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(54) **Title:** COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

(57) **Abstract:** The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.

COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FIELD OF THE INVENTION

The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.

BACKGROUND OF THE INVENTION

Malignant tumors (cancers) are the second leading cause of death in the United States, after heart disease (Boring et al., *CA Cancel J. Clin.* 43:7 (1993)). Cancer is characterized by the increase in the number of abnormal, or neoplastic, cells derived from a normal tissue which proliferate to form a tumor mass, the invasion of adjacent tissues by these neoplastic tumor cells, and the generation of malignant cells which eventually spread via the blood or lymphatic system to regional lymph nodes and to distant sites via a process called metastasis. In a cancerous state, a cell proliferates under conditions in which normal cells would not grow. Cancer manifests itself in a wide variety of forms, characterized by different degrees of invasiveness and aggressiveness.

In attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify transmembrane or otherwise membrane-associated polypeptides that are specifically expressed on the surface of one or more particular type(s) of cancer cell as compared to on one or more normal non-cancerous cell(s). Often, such membrane-associated polypeptides are more abundantly expressed on the surface of the cancer cells as compared to on the surface of the non-cancerous cells. The identification of such tumor-associated cell surface antigen polypeptides has given rise to the ability to specifically target cancer cells for destruction via antibody-based therapies. In this regard, it is noted that antibody-based therapy has proved very effective in the treatment of certain cancers. For example, HERCEPTIN® and RITUXAN® (both from Genentech Inc., South San Francisco, California) are antibodies that have been used successfully to treat breast cancer and non-Hodgkin's lymphoma, respectively. More specifically, HERCEPTIN® is a recombinant DNA-derived humanized monoclonal antibody that selectively binds to the extracellular domain of the human epidermal growth factor receptor 2 (HER2) proto-oncogene. HER2 protein overexpression is observed in 25-30% of primary breast cancers. RITUXAN® is a genetically engineered chimeric murine/human monoclonal antibody directed against the CD20 antigen found on the surface of normal and malignant B lymphocytes. Both these antibodies are recombinantly produced in CHO cells.

In other attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify (1) non-membrane-associated polypeptides that are specifically produced by one or more particular type(s) of cancer cell(s) as compared to by one or more particular type(s) of non-cancerous normal cell(s), (2) polypeptides that are produced by cancer cells at an expression level that is significantly higher than that of one or more normal non-cancerous cell(s), or (3) polypeptides whose expression is specifically limited

to only a single (or very limited number of different) tissue type(s) in both the cancerous and non-cancerous state (e.g., normal prostate and prostate tumor tissue). Such polypeptides may remain intracellularly located or may be secreted by the cancer cell. Moreover, such polypeptides may be expressed not by the cancer cell itself, but rather by cells which produce and/or secrete polypeptides having a potentiating or growth-enhancing effect on cancer cells. Such secreted polypeptides are often proteins that provide cancer cells with a growth advantage over normal cells and include such things as, for example, angiogenic factors, cellular adhesion factors, growth factors, and the like. Identification of antagonists of such non-membrane associated polypeptides would be expected to serve as effective therapeutic agents for the treatment of such cancers. Furthermore, identification of the expression pattern of such polypeptides would be useful for the diagnosis of particular cancers in mammals.

Despite the above identified advances in mammalian cancer therapy, there is a great need for additional diagnostic and therapeutic agents capable of detecting the presence of tumor in a mammal and for effectively inhibiting neoplastic cell growth, respectively. Accordingly, it is an objective of the present invention to identify: (1) cell membrane-associated polypeptides that are more abundantly expressed on one or more type(s) of cancer cell(s) as compared to on normal cells or on other different cancer cells, (2) non-membrane-associated polypeptides that are specifically produced by one or more particular type(s) of cancer cell(s) (or by other cells that produce polypeptides having a potentiating effect on the growth of cancer cells) as compared to by one or more particular type(s) of non-cancerous normal cell(s), (3) non-membrane-associated polypeptides that are produced by cancer cells at an expression level that is significantly higher than that of one or more normal non-cancerous cell(s), or (4) polypeptides whose expression is specifically limited to only a single (or very limited number of different) tissue type(s) in both a cancerous and non-cancerous state (e.g., normal prostate and prostate tumor tissue), and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of cancer in mammals. It is also an objective of the present invention to identify cell membrane-associated, secreted or intracellular polypeptides whose expression is limited to a single or very limited number of tissues, and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of cancer in mammals..

SUMMARY OF THE INVENTION

A. Embodiments

In the present specification, Applicants describe for the first time the identification of various cellular polypeptides (and their encoding nucleic acids or fragments thereof) which are expressed to a greater degree on the surface of or by one or more types of cancer cell(s) as compared to on the surface of or by one or more types of normal non-cancer cells. Alternatively, such polypeptides are expressed by cells which produce and/or secrete polypeptides having a potentiating or growth-enhancing effect on cancer cells. Again alternatively, such polypeptides may not be overexpressed by tumor cells as compared to normal cells of the same tissue type, but rather may be specifically expressed by both tumor cells and normal cells of only a single or very limited

number of tissue types (preferably tissues which are not essential for life, e.g., prostate, etc.). All of the above polypeptides are herein referred to as Tumor-associated Antigenic Target polypeptides ("TAT" polypeptides) and are expected to serve as effective targets for cancer therapy and diagnosis in mammals.

Accordingly, in one embodiment of the present invention, the invention provides an isolated nucleic acid molecule having a nucleotide sequence that encodes a tumor-associated antigenic target polypeptide or fragment thereof (a "TAT" polypeptide).

In certain aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule encoding a full-length TAT polypeptide having an amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule comprising the coding sequence of a full-length TAT polypeptide cDNA as disclosed herein, the coding sequence of a TAT polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In further aspects, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule that encodes the same mature polypeptide encoded by the full-length coding region of any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect of the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a TAT polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide(s) are disclosed herein. Therefore, soluble extracellular domains of the herein described TAT polypeptides are contemplated.

In other aspects, the present invention is directed to isolated nucleic acid molecules which hybridize to (a) a nucleotide sequence encoding a TAT polypeptide having a full-length amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular

domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the nucleotide sequence of (a). In this regard, an embodiment of the present invention is directed to fragments of a full-length TAT polypeptide coding sequence, or the complement thereof, as disclosed herein, that may find use as, for example, hybridization probes useful as, for example, diagnostic probes, antisense oligonucleotide probes, or for encoding fragments of a full-length TAT polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-TAT polypeptide antibody, a TAT binding oligopeptide or other small organic molecule that binds to a TAT polypeptide. Such nucleic acid fragments are usually at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a TAT polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the TAT polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which TAT polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such novel fragments of TAT polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the TAT polypeptide fragments encoded by these nucleotide molecule fragments, preferably those TAT polypeptide fragments that comprise a binding site for an anti-TAT antibody, a TAT binding oligopeptide or other small organic molecule that binds to a TAT polypeptide.

In another embodiment, the invention provides isolated TAT polypeptides encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated TAT polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity, to a TAT polypeptide having a full-length amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane TAT polypeptide protein, with or without the signal peptide, as disclosed herein, an amino acid sequence encoded by any of the nucleic acid sequences disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated TAT polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid

sequence identity, to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated TAT polypeptide without the N-terminal signal sequence and/or without the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the TAT polypeptide and recovering the TAT polypeptide from the cell culture.

Another aspect of the invention provides an isolated TAT polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the TAT polypeptide and recovering the TAT polypeptide from the cell culture.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cells comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides isolated chimeric polypeptides comprising any of the herein described TAT polypeptides fused to a heterologous (non-TAT) polypeptide. Example of such chimeric molecules comprise any of the herein described TAT polypeptides fused to a heterologous polypeptide such as, for example, an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, single-chain antibody or antibody that competitively inhibits the binding of an anti-TAT polypeptide antibody to its respective antigenic epitope. Antibodies of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies of the present invention may optionally be produced in CHO cells or bacterial cells and preferably induce death of a cell to which they bind. For diagnostic purposes, the antibodies of the present invention may be detectably labeled, attached to a solid support, or the like.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described antibodies. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described antibodies is further provided and comprises culturing host cells under conditions suitable for expression of the desired antibody and recovering the desired antibody from the cell culture.

In another embodiment, the invention provides oligopeptides ("TAT binding oligopeptides") which

bind, preferably specifically, to any of the above or below described TAT polypeptides. Optionally, the TAT binding oligopeptides of the present invention may be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The TAT binding oligopeptides of the present invention may optionally be produced in CHO cells or bacterial cells and preferably induce death of a cell to which they bind. For diagnostic purposes, the TAT binding oligopeptides of the present invention may be detectably labeled, attached to a solid support, or the like.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described TAT binding oligopeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described TAT binding oligopeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired oligopeptide and recovering the desired oligopeptide from the cell culture.

In another embodiment, the invention provides small organic molecules ("TAT binding organic molecules") which bind, preferably specifically, to any of the above or below described TAT polypeptides. Optionally, the TAT binding organic molecules of the present invention may be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The TAT binding organic molecules of the present invention preferably induce death of a cell to which they bind. For diagnostic purposes, the TAT binding organic molecules of the present invention may be detectably labeled, attached to a solid support, or the like.

In a still further embodiment, the invention concerns a composition of matter comprising a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

In yet another embodiment, the invention concerns an article of manufacture comprising a container and a composition of matter contained within the container, wherein the composition of matter may comprise a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein. The article may further optionally comprise a label affixed to the container, or a package insert included with the container, that refers to the use of the composition of matter for the therapeutic treatment or diagnostic detection of a tumor.

Another embodiment of the present invention is directed to the use of a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT polypeptide antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein, for the preparation of a medicament useful in the treatment of a condition which is responsive to the TAT polypeptide, chimeric TAT polypeptide, anti-TAT polypeptide antibody, TAT binding oligopeptide, or TAT

binding organic molecule.

B. Additional Embodiments

Another embodiment of the present invention is directed to a method for inhibiting the growth of a cell that expresses a TAT polypeptide, wherein the method comprises contacting the cell with an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, and wherein the binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide causes inhibition of the growth of the cell expressing the TAT polypeptide. In preferred embodiments, the cell is a cancer cell and binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide causes death of the cell expressing the TAT polypeptide. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and TAT binding oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of therapeutically treating a mammal having a cancerous tumor comprising cells that express a TAT polypeptide, wherein the method comprises administering to the mammal a therapeutically effective amount of an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby resulting in the effective therapeutic treatment of the tumor. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of determining the presence of a TAT polypeptide in a sample suspected of containing the TAT polypeptide, wherein the method comprises exposing the sample to an antibody, oligopeptide or small organic molecule that binds to the TAT polypeptide and determining binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide in the sample, wherein the presence of such binding is indicative of the presence of the TAT polypeptide in the sample. Optionally, the sample may contain cells (which may be cancer cells) suspected of expressing the TAT polypeptide. The antibody, TAT binding oligopeptide or TAT binding organic molecule employed in the method may optionally be detectably labeled, attached to a solid support, or the like.

A further embodiment of the present invention is directed to a method of diagnosing the presence of a tumor in a mammal, wherein the method comprises detecting the level of expression of a gene encoding a TAT polypeptide (a) in a test sample of tissue cells obtained from said mammal, and (b) in a control sample of known normal non-cancerous cells of the same tissue origin or type, wherein a higher level of expression of the

TAT polypeptide in the test sample, as compared to the control sample, is indicative of the presence of tumor in the mammal from which the test sample was obtained.

Another embodiment of the present invention is directed to a method of diagnosing the presence of a tumor in a mammal, wherein the method comprises (a) contacting a test sample comprising tissue cells obtained from the mammal with an antibody, oligopeptide or small organic molecule that binds to a TAT polypeptide and (b) detecting the formation of a complex between the antibody, oligopeptide or small organic molecule and the TAT polypeptide in the test sample, wherein the formation of a complex is indicative of the presence of a tumor in the mammal. Optionally, the antibody, TAT binding oligopeptide or TAT binding organic molecule employed is detectably labeled, attached to a solid support, or the like, and/or the test sample of tissue cells is obtained from an individual suspected of having a cancerous tumor.

Yet another embodiment of the present invention is directed to a method for treating or preventing a cell proliferative disorder associated with altered, preferably increased, expression or activity of a TAT polypeptide, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of a TAT polypeptide. Preferably, the cell proliferative disorder is cancer and the antagonist of the TAT polypeptide is an anti-TAT polypeptide antibody, TAT binding oligopeptide, TAT binding organic molecule or antisense oligonucleotide. Effective treatment or prevention of the cell proliferative disorder may be a result of direct killing or growth inhibition of cells that express a TAT polypeptide or by antagonizing the cell growth potentiating activity of a TAT polypeptide.

Yet another embodiment of the present invention is directed to a method of binding an antibody, oligopeptide or small organic molecule to a cell that expresses a TAT polypeptide, wherein the method comprises contacting a cell that expresses a TAT polypeptide with said antibody, oligopeptide or small organic molecule under conditions which are suitable for binding of the antibody, oligopeptide or small organic molecule to said TAT polypeptide and allowing binding therebetween.

Other embodiments of the present invention are directed to the use of (a) a TAT polypeptide, (b) a nucleic acid encoding a TAT polypeptide or a vector or host cell comprising that nucleic acid, (c) an anti-TAT polypeptide antibody, (d) a TAT-binding oligopeptide, or (e) a TAT-binding small organic molecule in the preparation of a medicament useful for (i) the therapeutic treatment or diagnostic detection of a cancer or tumor, or (ii) the therapeutic treatment or prevention of a cell proliferative disorder.

Another embodiment of the present invention is directed to a method for inhibiting the growth of a cancer cell, wherein the growth of said cancer cell is at least in part dependent upon the growth potentiating effect(s) of a TAT polypeptide (wherein the TAT polypeptide may be expressed either by the cancer cell itself or a cell that produces polypeptide(s) that have a growth potentiating effect on cancer cells), wherein the method comprises contacting the TAT polypeptide with an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby antagonizing the growth-potentiating activity of the TAT polypeptide and, in turn, inhibiting the growth of the cancer cell. Preferably the growth of the cancer cell is completely inhibited. Even more preferably, binding of the antibody, oligopeptide or small organic molecule to the TAT polypeptide induces the death of the cancer cell. Optionally, the antibody is a monoclonal antibody, antibody fragment,

chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and TAT binding oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of therapeutically treating a tumor in a mammal, wherein the growth of said tumor is at least in part dependent upon the growth potentiating effect(s) of a TAT polypeptide, wherein the method comprises administering to the mammal a therapeutically effective amount of an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby antagonizing the growth potentiating activity of said TAT polypeptide and resulting in the effective therapeutic treatment of the tumor. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet further embodiments of the present invention will be evident to the skilled artisan upon a reading of the present specification.

BRIEF DESCRIPTION OF THE DRAWINGS

In the list of figures for the present application, specific cDNA sequences which are upregulated in certain tumor tissues as compared to their normal tissue counterparts are individually identified with a designation beginning with the letters "DNA" followed by a specific numerical designation. A full or partial length protein sequence that is encoded by a cDNA sequence identified and shown herein is individually identified with a designation beginning with the letters "PRO" followed by a specific numerical designation. Figures showing encoded amino acid sequences immediately follow the figure showing the cDNA sequence encoding that specific amino acid sequence. If start and/or stop codons have been identified in a cDNA sequence shown in the attached figures, they are shown in bold and underlined font.

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Figure 148: DNA323804, NM_003757, gen.NM_003757
Figure 149: PRO80553
Figure 150: DNA323805, NM_004964, gen.NM_004964
Figure 151: PRO80554
Figure 152: DNA323806, NM_023009, gen.NM_023009
Figure 153: PRO80555
Figure 154: DNA323807, XM_030423, gen.XM_030423
Figure 155A-B: DNA323808, XM_036299, gen.XM_036299
Figure 156: PRO80557
Figure 157: DNA227213, NM_003680, gen.NM_003680
Figure 158: PRO37676
Figure 159: DNA323809, NM_006112, gen.NM_006112
Figure 160: PRO80558
Figure 161: DNA323810, XM_018136, gen.XM_018136
Figure 162: PRO80559
Figure 163: DNA323811, XM_117184, gen.XM_117184
Figure 164: PRO80560
Figure 165: DNA323812, NM_017825, gen.NM_017825
Figure 166: PRO80561
Figure 167: DNA189315, NM_014408, gen.NM_014408
Figure 168: PRO22262
Figure 169A-B: DNA323813, XM_029031, gen.XM_029031
Figure 170: PRO80562
Figure 171: DNA323814, XM_059171,

gen.XM_059171
Figure 172: PRO80563
Figure 173: DNA83085, NM_000760, gen.NM_000760
Figure 174: PRO2583
Figure 175: DNA323815, XM_165984, gen.XM_165984
Figure 176: DNA323816, XM_029842, gen.XM_029842
Figure 177: PRO2851
Figure 178: DNA323817, XM_086384, gen.XM_086384
Figure 179: PRO80565
Figure 180A-C: DNA274487, NM_014747, gen.NM_014747
Figure 181: PRO62389
Figure 182: DNA323818, XM_010712, gen.XM_010712
Figure 183: DNA323819, NM_024664, gen.NM_024664
Figure 184: PRO80567
Figure 185: DNA323820, XM_059214, gen.XM_059214
Figure 186: PRO80568
Figure 187: DNA323821, XM_046349, gen.XM_046349
Figure 188: DNA103253, NM_006516, gen.NM_006516
Figure 189: PRO4583
Figure 190: DNA323822, XM_086543, gen.XM_086543
Figure 191: PRO80570
Figure 192: DNA274745, NM_006824, gen.NM_006824
Figure 193: PRO62518
Figure 194: DNA273060, NM_001255, gen.NM_001255 .
Figure 195: PRO61125
Figure 196: DNA323823, NM_030587, gen.NM_030587
Figure 197: PRO80571
Figure 198: DNA323824, XM_097649, gen.XM_097649
Figure 199: DNA256503, NM_003780, gen.NM_003780
Figure 200: PRO51539
Figure 201: DNA323825, XM_046450, gen.XM_046450
Figure 202A-B: DNA272024, NM_014663, gen.NM_014663
Figure 203: PRO60298
Figure 204: DNA323826, XM_046565, gen.XM_046565
Figure 205: PRO80574
Figure 206: DNA323827, NM_024602, gen.NM_024602
Figure 207: PRO80575
Figure 208: DNA323828, XM_046557, gen.XM_046557
Figure 209: PRO80576
Figure 210: DNA323829, NM_001012, gen.NM_001012
Figure 211: PRO10760
Figure 212: DNA323830, XM_046551, gen.XM_046551
Figure 213A-B: DNA323831, XM_027983, gen.XM_027983
Figure 214: DNA323832, XM_086324, gen.XM_086324
Figure 215: PRO80579
Figure 216: DNA323833, XM_032391, gen.XM_032391
Figure 217: PRO80580
Figure 218: DNA103214, NM_006066, gen.NM_006066
Figure 219: PRO4544
Figure 220: DNA304686, NM_002574, gen.NM_002574
Figure 221: PRO71112
Figure 222: DNA323834, NM_032756, gen.NM_032756
Figure 223: PRO80581
Figure 224: DNA323835, XM_059133, gen.XM_059133
Figure 225: PRO80582
Figure 226: DNA323836, XM_027313, gen.XM_027313
Figure 227: PRO80583
Figure 228: DNA323837, XM_054868, gen.XM_054868
Figure 229: DNA323838, NM_001262, gen.NM_001262
Figure 230: PRO59546
Figure 231: DNA323839, XM_086391, gen.XM_086391
Figure 232: PRO80584
Figure 233: DNA323840, XM_114798, gen.XM_114798
Figure 234: PRO80585
Figure 235: DNA272748, NM_002979, gen.NM_002979
Figure 236: PRO60860
Figure 237: DNA323841, XM_038911, gen.XM_038911
Figure 238: PRO80586
Figure 239: DNA323842, NM_018070, gen.NM_018070
Figure 240: PRO80587
Figure 241: DNA323843, NM_024603, gen.NM_024603
Figure 242: PRO80588
Figure 243: DNA323844, XM_086389, gen.XM_086389

Figure 244: DNA323845, XM_038852, gen.XM_038852
Figure 245: DNA323846, NM_032864, gen.NM_032864
Figure 246: PRO80591
Figure 247: DNA323847, NM_024586, gen.NM_024586
Figure 248: PRO80592
Figure 249A-B: DNA323848, XM_097565, gen.XM_097565
Figure 250: DNA323849, XM_001472, gen.XM_001472
Figure 251A-C: DNA323850, XM_055481, gen.XM_055481
Figure 252: PRO80593
Figure 253: DNA323851, XM_010615, gen.XM_010615
Figure 254A-B: DNA323852, XM_089138, gen.XM_089138
Figure 255: PRO80595
Figure 256A-B: DNA323853, XM_059180, gen.XM_059180
Figure 257: DNA323854, XM_015717, gen.XM_015717
Figure 258: PRO80597
Figure 259: DNA323855, XM_114125, gen.XM_114125
Figure 260: DNA323856, NM_015640, gen.NM_015640
Figure 261: PRO80599
Figure 262: DNA323857, NM_017768, gen.NM_017768
Figure 263: PRO80600
Figure 264: DNA323858, XM_165977, gen.XM_165977
Figure 265: DNA323859, XM_086343, gen.XM_086343
Figure 266: PRO80602
Figure 267: DNA269708, NM_007034, gen.NM_007034
Figure 268: PRO58118
Figure 269: DNA323860, NM_001554, gen.NM_001554
Figure 270: PRO80603
Figure 271: DNA226260, NM_006769, gen.NM_006769
Figure 272: PRO36723
Figure 273: DNA323861, NM_004261, gen.NM_004261
Figure 274: PRO80604
Figure 275: DNA323862, XM_165983, gen.XM_165983
Figure 276: DNA323863, XM_016164, gen.XM_016164
Figure 277: DNA323864, XM_086164, gen.XM_086164
Figure 278: PRO80607
Figure 279: DNA323865, XM_086165, gen.XM_086165
Figure 280: DNA323866, XM_086167, gen.XM_086167
Figure 281: DNA323867, XM_086166, gen.XM_086166
Figure 282: DNA323868, XM_086138, gen.XM_086138
Figure 283: PRO80611
Figure 284: DNA323869, NM_000969, gen.NM_000969
Figure 285: PRO80612
Figure 286: DNA323870, XM_088863, gen.XM_088863
Figure 287: PRO80613
Figure 288: DNA271003, NM_003729, gen.NM_003729
Figure 289: PRO59332
Figure 290: DNA323871, XM_165981, gen.XM_165981
Figure 291: PRO80614
Figure 292: DNA275139, NM_013296, gen.NM_013296
Figure 293: PRO62849
Figure 294: DNA323872, XM_058702, gen.XM_058702
Figure 295: DNA323873, XM_054978, gen.XM_054978
Figure 296: DNA323874, NM_032636, gen.NM_032636
Figure 297: PRO80617
Figure 298: DNA323875, NM_006513, gen.NM_006513
Figure 299: PRO80618
Figure 300: DNA323876, NM_006621, gen.NM_006621
Figure 301: PRO80619
Figure 302A-B: DNA323877, NM_007158, gen.NM_007158
Figure 303: PRO80620
Figure 304: DNA323878, XM_086132, gen.XM_086132
Figure 305: PRO80621
Figure 306: DNA323879, NM_004000, gen.NM_004000
Figure 307: PRO80622
Figure 308: DNA323880, NM_001688, gen.NM_001688
Figure 309: PRO80623
Figure 310: DNA323881, NM_019099, gen.NM_019099
Figure 311: PRO80624
Figure 312A-B: DNA323882, NM_000701, gen.NM_000701
Figure 313: PRO80625

Figure 314A-B: DNA323883, XM_018332, gen.XM_018332
Figure 315A-B: DNA323884, XM_040709, gen.XM_040709
Figure 316: PRO80627
Figure 317: DNA323885, XM_086518, gen.XM_086518
Figure 318A-D: DNA323886, XM_034671, gen.XM_034671
Figure 319: DNA323887, XM_034662, gen.XM_034662
Figure 320: PRO80630
Figure 321: DNA323888, XM_039721, gen.XM_039721
Figure 322: PRO80631
Figure 323A-B: DNA323889, XM_086397, gen.XM_086397
Figure 324A-B: DNA323890, XM_086515, gen.XM_086515
Figure 325: PRO80633
Figure 326: DNA323891, XM_016480, gen.XM_016480
Figure 327: DNA323892, XM_165975, gen.XM_165975
Figure 328: DNA323893, NM_016361, gen.NM_016361
Figure 329: PRO231
Figure 330: DNA323894, XM_059210, gen.XM_059210
Figure 331: DNA323895, XM_086296, gen.XM_086296
Figure 332: DNA323896, NM_030920, gen.NM_030920
Figure 333: PRO80638
Figure 334: DNA323897, NM_016022, gen.NM_016022
Figure 335: PRO80639
Figure 336: DNA323898, NM_031901, gen.NM_031901
Figure 337: PRO80640
Figure 338A-B: DNA323899, XM_088788, gen.XM_088788
Figure 339: PRO80641
Figure 340: DNA274759, NM_005620, gen.NM_005620
Figure 341: PRO62529
Figure 342: DNA323900, XM_001468, gen.XM_001468
Figure 343: PRO49642
Figure 344: DNA323901, NM_006862, gen.NM_006862
Figure 345: PRO80642
Figure 346: DNA227529, NM_002796, gen.NM_002796
Figure 347: PRO37992
Figure 348: DNA323902, NM_002810, gen.NM_002810
Figure 349: PRO61638
Figure 350: DNA290284, NM_005997, gen.NM_005997
Figure 351: PRO70433
Figure 352: DNA323903, XM_097639, gen.XM_097639
Figure 353: DNA323904, XM_041879, gen.XM_041879
Figure 354: DNA323905, XM_041884, gen.XM_041884
Figure 355: PRO80644
Figure 356: DNA225809, NM_000396, gen.NM_000396
Figure 357: PRO36272
Figure 358: DNA323906, NM_025150, gen.NM_025150
Figure 359: PRO80645
Figure 360: DNA323907, XM_114098, gen.XM_114098
Figure 361: DNA323908, XM_113369, gen.XM_113369
Figure 362: PRO80646
Figure 363: DNA323909, XM_099467, gen.XM_099467
Figure 364: DNA323910, NM_002965, gen.NM_002965
Figure 365: PRO80648
Figure 366: DNA323911, XM_086400, gen.XM_086400
Figure 367: DNA210134, NM_014624, gen.NM_014624
Figure 368: PRO33679
Figure 369: DNA304666, NM_002961, gen.NM_002961
Figure 370: PRO71093
Figure 371: DNA304720, NM_019554, gen.NM_019554
Figure 372: PRO71146
Figure 373: DNA323912, XM_165976, gen.XM_165976
Figure 374: DNA227577, NM_006271, gen.NM_006271
Figure 375: PRO38040
Figure 376: DNA323913, XM_114097, gen.XM_114097
Figure 377: DNA323914, XM_040009, gen.XM_040009
Figure 378: PRO80651
Figure 379: DNA323915, NM_024330, gen.NM_024330
Figure 380: PRO703
Figure 381: DNA323916, NM_012437, gen.NM_012437
Figure 382: PRO80652
Figure 383: DNA323917, XM_086271,

gen.XM_086271
Figure 384: DNA323918, XM_114055, gen.XM_114055
Figure 385: PRO37535
Figure 386: DNA323919, XM_113360, gen.XM_113360
Figure 387: PRO80654
Figure 388: DNA323920, XM_086564, gen.XM_086564
Figure 389: DNA323921, NM_005973, gen.NM_005973
Figure 390: PRO80656
Figure 391: DNA323922, XM_044077, gen.XM_044077
Figure 392: DNA323923, NM_001878, gen.NM_001878
Figure 393: PRO80657
Figure 394: DNA323924, NM_021948, gen.NM_021948
Figure 395: PRO6018
Figure 396: DNA273088, NM_006365, gen.NM_006365
Figure 397: PRO61146
Figure 398: DNA323925, XM_044127, gen.XM_044127
Figure 399: PRO80658
Figure 400: DNA323926, XM_053245, gen.XM_053245
Figure 401: PRO80659
Figure 402: DNA257916, NM_032323, gen.NM_032323
Figure 403: PRO52449
Figure 404: DNA323927, NM_005572, gen.NM_005572
Figure 405: PRO80660
Figure 406: DNA323928, XM_044166, gen.XM_044166
Figure 407: PRO80661
Figure 408: DNA323929, XM_044128, gen.XM_044128
Figure 409: DNA226125, NM_003145, gen.NM_003145
Figure 410: PRO36588
Figure 411A-B: DNA323930, XM_044172, gen.XM_044172
Figure 412: DNA323931, NM_032292, gen.NM_032292
Figure 413: PRO80664
Figure 414: DNA323932, NM_004632, gen.NM_004632
Figure 415: PRO80665
Figure 416: DNA323933, XM_044075, gen.XM_044075
Figure 417: PRO80666
Figure 418: DNA323934, NM_018253, gen.NM_018253
Figure 419: PRO80667
Figure 420: DNA323935, NM_018116, gen.NM_018116
Figure 421: PRO80668
Figure 422: DNA323936, NM_002004, gen.NM_002004
Figure 423: PRO80669
Figure 424: DNA323937, NM_005698, gen.NM_005698
Figure 425: PRO80670
Figure 426: DNA323938, NM_052837, gen.NM_052837
Figure 427: PRO80671
Figure 428: DNA194600, NM_006589, gen.NM_006589
Figure 429: PRO23942
Figure 430: DNA323939, XM_086567, gen.XM_086567
Figure 431: PRO80672
Figure 432: DNA323940, XM_086552, gen.XM_086552
Figure 433: DNA323941, XM_036744, gen.XM_036744
Figure 434: DNA323942, NM_130898, gen.NM_130898
Figure 435: PRO80675
Figure 436: DNA226793, NM_006694, gen.NM_006694
Figure 437: PRO37256
Figure 438: DNA294794, NM_002870, gen.NM_002870
Figure 439: PRO70754
Figure 440: DNA323943, NM_001030, gen.NM_001030
Figure 441: PRO80676
Figure 442: DNA323944, XM_036829, gen.XM_036829
Figure 443: PRO80677
Figure 444: DNA323945, NM_015449, gen.NM_015449
Figure 445: PRO80678
Figure 446: DNA323946, NM_014847, gen.NM_014847
Figure 447: PRO80679
Figure 448: DNA323947, XM_036934, gen.XM_036934
Figure 449: PRO80680
Figure 450A-B: DNA323948, XM_036845, gen.XM_036845
Figure 451: DNA323949, XM_010636, gen.XM_010636
Figure 452: DNA323950, NM_006556, gen.NM_006556
Figure 453: PRO62574
Figure 454: DNA323951, XM_034082, gen.XM_034082

Figure 455: DNA323952, NM_025207, gen.NM_025207
Figure 456: PRO80684
Figure 457: DNA103436, NM_003815, gen.NM_003815
Figure 458: PRO4763
Figure 459: DNA323953, NM_003516, gen.NM_003516
Figure 460: PRO80685
Figure 461: DNA323954, NM_005850, gen.NM_005850
Figure 462: PRO59725
Figure 463A-B: DNA323955, NM_014849, gen.NM_014849
Figure 464: PRO80686
Figure 465: DNA323956, XM_059094, gen.XM_059094
Figure 466: DNA323957, XM_058247, gen.XM_058247
Figure 467: PRO80688
Figure 468: DNA323958, NM_003779, gen.NM_003779
Figure 469: PRO80689
Figure 470: DNA323959, NM_004550, gen.NM_004550
Figure 471: PRO58974
Figure 472: DNA323960, XM_085581, gen.XM_085581
Figure 473: DNA323961, XM_113379, gen.XM_113379
Figure 474: DNA226619, NM_003564, gen.NM_003564
Figure 475: PRO37082
Figure 476A-B: DNA323962, XM_049680, gen.XM_049680
Figure 477: DNA323963, XM_165443, gen.XM_165443
Figure 478: PRO80693
Figure 479: DNA323964, XM_086381, gen.XM_086381
Figure 480: PRO80694
Figure 481A-B: DNA323965, NM_002857, gen.NM_002857
Figure 482: PRO80695
Figure 483A-B: DNA323966, XM_049690, gen.XM_049690
Figure 484: DNA323967, XM_114153, gen.XM_114153
Figure 485: DNA323968, XM_086378, gen.XM_086378
Figure 486: DNA323969, XM_001897, gen.XM_001897
Figure 487: PRO10002
Figure 488: DNA323970, NM_052862, gen.NM_052862
Figure 489: PRO80699
Figure 490: DNA323971, XM_086481, gen.XM_086481
Figure 491: PRO80700
Figure 492: DNA323972, XM_059191, gen.XM_059191
Figure 493: DNA323973, XM_086485, gen.XM_086485
Figure 494: DNA323974, XM_086484, gen.XM_086484
Figure 495: DNA323975, XM_047479, gen.XM_047479
Figure 496: PRO80704
Figure 497: DNA323976, NM_003617, gen.NM_003617
Figure 498: PRO37806
Figure 499: DNA254298, NM_025226, gen.NM_025226
Figure 500: PRO49409
Figure 501: DNA323977, XM_034000, gen.XM_034000
Figure 502: PRO80705
Figure 503: DNA323978, NM_032738, gen.NM_032738
Figure 504: PRO329
Figure 505: DNA323979, NM_000569, gen.NM_000569
Figure 506: PRO80706
Figure 507: DNA323980, XM_088945, gen.XM_088945
Figure 508: PRO80707
Figure 509: DNA323981, XM_060331, gen.XM_060331
Figure 510: PRO80708
Figure 511: DNA323982, NM_004905, gen.NM_004905
Figure 512: PRO80709
Figure 513: DNA323983, NM_017847, gen.NM_017847
Figure 514: PRO80710
Figure 515A-B: DNA323984, XM_051877, gen.XM_051877
Figure 516: PRO62077
Figure 517: DNA323985, NM_005717, gen.NM_005717
Figure 518: PRO80711
Figure 519A-B: DNA271986, NM_014837, gen.NM_014837
Figure 520: PRO60261
Figure 521A-B: DNA323986, XM_056923, gen.XM_056923
Figure 522: DNA323987, XM_046464, gen.XM_046464
Figure 523: DNA323988, XM_002068, gen.XM_002068
Figure 524A-B: DNA323989, XM_001289, gen.XM_001289

Figure 525: DNA323990, XM_114109, gen.XM_114109
Figure 526: PRO80714
Figure 527: DNA323991, NM_022371, gen.NM_022371
Figure 528: PRO80715
Figure 529: DNA323992, NM_004673, gen.NM_004673
Figure 530: PRO188
Figure 531: DNA323993, XM_060517, gen.XM_060517
Figure 532: DNA323994, XM_165978, gen.XM_165978
Figure 533: PRO80717
Figure 534: DNA323995, XM_117181, gen.XM_117181
Figure 535: DNA323996, NM_018122, gen.NM_018122
Figure 536: PRO80719
Figure 537: DNA323997, XM_042967, gen.XM_042967
Figure 538: DNA323998, XM_086494, gen.XM_086494
Figure 539: PRO80720
Figure 540: DNA290234, NM_002923, gen.NM_002923
Figure 541: PRO70333
Figure 542: DNA323999, XM_086328, gen.XM_086328
Figure 543: DNA324000, XM_086282, gen.XM_086282
Figure 544: DNA324001, XM_053633, gen.XM_053633
Figure 545: DNA256905, NM_138391, gen.NM_138391
Figure 546: PRO51836
Figure 547: DNA324002, XM_015434, gen.XM_015434
Figure 548: DNA324003, NM_006763, gen.NM_006763
Figure 549: PRO80725
Figure 550: DNA227246, NM_005686, gen.NM_005686
Figure 551: PRO37709
Figure 552: DNA324004, XM_058405, gen.XM_058405
Figure 553A-B: DNA226005, NM_000228, gen.NM_000228
Figure 554: PRO36468
Figure 555: DNA324005, NM_015714, gen.NM_015714
Figure 556: PRO11582
Figure 557: DNA324006, XM_086142, gen.XM_086142
Figure 558: DNA83046, NM_000574, gen.NM_000574
Figure 559: PRO2569
Figure 560A-B: DNA324007, XM_114030, gen.XM_114030
Figure 561: DNA324008, XM_097519, gen.XM_097519
Figure 562: DNA324009, XM_059120, gen.XM_059120
Figure 563: PRO80730
Figure 564: DNA324010, NM_016456, gen.NM_016456
Figure 565: PRO1248
Figure 566: DNA324011, XM_036556, gen.XM_036556
Figure 567: DNA324012, XM_001914, gen.XM_001914
Figure 568: DNA324013, XM_001916, gen.XM_001916
Figure 569: DNA324014, NM_018085, gen.NM_018085
Figure 570: PRO80734
Figure 571: DNA324015, NM_006335, gen.NM_006335
Figure 572: PRO80735
Figure 573: DNA324016, XM_036500, gen.XM_036500
Figure 574: PRO80736
Figure 575: DNA324017, XM_036507, gen.XM_036507
Figure 576: DNA196344, NM_004767, gen.NM_004767
Figure 577: PRO24851
Figure 578: DNA247474, NM_014176, gen.NM_014176
Figure 579: PRO44999
Figure 580A-B: DNA324018, XM_084055, gen.XM_084055
Figure 581: DNA324019, XM_010682, gen.XM_010682
Figure 582: DNA324020, XM_117185, gen.XM_117185
Figure 583: DNA324021, XM_055880, gen.XM_055880
Figure 584: PRO80740
Figure 585: DNA193882, NM_014184, gen.NM_014184
Figure 586: PRO23300
Figure 587: DNA324022, NM_018212, gen.NM_018212
Figure 588: PRO80741
Figure 589: DNA324023, XM_086431, gen.XM_086431
Figure 590: PRO80742
Figure 591: DNA324024, XM_037329, gen.XM_037329
Figure 592: DNA324025, XM_086432, gen.XM_086432
Figure 593A-B: DNA324026, XM_010732,

gen.XM_010732
Figure 594: DNA227504, NM_000447, gen.NM_000447
Figure 595: PRO37967
Figure 596: DNA324027, NM_012486, gen.NM_012486
Figure 597: PRO80745
Figure 598A-B: DNA324028, XM_113361, gen.XM_113361
Figure 599A-B: DNA324029, XM_001958, gen.XM_001958
Figure 600: DNA324030, XM_016199, gen.XM_016199
Figure 601: DNA324031, XM_086244, gen.XM_086244
Figure 602: DNA324032, XM_086245, gen.XM_086245
Figure 603: DNA254346, NM_024709, gen.NM_024709
Figure 604: PRO49457
Figure 605: DNA324033, XM_088107, gen.XM_088107
Figure 606: DNA324034, NM_032890, gen.NM_032890
Figure 607: PRO80752
Figure 608: DNA324035, XM_052974, gen.XM_052974
Figure 609: PRO80753
Figure 610: DNA324036, XM_047499, gen.XM_047499
Figure 611: PRO80754
Figure 612: DNA324037, NM_000858, gen.NM_000858
Figure 613: PRO80755
Figure 614: DNA324038, NM_024319, gen.NM_024319
Figure 615: PRO80756
Figure 616: DNA324039, XM_047545, gen.XM_047545
Figure 617: PRO4914
Figure 618A-B: DNA324040, XM_056884, gen.XM_056884
Figure 619: DNA324041, XM_098599, gen.XM_098599
Figure 620: DNA324042, XM_165439, gen.XM_165439
Figure 621: PRO80759
Figure 622: DNA324043, XM_089030, gen.XM_089030
Figure 623: PRO80760
Figure 624: DNA82328, NM_000029, gen.NM_000029
Figure 625: PRO1707
Figure 626: DNA324044, NM_014236, gen.NM_014236
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Figure 628: DNA324045, XM_056970, gen.XM_056970
Figure 629: PRO80762
Figure 630: DNA324046, NM_032324, gen.NM_032324
Figure 631: PRO80763
Figure 632: DNA324047, XM_086257, gen.XM_086257
Figure 633: PRO80764
Figure 634: DNA324048, XM_114137, gen.XM_114137
Figure 635: PRO80765
Figure 636: DNA324049, NM_000143, gen.NM_000143
Figure 637: PRO62607
Figure 638: DNA324050, XM_090833, gen.XM_090833
Figure 639: DNA324051, NM_130398, gen.NM_130398
Figure 640: PRO80767
Figure 641: DNA324052, XM_117196, gen.XM_117196
Figure 642: DNA324053, XM_018041, gen.XM_018041
Figure 643: DNA324054, NM_001011, gen.NM_001011
Figure 644: PRO10692
Figure 645: DNA324055, NM_024027, gen.NM_024027
Figure 646: PRO1182
Figure 647: DNA324056, NM_016030, gen.NM_016030
Figure 648: PRO80770
Figure 649: DNA103217, NM_003310, gen.NM_003310
Figure 650: PRO4547
Figure 651: DNA275195, NM_001034, gen.NM_001034
Figure 652: PRO62893
Figure 653: DNA324057, XM_059368, gen.XM_059368
Figure 654: PRO80771
Figure 655: DNA324058, NM_006826, gen.NM_006826
Figure 656: PRO70258
Figure 657: DNA324059, NM_005378, gen.NM_005378
Figure 658: PRO80772
Figure 659: DNA324060, NM_002539, gen.NM_002539
Figure 660: PRO80773
Figure 661: DNA324061, XM_096149, gen.XM_096149
Figure 662: DNA275049, NM_004939, gen.NM_004939
Figure 663: PRO62770
Figure 664A-B: DNA324062, XM_036450,

gen.XM_036450
Figure 665: DNA324063, XM_103946, gen.XM_103946
Figure 666: PRO80775
Figure 667: DNA324064, NM_014713, gen.NM_014713
Figure 668: PRO80776
Figure 669: DNA324065, XM_087206, gen.XM_087206
Figure 670: DNA324066, NM_106552, gen.NM_106552
Figure 671: PRO80778
Figure 672: DNA324067, XM_092135, gen.XM_092135
Figure 673: PRO80779
Figure 674: DNA324068, NM_017910, gen.NM_017910
Figure 675: PRO80780
Figure 676: DNA324069, XM_092517, gen.XM_092517
Figure 677: PRO80781
Figure 678A-B: DNA324070, NM_025203, gen.NM_025203
Figure 679: PRO80782
Figure 680: DNA324071, XM_002480, gen.XM_002480
Figure 681: DNA324072, NM_002707, gen.NM_002707
Figure 682: PRO12199
Figure 683: DNA324073, XM_087151, gen.XM_087151
Figure 684: DNA227165, NM_014748, gen.NM_014748
Figure 685: PRO37628
Figure 686: DNA324074, NM_015636, gen.NM_015636
Figure 687: PRO80785
Figure 688: DNA273800, NM_001521, gen.NM_001521
Figure 689: PRO61761
Figure 690: DNA324075, XM_047175, gen.XM_047175
Figure 691: PRO80786
Figure 692A-B: DNA324076, NM_004341, gen.NM_004341
Figure 693: PRO80787
Figure 694: DNA324077, NM_016085, gen.NM_016085
Figure 695: PRO80788
Figure 696: DNA324078, NM_080592, gen.NM_080592
Figure 697: PRO80789
Figure 698: DNA227545, NM_021095, gen.NM_021095
Figure 699: PRO38008
Figure 700: DNA324079, XM_002435, gen.XM_002435
Figure 701: DNA324080, NM_000221, gen.NM_000221
Figure 702: PRO80790
Figure 703: DNA271243, NM_006488, gen.NM_006488
Figure 704: PRO59558
Figure 705: DNA324081, NM_007046, gen.NM_007046
Figure 706: PRO9886
Figure 707: DNA324082, NM_021831, gen.NM_021831
Figure 708: PRO80791
Figure 709: DNA324083, NM_020134, gen.NM_020134
Figure 710: PRO80792
Figure 711: DNA103593, NM_000183, gen.NM_000183
Figure 712: PRO4917
Figure 713: DNA324084, NM_000182, gen.NM_000182
Figure 714: PRO80793
Figure 715: DNA324085, XM_097976, gen.XM_097976
Figure 716A-B: DNA324086, XM_039712, gen.XM_039712
Figure 717: DNA324087, NM_022552, gen.NM_022552
Figure 718: PRO80796
Figure 719: DNA324088, NM_024572, gen.NM_024572
Figure 720: PRO80797
Figure 721: DNA324089, NM_018607, gen.NM_018607
Figure 722: PRO80798
Figure 723: DNA324090, XM_165448, gen.XM_165448
Figure 724: PRO80799
Figure 725: DNA324091, XM_087195, gen.XM_087195
Figure 726: DNA324092, XM_087193, gen.XM_087193
Figure 727: DNA324093, NM_138801, gen.NM_138801
Figure 728: PRO80802
Figure 729: DNA324094, XM_098004, gen.XM_098004
Figure 730: PRO80803
Figure 731: DNA324095, XM_031519, gen.XM_031519
Figure 732: PRO80804
Figure 733A-B: DNA324096, XM_031527, gen.XM_031527
Figure 734: DNA324097, XM_038576, gen.XM_038576
Figure 735: PRO80806

Figure 736: DNA324098, XM_117264, gen.XM_117264
Figure 737: PRO80807
Figure 738A-B: DNA324099, XM_031626, gen.XM_031626
Figure 739: PRO80808
Figure 740: DNA324100, XM_057664, gen.XM_057664
Figure 741: DNA226428, NM_000251, gen.NM_000251
Figure 742: PRO36891
Figure 743: DNA324101, XM_087211, gen.XM_087211
Figure 744A-B: DNA275066, NM_000179, gen.NM_000179
Figure 745: PRO62786
Figure 746A-C: DNA270154, NM_003128, gen.NM_003128
Figure 747: PRO58543
Figure 748: DNA324102, XM_087051, gen.XM_087051
Figure 749: DNA324103, NM_002954, gen.NM_002954
Figure 750: PRO62239
Figure 751: DNA271060, NM_002453, gen.NM_002453
Figure 752: PRO59384
Figure 753: DNA324104, XM_048088, gen.XM_048088
Figure 754: PRO80811
Figure 755: DNA324105, XM_010886, gen.XM_010886
Figure 756: PRO80812
Figure 757: DNA324106, XM_045283, gen.XM_045283
Figure 758: PRO80813
Figure 759: DNA324107, NM_006430, gen.NM_006430
Figure 760: PRO80814
Figure 761A-B: DNA324108, NM_003400, gen.NM_003400
Figure 762: PRO59544
Figure 763: DNA324109, XM_018301, gen.XM_018301
Figure 764: DNA324110, NM_005917, gen.NM_005917
Figure 765: PRO4918
Figure 766: DNA324111, XM_016843, gen.XM_016843
Figure 767: PRO80816
Figure 768: DNA324112, XM_088638, gen.XM_088638
Figure 769: PRO80817
Figure 770: DNA324113, XM_002647, gen.XM_002647
Figure 771: DNA324114, XM_010881, gen.XM_010881
Figure 772: DNA324115, XM_087069, gen.XM_087069
Figure 773: DNA324116, XM_016625, gen.XM_016625
Figure 774: PRO80820
Figure 775: DNA324117, XM_087068, gen.XM_087068
Figure 776: DNA324118, XM_002674, gen.XM_002674
Figure 777: DNA324119, XM_065884, gen.XM_065884
Figure 778: PRO80823
Figure 779A-B: DNA324120, XM_002739, gen.XM_002739
Figure 780: DNA324121, XM_031596, gen.XM_031596
Figure 781: PRO61325
Figure 782: DNA324122, XM_031585, gen.XM_031585
Figure 783: DNA324123, XM_031586, gen.XM_031586
Figure 784: DNA324124, XM_018039, gen.XM_018039
Figure 785: DNA324125, NM_032822, gen.NM_032822
Figure 786: PRO80827
Figure 787A-B: DNA324126, XM_096172, gen.XM_096172
Figure 788A-B: DNA324127, XM_002727, gen.XM_002727
Figure 789: DNA324128, NM_003124, gen.NM_003124
Figure 790: PRO80830
Figure 791: DNA324129, XM_086980, gen.XM_086980
Figure 792: DNA227795, NM_006429, gen.NM_006429
Figure 793: PRO38258
Figure 794: DNA287167, NM_006636, gen.NM_006636
Figure 795: PRO59136
Figure 796: DNA324130, NM_033046, gen.NM_033046
Figure 797: PRO80832
Figure 798: DNA324131, NM_133637, gen.NM_133637
Figure 799: PRO80833
Figure 800: DNA324132, XM_035220, gen.XM_035220
Figure 801: DNA324133, NM_013247, gen.NM_013247
Figure 802: PRO80835
Figure 803: DNA227528, NM_021103, gen.NM_021103
Figure 804: PRO37991

Figure 805: DNA324134, XM_086920, gen.XM_086920
Figure 806: DNA150725, NM_001747, gen.NM_001747
Figure 807: PRO12792
Figure 808: DNA324135, NM_005911, gen.NM_005911
Figure 809: PRO80837
Figure 810: DNA324136, NM_032827, gen.NM_032827
Figure 811: PRO80838
Figure 812: DNA324137, NM_017952, gen.NM_017952
Figure 813: PRO80839
Figure 814: DNA227190, NM_006839, gen.NM_006839
Figure 815: PRO37653
Figure 816: DNA324138, XM_114215, gen.XM_114215
Figure 817: DNA324139, XM_052989, gen.XM_052989
Figure 818: DNA324140, XM_049116, gen.XM_049116
Figure 819: PRO80842
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Figure 821: PRO80843
Figure 822: DNA324142, XM_049113, gen.XM_049113
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Figure 824A-B: DNA324144, XM_114247, gen.XM_114247
Figure 825: DNA324145, NM_017789, gen.NM_017789
Figure 826: PRO80846
Figure 827: DNA324146, NM_001862, gen.NM_001862
Figure 828: PRO80847
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Figure 833: PRO11197
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Figure 835: PRO80850
Figure 836: DNA324151, NM_001450, gen.NM_001450
Figure 837: PRO80851
Figure 838: DNA324152, XM_114229, gen.XM_114229
Figure 839: DNA324153, XM_087122, gen.XM_087122
Figure 840: PRO80853
Figure 841: DNA324154, XM_018540, gen.XM_018540
Figure 842: DNA324155, XM_087040, gen.XM_087040
Figure 843: DNA324156, NM_032212, gen.NM_032212
Figure 844: PRO80856
Figure 845: DNA324157, XM_002217, gen.XM_002217
Figure 846: PRO80857
Figure 847: DNA324158, NM_000576, gen.NM_000576
Figure 848: PRO65
Figure 849: DNA324159, XM_086923, gen.XM_086923
Figure 850: DNA324160, XM_086925, gen.XM_086925
Figure 851A-B: DNA324161, XM_114266, gen.XM_114266
Figure 852: PRO80860
Figure 853: DNA324162, XM_002704, gen.XM_002704
Figure 854: DNA194740, NM_005291, gen.NM_005291
Figure 855: PRO24028
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Figure 857: DNA324164, XM_034952, gen.XM_034952
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Figure 859A-B: DNA255531, NM_017751, gen.NM_017751
Figure 860: PRO50596
Figure 861: DNA324166, XM_017698, gen.XM_017698 .
Figure 862: DNA324167, XM_030529, gen.XM_030529
Figure 863: PRO80866
Figure 864: DNA275240, NM_005915, gen.NM_005915
Figure 865: PRO62927
Figure 866: DNA324168, XM_043173, gen.XM_043173
Figure 867: DNA324169, XM_092489, gen.XM_092489
Figure 868: PRO80868
Figure 869: DNA324170, XM_115672, gen.XM_115672
Figure 870: PRO80869
Figure 871: DNA324171, NM_020548, gen.NM_020548
Figure 872: PRO60753
Figure 873: DNA324172, XM_037101,

gen.XM_037101
Figure 874: PRO80870
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Figure 876: PRO80871
Figure 877: DNA324174, XM_002447, gen.XM_002447
Figure 878: DNA324175, NM_033416, gen.NM_033416
Figure 879: PRO80873
Figure 880: DNA324176, XM_016288, gen.XM_016288
Figure 881: DNA272127, NM_003937, gen.NM_003937
Figure 882: PRO60397
Figure 883: DNA324177, XM_030582, gen.XM_030582
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Figure 885: DNA324178, NM_015702, gen.NM_015702
Figure 886: PRO80876
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Figure 888: PRO80877
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Figure 890: PRO80878
Figure 891: DNA324181, XM_087118, gen.XM_087118
Figure 892: PRO80879
Figure 893: DNA324182, XM_165998, gen.XM_165998
Figure 894: DNA324183, NM_001935, gen.NM_001935
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Figure 900: DNA324185, XM_166008, gen.XM_166008
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Figure 902: PRO11403
Figure 903: DNA324187, NM_013341, gen.NM_013341
Figure 904: PRO80883
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Figure 906: PRO69531
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Figure 910: DNA324190, XM_166007, gen.XM_166007
Figure 911: DNA324191, XM_015922, gen.XM_015922
Figure 912: DNA324192, XM_087061, gen.XM_087061
Figure 913: PRO80888
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Figure 915: PRO80889
Figure 916: DNA324194, NM_001463, gen.NM_001463
Figure 917: PRO80890
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Figure 922: PRO2665
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Figure 924: PRO37675
Figure 925: DNA324199, XM_010778, gen.XM_010778
Figure 926: DNA324200, XM_086961, gen.XM_086961
Figure 927: DNA324201, XM_165994, gen.XM_165994
Figure 928: DNA324202, XM_045170, gen.XM_045170
Figure 929: DNA324203, XM_113390, gen.XM_113390
Figure 930: DNA299899, NM_002157, gen.NM_002157
Figure 931: PRO62760
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Figure 933: DNA324205, XM_086944, gen.XM_086944
Figure 934: DNA271608, NM_014670, gen.NM_014670
Figure 935: PRO59895
Figure 936: DNA324206, XM_027963, gen.XM_027963
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Figure 938: DNA324207, XM_010852, gen.XM_010852
Figure 939: PRO80901
Figure 940: DNA324208, XM_028034, gen.XM_028034
Figure 941: DNA324209, NM_015934, gen.NM_015934
Figure 942: DNA324210, XM_087028, gen.XM_087028

Figure 943: PRO80903
Figure 944: DNA324211, XM_092346, gen.XM_092346
Figure 945: PRO80904
Figure 946: DNA324212, XM_002669, gen.XM_002669
Figure 947: PRO80905
Figure 948: DNA324213, NM_021121, gen.NM_021121
Figure 949: PRO23124
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Figure 960A-B: DNA324220, XM_098048, gen.XM_098048
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Figure 963: PRO80911
Figure 964: DNA324222, XM_002636, gen.XM_002636
Figure 965: DNA324223, XM_087181, gen.XM_087181
Figure 966: DNA324224, NM_000998, gen.NM_000998
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Figure 987: PRO80920
Figure 988: DNA324236, NM_022453, gen.NM_022453
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Figure 994: DNA254204, NM_001087, gen.NM_001087
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Figure 1007: DNA324245, XM_048690, gen.XM_048690
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Figure 1013: PRO80932

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Figure 1034: DNA324259, NM_004404, gen.NM_004404
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Figure 1036: DNA324260, XM_002742, gen.XM_002742
Figure 1037: DNA324261, NM_138483, gen.NM_138483
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Figure 1039: DNA324262, XM_115706, gen.XM_115706
Figure 1040: DNA324263, XM_115722, gen.XM_115722
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Figure 1048: PRO80951
Figure 1049: DNA324269, NM_006354, gen.NM_006354
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Figure 1053: DNA324271, NM_133481, gen.NM_133481
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Figure 1057: DNA324273, NM_015644, gen.NM_015644
Figure 1058: PRO80956
Figure 1059: DNA324274, XM_059561, gen.XM_059561
Figure 1060: DNA324275, XM_052310, gen.XM_052310
Figure 1061: PRO80958
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Figure 1063: PRO58308
Figure 1064: DNA324276, NM_000994, gen.NM_000994
Figure 1065: PRO80959
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Figure 1067: PRO12841
Figure 1068: DNA324277, XM_059557, gen.XM_059557
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Figure 1071: PRO80961
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Figure 1073: PRO80962
Figure 1074: DNA324280, XM_053712, gen.XM_053712
Figure 1075: DNA324281, XM_087284, gen.XM_087284
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Figure 1077: PRO6360
Figure 1078: DNA324283, XM_053323, gen.XM_053323
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Figure 1080: PRO80966
Figure 1081: DNA252367, NM_017801, gen.NM_017801
Figure 1082: PRO48357
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Figure 1084: PRO80967

Figure 1085: DNA324286, XM_046401, gen.XM_046401
Figure 1086: DNA324287, NM_022461, gen.NM_022461
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Figure 1088: DNA324288, XM_113410, gen.XM_113410
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Figure 1105: DNA324293, XM_017364, gen.XM_017364
Figure 1106: DNA324294, XM_087349, gen.XM_087349
Figure 1107: PRO80974
Figure 1108: DNA226547, NM_002295, gen.NM_002295
Figure 1109: PRO37010
Figure 1110: DNA324295, NM_003973, gen.NM_003973
Figure 1111: PRO80975
Figure 1112: DNA324296, XM_030417, gen.XM_030417
Figure 1113: DNA324297, NM_020347, gen.NM_020347
Figure 1114: PRO80977
Figure 1115: DNA324298, XM_087346, gen.XM_087346
Figure 1116: PRO80978
Figure 1117: DNA324299, XM_096198, gen.XM_096198
Figure 1118: PRO80979
Figure 1119: DNA324300, XM_003222, gen.XM_003222
Figure 1120: DNA324301, XM_087588, gen.XM_087588
Figure 1121: DNA324302, XM_166011, gen.XM_166011
Figure 1122A-B: DNA324303, XM_114364, gen.XM_114364
Figure 1123A-B: DNA324304, XM_033294, gen.XM_033294
Figure 1124: PRO80983
Figure 1125: DNA324305, NM_138614, gen.NM_138614
Figure 1126: PRO80984
Figure 1127: DNA324306, XM_002899, gen.XM_002899
Figure 1128: DNA225910, NM_004345, gen.NM_004345
Figure 1129: PRO36373
Figure 1130: DNA324307, XM_010953, gen.XM_010953
Figure 1131: DNA324308, XM_051518, gen.XM_051518
Figure 1132A-D: DNA324309, NM_001407, gen.NM_001407
Figure 1133: PRO50095
Figure 1134: DNA324310, NM_003365, gen.NM_003365
Figure 1135: PRO80988
Figure 1136: DNA324311, XM_003245, gen.XM_003245
Figure 1137: DNA324312, XM_047561, gen.XM_047561
Figure 1138: PRO80990
Figure 1139: DNA324313, XM_116853, gen.XM_116853
Figure 1140A-B: DNA324314, XM_113405, gen.XM_113405
Figure 1141: DNA324315, XM_114323, gen.XM_114323
Figure 1142: PRO80993
Figure 1143: DNA324316, XM_002828, gen.XM_002828
Figure 1144: PRO80994
Figure 1145: DNA150976, NM_022171, gen.NM_022171
Figure 1146: PRO12565
Figure 1147: DNA324317, XM_041507, gen.XM_041507
Figure 1148: PRO71103
Figure 1149: DNA103505, NM_004636, gen.NM_004636
Figure 1150: PRO4832
Figure 1151: DNA324318, NM_006764, gen.NM_006764
Figure 1152: PRO80995
Figure 1153: DNA150562, NM_007275, gen.NM_007275
Figure 1154: PRO12779

Figure 1155: DNA254582, NM_004635, gen.NM_004635
Figure 1156: PRO49685
Figure 1157: DNA324319, NM_052859, gen.NM_052859
Figure 1158: PRO80996
Figure 1159: DNA324320, NM_001064, gen.NM_001064
Figure 1160: PRO80997
Figure 1161: DNA324321, XM_041211, gen.XM_041211
Figure 1162: DNA324322, XM_003213, gen.XM_003213
Figure 1163A-C: DNA324323, XM_037423, gen.XM_037423
Figure 1164: PRO80999
Figure 1165A-B: DNA227307, NM_007184, gen.NM_007184
Figure 1166: PRO37770
Figure 1167: DNA324324, NM_000688, gen.NM_000688
Figure 1168: PRO81000
Figure 1169: DNA324325, XM_067715, gen.XM_067715
Figure 1170: DNA324326, NM_000992, gen.NM_000992
Figure 1171: PRO62153
Figure 1172: DNA324327, NM_000666, gen.NM_000666
Figure 1173: PRO81002
Figure 1174: DNA324328, NM_032750, gen.NM_032750
Figure 1175: PRO81003
Figure 1176: DNA324329, NM_033008, gen.NM_033008
Figure 1177: PRO81004
Figure 1178: DNA324330, NM_033010, gen.NM_033010
Figure 1179: PRO81005
Figure 1180: DNA324331, NM_020418, gen.NM_020418
Figure 1181: PRO81006
Figure 1182: DNA273919, NM_004704, gen.NM_004704
Figure 1183: PRO61870
Figure 1184A-B: DNA324332, XM_087448, gen.XM_087448
Figure 1185: PRO81007
Figure 1186: DNA324333, XM_002855, gen.XM_002855
Figure 1187: DNA324334, XM_002854, gen.XM_002854
Figure 1188: DNA0, NM_002854, gen.NM_002854
Figure 1189: PRO
Figure 1190: DNA324335, XM_096195, gen.XM_096195
Figure 1191: PRO81010
Figure 1192: DNA324336, XM_166015, gen.XM_166015
Figure 1193: DNA324337, XM_113395, gen.XM_113395
Figure 1194: PRO81012
Figure 1195: DNA269730, NM_014814, gen.NM_014814
Figure 1196: PRO58140
Figure 1197: DNA324338, XM_036938, gen.XM_036938
Figure 1198: DNA324339, XM_029369, gen.XM_029369
Figure 1199: DNA324340, XM_076414, gen.XM_076414
Figure 1200: PRO81015
Figure 1201: DNA324341, XM_093546, gen.XM_093546
Figure 1202: DNA324342, XM_113409, gen.XM_113409
Figure 1203: DNA324343, XM_087268, gen.XM_087268
Figure 1204: DNA324344, XM_116071, gen.XM_116071
Figure 1205: DNA324345, XM_116072, gen.XM_116072
Figure 1206: DNA324346, NM_000986, gen.NM_000986
Figure 1207: PRO10602
Figure 1208: DNA324347, XM_015462, gen.XM_015462
Figure 1209: DNA324348, XM_167366, gen.XM_167366
Figure 1210: PRO81022
Figure 1211: DNA324349, XM_087331, gen.XM_087331
Figure 1212: PRO81023
Figure 1213: DNA324350, XM_039952, gen.XM_039952
Figure 1214: DNA324351, XM_045290, gen.XM_045290
Figure 1215: PRO81025
Figure 1216A-B: DNA324352, NM_007085, gen.NM_007085
Figure 1217: PRO2077
Figure 1218: DNA324353, NM_004547, gen.NM_004547
Figure 1219: PRO81026
Figure 1220: DNA324354, XM_027161, gen.XM_027161
Figure 1221A-B: DNA324355, XM_032269, gen.XM_032269
Figure 1222: PRO81028
Figure 1223: DNA88547, NM_006810, gen.NM_006810
Figure 1224: PRO2837

Figure 1225: DNA324356, XM_114301, gen.XM_114301
Figure 1226: PRO81029
Figure 1227: DNA324357, XM_098173, gen.XM_098173
Figure 1228: PRO81030
Figure 1229: DNA324358, XM_042618, gen.XM_042618
Figure 1230: PRO81031
Figure 1231: DNA324359, XM_084129, gen.XM_084129
Figure 1232: DNA324360, XM_098154, gen.XM_098154
Figure 1233: PRO81033
Figure 1234: DNA324361, XM_050552, gen.XM_050552
Figure 1235: DNA324362, NM_032343, gen.NM_032343
Figure 1236: PRO81034
Figure 1237: DNA324363, XM_051264, gen.XM_051264
Figure 1238A-B: DNA324364, NM_013336, gen.NM_013336
Figure 1239: PRO1314
Figure 1240: DNA324365, XM_067264, gen.XM_067264
Figure 1241: PRO81036
Figure 1242: DNA324366, XM_114309, gen.XM_114309
Figure 1243: DNA324367, XM_084111, gen.XM_084111
Figure 1244: DNA324368, XM_113397, gen.XM_113397
Figure 1245: DNA324369, XM_098111, gen.XM_098111
Figure 1246: DNA324370, NM_004637, gen.NM_004637
Figure 1247: PRO81040
Figure 1248: DNA324371, NM_020701, gen.NM_020701
Figure 1249: PRO81041
Figure 1250: DNA324372, NM_003418, gen.NM_003418
Figure 1251: PRO81042
Figure 1252: DNA324373, XM_059583, gen.XM_059583
Figure 1253: PRO81043
Figure 1254: DNA324374, XM_113417, gen.XM_113417
Figure 1255: DNA324375, XM_093487, gen.XM_093487
Figure 1256A-B: DNA324376, XM_030812, gen.XM_030812
Figure 1257: PRO58177
Figure 1258A-B: DNA324377, XM_039805, gen.XM_039805
Figure 1259: PRO81046
Figure 1260: DNA324378, NM_000532, gen.NM_000532
Figure 1261: PRO81047
Figure 1262: DNA324379, XM_036118, gen.XM_036118
Figure 1263: DNA324380, XM_084123, gen.XM_084123
Figure 1264: DNA324381, XM_018149, gen.XM_018149
Figure 1265: DNA324382, XM_087342, gen.XM_087342
Figure 1266: DNA324383, XM_059516, gen.XM_059516
Figure 1267: DNA324384, XM_087341, gen.XM_087341
Figure 1268: DNA324385, XM_165451, gen.XM_165451
Figure 1269: PRO81053
Figure 1270: DNA269858, NM_004766, gen.NM_004766
Figure 1271: PRO58259
Figure 1272: DNA324386, NM_030921, gen.NM_030921
Figure 1273: PRO51109
Figure 1274: DNA324387, XM_002859, gen.XM_002859
Figure 1275: DNA324388, XM_166014, gen.XM_166014
Figure 1276: DNA324389, NM_013363, gen.NM_013363
Figure 1277: PRO287
Figure 1278: DNA324390, XM_058267, gen.XM_058267
Figure 1279: PRO81056
Figure 1280A-B: DNA324391, NM_032383, gen.NM_032383
Figure 1281: PRO81057
Figure 1282: DNA324392, NM_015472, gen.NM_015472
Figure 1283: PRO81058
Figure 1284: DNA324393, NM_014445, gen.NM_014445
Figure 1285: PRO11048
Figure 1286: DNA324394, XM_042168, gen.XM_042168
Figure 1287: PRO81059
Figure 1288A-B: DNA324395, XM_114356, gen.XM_114356
Figure 1289: DNA324396, XM_105236, gen.XM_105236
Figure 1290: DNA324397, XM_010978, gen.XM_010978
Figure 1291: DNA324398, XM_017356, gen.XM_017356
Figure 1292A-B: DNA324399, XM_039796,

gen.XM_039796
Figure 1293: PRO81064
Figure 1294: DNA324400, XM_016334, gen.XM_016334
Figure 1295: DNA324401, XM_116058, gen.XM_116058
Figure 1296: DNA324402, XM_113408, gen.XM_113408
Figure 1297: DNA324403, NM_002492, gen.NM_002492
Figure 1298: PRO81068
Figure 1299: DNA324404, XM_037381, gen.XM_037381
Figure 1300: DNA324405, XM_037377, gen.XM_037377
Figure 1301: PRO69681
Figure 1302A-B: DNA324406, XM_087254, gen.XM_087254
Figure 1303: PRO81070
Figure 1304: DNA324407, XM_037600, gen.XM_037600
Figure 1305: PRO81071
Figure 1306: DNA324408, NM_018023, gen.NM_018023
Figure 1307: PRO81072
Figure 1308: DNA324409, XM_093423, gen.XM_093423
Figure 1309: PRO81073
Figure 1310: DNA324410, XM_029136, gen.XM_029136
Figure 1311: PRO81074
Figure 1312: DNA324411, XM_087322, gen.XM_087322
Figure 1313A-B: DNA324412, XM_029132, gen.XM_029132
Figure 1314A-B: DNA324413, XM_029104, gen.XM_029104
Figure 1315: DNA324414, XM_084120, gen.XM_084120
Figure 1316: DNA254620, NM_005787, gen.NM_005787
Figure 1317: PRO49722
Figure 1318: DNA324415, NM_032331, gen.NM_032331
Figure 1319: PRO81079
Figure 1320: DNA324416, XM_011074, gen.XM_011074
Figure 1321: PRO81080
Figure 1322: DNA324417, XM_087295, gen.XM_087295
Figure 1323: DNA324418, XM_087289, gen.XM_087289
Figure 1324: PRO81082
Figure 1325: DNA324419, XM_105658, gen.XM_105658
Figure 1326: PRO81083
Figure 1327: DNA89239, NM_000893, gen.NM_000893
Figure 1328: PRO2906
Figure 1329: DNA324420, XM_113422, gen.XM_113422
Figure 1330: DNA225592, NM_001622, gen.NM_001622
Figure 1331: PRO36055
Figure 1332: DNA324421, XM_005180, gen.XM_005180
Figure 1333: DNA324422, XM_087392, gen.XM_087392
Figure 1334: PRO81086
Figure 1335A-B: DNA272605, NM_003722, gen.NM_003722
Figure 1336: PRO60741
Figure 1337: DNA324423, XM_117311, gen.XM_117311
Figure 1338: DNA324424, XM_116034, gen.XM_116034
Figure 1339: PRO81088
Figure 1340A-B: DNA324425, XM_084110, gen.XM_084110
Figure 1341: DNA324426, XM_038243, gen.XM_038243
Figure 1342: PRO81090
Figure 1343: DNA324427, XM_087359, gen.XM_087359
Figure 1344: DNA324428, XM_114328, gen.XM_114328
Figure 1345: DNA324429, XM_098109, gen.XM_098109
Figure 1346: PRO81093
Figure 1347: DNA324430, XM_087410, gen.XM_087410
Figure 1348: DNA324431, NM_033316, gen.NM_033316
Figure 1349: PRO81095
Figure 1350: DNA324432, XM_166017, gen.XM_166017
Figure 1351: PRO81096
Figure 1352: DNA79129, NM_001647, gen.NM_001647
Figure 1353: PRO2551
Figure 1354: DNA324433, NM_032288, gen.NM_032288
Figure 1355: PRO81097
Figure 1356: DNA324434, XM_086228, gen.XM_086228
Figure 1357: PRO81098
Figure 1358: DNA324435, XM_087278, gen.XM_087278
Figure 1359: DNA324436, XM_018523, gen.XM_018523
Figure 1360: DNA324437, XM_087297, gen.XM_087297

Figure 1361: DNA324438, XM_002255, gen.XM_002255
Figure 1362: PRO81102
Figure 1363: DNA324439, XM_053122, gen.XM_053122
Figure 1364: DNA324440, XM_042695, gen.XM_042695
Figure 1365: DNA324441, XM_011160, gen.XM_011160
Figure 1366: DNA324442, NM_007100, gen.NM_007100
Figure 1367: PRO81106
Figure 1368: DNA139747, NM_002477, gen.NM_002477
Figure 1369: PRO9785
Figure 1370: DNA253804, NM_032219, gen.NM_032219
Figure 1371: PRO49209
Figure 1372: DNA324443, NM_138385, gen.NM_138385
Figure 1373: PRO81107
Figure 1374: DNA324444, NM_006342, gen.NM_006342
Figure 1375: PRO81108
Figure 1376A-C: DNA324445, NM_133330, gen.NM_133330
Figure 1377: PRO81109
Figure 1378A-C: DNA324446, NM_014919, gen.NM_014919
Figure 1379: PRO81110
Figure 1380A-C: DNA324447, NM_133332, gen.NM_133332
Figure 1381: PRO81111
Figure 1382: DNA324448, NM_005663, gen.NM_005663
Figure 1383: PRO81112
Figure 1384A-B: DNA324449, XM_098248, gen.XM_098248
Figure 1385: PRO81113
Figure 1386: DNA270615, NM_002938, gen.NM_002938
Figure 1387: PRO58986
Figure 1388A-B: DNA324450, NM_014190, gen.NM_014190
Figure 1389: PRO81114
Figure 1390A-B: DNA324451, NM_014189, gen.NM_014189
Figure 1391: PRO81115
Figure 1392: DNA324452, XM_035572, gen.XM_035572
Figure 1393: PRO81116
Figure 1394A-B: DNA324453, NM_014556, gen.NM_014556
Figure 1395: PRO81117
Figure 1396: DNA324454, NM_001313, gen.NM_001313
Figure 1397: PRO60542
Figure 1398A-B: DNA324455, XM_052626, gen.XM_052626
Figure 1399: PRO81118
Figure 1400: DNA324456, NM_016930, gen.NM_016930
Figure 1401: PRO81119
Figure 1402: DNA324457, XM_035824, gen.XM_035824
Figure 1403: PRO81120
Figure 1404: DNA324458, NM_033296, gen.NM_033296
Figure 1405: PRO81121
Figure 1406: DNA324459, NM_138699, gen.NM_138699
Figure 1407: PRO81122
Figure 1408: DNA324460, XM_116285, gen.XM_116285
Figure 1409: PRO81123
Figure 1410: DNA324461, XM_041221, gen.XM_041221
Figure 1411: PRO81124
Figure 1412: DNA324462, XM_117351, gen.XM_117351
Figure 1413: DNA324463, XM_039165, gen.XM_039165
Figure 1414: DNA324464, NM_025205, gen.NM_025205
Figure 1415: PRO81127
Figure 1416: DNA324465, XM_039173, gen.XM_039173
Figure 1417: DNA324466, XM_039176, gen.XM_039176
Figure 1418: DNA324467, XM_087583, gen.XM_087583
Figure 1419: DNA324468, NM_017491, gen.NM_017491
Figure 1420: PRO12077
Figure 1421: DNA324469, NM_005112, gen.NM_005112
Figure 1422: PRO81131
Figure 1423: DNA324470, XM_011129, gen.XM_011129
Figure 1424A-B: DNA324471, XM_052530, gen.XM_052530
Figure 1425: DNA324472, NM_000661, gen.NM_000661
Figure 1426: PRO81134
Figure 1427A-B: DNA324473, NM_002913, gen.NM_002913
Figure 1428: PRO81135
Figure 1429A-B: DNA324474, XM_047477, gen.XM_047477
Figure 1430: DNA324475, NM_004181, gen.NM_004181
Figure 1431: PRO81137

Figure 1432: DNA324476, XM_003435, gen.XM_003435
Figure 1433: DNA324478, XM_010941, gen.XM_010941
Figure 1434: DNA324479, XM_059593, gen.XM_059593
Figure 1435: DNA324480, NM_001553, gen.NM_001553
Figure 1436: PRO81141
Figure 1437: DNA257511, NM_032313, gen.NM_032313
Figure 1438: PRO52083
Figure 1439: DNA324481, XM_071623, gen.XM_071623
Figure 1440A-B: DNA324482, XM_036002, gen.XM_036002
Figure 1441: DNA324483, XM_058927, gen.XM_058927
Figure 1442: DNA324484, XM_059628, gen.XM_059628
Figure 1443: DNA324485, XM_046057, gen.XM_046057
Figure 1444: PRO81146
Figure 1445: DNA324486, XM_031320, gen.XM_031320
Figure 1446: DNA225919, NM_001134, gen.NM_001134
Figure 1447: PRO36382
Figure 1448A-B: DNA324487, XM_003511, gen.XM_003511
Figure 1449: DNA324488, NM_006835, gen.NM_006835
Figure 1450: PRO4605
Figure 1451: DNA324489, XM_003305, gen.XM_003305
Figure 1452: DNA324490, XM_113425, gen.XM_113425
Figure 1453: DNA324491, XM_001389, gen.XM_001389
Figure 1454: PRO81148
Figure 1455: DNA324492, XM_087527, gen.XM_087527
Figure 1456: DNA324493, XM_035986, gen.XM_035986
Figure 1457A-B: DNA324494, NM_014933, gen.NM_014933
Figure 1458: PRO81150
Figure 1459: DNA290585, NM_000582, gen.NM_000582
Figure 1460: PRO70536
Figure 1461: DNA324495, XM_055551, gen.XM_055551
Figure 1462: PRO81151
Figure 1463: DNA324496, XM_087498, gen.XM_087498
Figure 1464: DNA324497, XM_096203, gen.XM_096203
Figure 1465: DNA324498, XM_084158, gen.XM_084158
Figure 1466: DNA324499, XM_034710, gen.XM_034710
Figure 1467: PRO81156
Figure 1468: DNA324500, XM_034713, gen.XM_034713
Figure 1469: DNA324501, XM_059633, gen.XM_059633
Figure 1470: DNA324502, XM_114426, gen.XM_114426
Figure 1471: DNA324503, XM_056957, gen.XM_056957
Figure 1472: DNA324504, XM_088472, gen.XM_088472
Figure 1473: DNA324505, XM_114424, gen.XM_114424
Figure 1474A-B: DNA324506, XM_042301, gen.XM_042301
Figure 1475: PRO81163
Figure 1476: DNA324507, XM_017925, gen.XM_017925
Figure 1477: DNA324508, XM_052336, gen.XM_052336
Figure 1478: DNA324509, NM_002106, gen.NM_002106
Figure 1479: PRO10297
Figure 1480: DNA324510, XM_085068, gen.XM_085068
Figure 1481: PRO81166
Figure 1482: DNA324511, XM_165473, gen.XM_165473
Figure 1483: DNA324512, XM_087514, gen.XM_087514
Figure 1484: DNA324513, XM_116247, gen.XM_116247
Figure 1485: DNA324514, NM_002358, gen.NM_002358
Figure 1486: PRO81169
Figure 1487: DNA324515, XM_050200, gen.XM_050200
Figure 1488: PRO81170
Figure 1489: DNA225584, NM_001154, gen.NM_001154
Figure 1490: PRO36047
Figure 1491: DNA324516, NM_024900, gen.NM_024900
Figure 1492: PRO81171
Figure 1493: DNA324517, XM_040752, gen.XM_040752
Figure 1494: DNA324518, NM_002413, gen.NM_002413
Figure 1495: PRO60956
Figure 1496: DNA324519, XM_114401, gen.XM_114401

Figure 1497: DNA324520, XM_068164, gen.XM_068164
Figure 1498: PRO81174
Figure 1499: DNA324521, XM_060067, gen.XM_060067
Figure 1500: DNA324522, XM_003555, gen.XM_003555
Figure 1501: PRO81176
Figure 1502: DNA324523, XM_034321, gen.XM_034321
Figure 1503: PRO81177
Figure 1504: DNA324524, NM_006439, gen.NM_006439
Figure 1505: PRO81178
Figure 1506: DNA324525, NM_001006, gen.NM_001006
Figure 1507: PRO81179
Figure 1508: DNA227575, NM_005141, gen.NM_005141
Figure 1509: PRO38038
Figure 1510: DNA324526, XM_114368, gen.XM_114368
Figure 1511A-B: DNA225920, NM_000508, gen.NM_000508
Figure 1512: PRO36383
Figure 1513: DNA324527, NM_021871, gen.NM_021871
Figure 1514: PRO81181
Figure 1515: DNA225921, NM_000509, gen.NM_000509
Figure 1516: PRO36384
Figure 1517: DNA324528, NM_021870, gen.NM_021870
Figure 1518: PRO81182
Figure 1519: DNA324529, XM_059623, gen.XM_059623
Figure 1520: DNA324530, XM_106246, gen.XM_106246
Figure 1521: PRO81184
Figure 1522: DNA324531, NM_002129, gen.NM_002129
Figure 1523: PRO81185
Figure 1524: DNA324532, XM_040321, gen.XM_040321
Figure 1525: DNA324533, XM_015563, gen.XM_015563
Figure 1526: DNA324534, NM_024748, gen.NM_024748
Figure 1527: PRO81188
Figure 1528: DNA324535, XM_165470, gen.XM_165470
Figure 1529: PRO81189
Figure 1530A-E: DNA324536, XM_003477, gen.XM_003477
Figure 1531: DNA324537, XM_165465, gen.XM_165465
Figure 1532: DNA324538, XM_116204, gen.XM_116204
Figure 1533: DNA324539, XM_116205, gen.XM_116205
Figure 1534: DNA324540, XM_098405, gen.XM_098405
Figure 1535: DNA324541, XM_052313, gen.XM_052313
Figure 1536: PRO81195
Figure 1537: DNA324542, XM_087659, gen.XM_087659
Figure 1538: PRO81196
Figure 1539: DNA324543, XM_029096, gen.XM_029096
Figure 1540: DNA324544, XM_003825, gen.XM_003825
Figure 1541: DNA324545, XM_057994, gen.XM_057994
Figure 1542: PRO81199
Figure 1543: DNA324546, XM_087686, gen.XM_087686
Figure 1544: DNA324547, XM_017641, gen.XM_017641
Figure 1545: DNA324548, NM_030782, gen.NM_030782
Figure 1546: PRO81202
Figure 1547: DNA324549, XM_084168, gen.XM_084168
Figure 1548: DNA324550, XM_057492, gen.XM_057492
Figure 1549: DNA324551, XM_087597, gen.XM_087597
Figure 1550: DNA324552, XM_087601, gen.XM_087601
Figure 1551: DNA324554, XM_087599, gen.XM_087599
Figure 1552: DNA324555, XM_114435, gen.XM_114435
Figure 1553: DNA324556, XM_087600, gen.XM_087600
Figure 1554: DNA324557, XM_016170, gen.XM_016170
Figure 1555: DNA324558, XM_114434, gen.XM_114434
Figure 1556: DNA324559, XM_113452, gen.XM_113452
Figure 1557: DNA324560, XM_071580, gen.XM_071580
Figure 1558: PRO81213
Figure 1559: DNA324561, XM_087713, gen.XM_087713
Figure 1560: PRO81214
Figure 1561: DNA324562, XM_094440, gen.XM_094440
Figure 1562: DNA324563, XM_106739, gen.XM_106739

Figure 1563: PRO81216
Figure 1564: DNA324564, XM_087614, gen.XM_087614
Figure 1565: DNA324565, XM_004009, gen.XM_004009
Figure 1566: PRO81219
Figure 1567: DNA324566, XM_114437, gen.XM_114437
Figure 1568: DNA324567, XM_043771, gen.XM_043771
Figure 1569: PRO81221
Figure 1570: DNA324568, NM_000997, gen.NM_000997
Figure 1571: PRO11077
Figure 1572: DNA324569, XM_003869, gen.XM_003869
Figure 1573: DNA227173, NM_001465, gen.NM_001465
Figure 1574: PRO37636
Figure 1575: DNA324570, NM_018034, gen.NM_018034
Figure 1576: PRO81223
Figure 1577: DNA324571, NM_032637, gen.NM_032637
Figure 1578: PRO81224
Figure 1579: DNA324572, NM_005983, gen.NM_005983
Figure 1580: PRO81225
Figure 1581A-B: DNA324573, XM_003896, gen.XM_003896
Figure 1582: DNA287282, NM_002130, gen.NM_002130
Figure 1583: PRO69554
Figure 1584: DNA324574, XM_114442, gen.XM_114442
Figure 1585: PRO81227
Figure 1586: DNA324575, XM_114439, gen.XM_114439
Figure 1587: DNA324576, XM_114440, gen.XM_114440
Figure 1588A-B: DNA324577, XM_032902, gen.XM_032902
Figure 1589: PRO81230
Figure 1590: DNA324578, XM_032895, gen.XM_032895
Figure 1591: DNA324579, XM_084179, gen.XM_084179
Figure 1592: DNA324580, XM_041712, gen.XM_041712
Figure 1593: DNA324581, XM_116439, gen.XM_116439
Figure 1594: PRO81234
Figure 1595: DNA324582, XM_087611, gen.XM_087611
Figure 1596: DNA324583, XM_059653, gen.XM_059653
Figure 1597: DNA324584, XM_087610, gen.XM_087610
Figure 1598: DNA288259, NM_031966, gen.NM_031966
Figure 1599: PRO4676
Figure 1600: DNA324585, XM_042025, gen.XM_042025
Figure 1601: PRO81238
Figure 1602: DNA324586, NM_005713, gen.NM_005713
Figure 1603: PRO81239
Figure 1604: DNA324587, XM_059709, gen.XM_059709
Figure 1605: PRO81240
Figure 1606: DNA324588, XM_116447, gen.XM_116447
Figure 1607: PRO81241
Figure 1608: DNA324589, XM_037260, gen.XM_037260
Figure 1609: DNA324590, XM_098351, gen.XM_098351
Figure 1610: DNA324591, XM_098354, gen.XM_098354
Figure 1611: DNA324592, XM_098352, gen.XM_098352
Figure 1612: DNA324593, XM_166037, gen.XM_166037
Figure 1613: PRO81246
Figure 1614: DNA324594, XM_041694, gen.XM_041694
Figure 1615: DNA324595, XM_165488, gen.XM_165488
Figure 1616: PRO81248
Figure 1617: DNA324596, XM_059669, gen.XM_059669
Figure 1618: PRO81249
Figure 1619: DNA324597, XM_027964, gen.XM_027964
Figure 1620: PRO81250
Figure 1621: DNA324598, XM_088020, gen.XM_088020
Figure 1622: DNA324599, XM_117387, gen.XM_117387
Figure 1623: DNA324600, XM_114469, gen.XM_114469
Figure 1624: DNA324601, NM_001207, gen.NM_001207
Figure 1625: PRO22771
Figure 1626A-B: DNA324602, XM_032553, gen.XM_032553
Figure 1627: DNA254147, NM_000521, gen.NM_000521
Figure 1628: PRO49262
Figure 1629: DNA324603, NM_031482, gen.NM_031482
Figure 1630: PRO81254

Figure 1631: DNA324604, XM_087790, gen.XM_087790
Figure 1632: DNA324605, NM_001025, gen.NM_001025
Figure 1633: PRO10685
Figure 1634: DNA324606, XM_098362, gen.XM_098362
Figure 1635: PRO81256
Figure 1636: DNA324607, NM_003401, gen.NM_003401
Figure 1637: PRO70327
Figure 1638: DNA290231, NM_022550, gen.NM_022550
Figure 1639: PRO70327
Figure 1640: DNA324608, XM_017857, gen.XM_017857
Figure 1641: DNA324609, XM_117398, gen.XM_117398
Figure 1642A-B: DNA257253, NM_032280, gen.NM_032280
Figure 1643: PRO51851
Figure 1644: DNA324610, XM_003771, gen.XM_003771
Figure 1645: PRO81259
Figure 1646A-B: DNA269816, NM_002397, gen.NM_002397
Figure 1647: PRO58219
Figure 1648: DNA324611, XM_116427, gen.XM_116427
Figure 1649: PRO81260
Figure 1650: DNA324612, NM_004772, gen.NM_004772
Figure 1651: PRO81261
Figure 1652: DNA324613, XM_016674, gen.XM_016674
Figure 1653: PRO81262
Figure 1654: DNA324614, XM_113463, gen.XM_113463
Figure 1655: DNA324615, XM_034744, gen.XM_034744
Figure 1656: DNA324616, XM_087745, gen.XM_087745
Figure 1657: PRO81264
Figure 1658: DNA324617, XM_018473, gen.XM_018473
Figure 1659: PRO81265
Figure 1660: DNA324618, XM_087635, gen.XM_087635
Figure 1661: PRO81266
Figure 1662: DNA324619, XM_087637, gen.XM_087637
Figure 1663: DNA324620, XM_166027, gen.XM_166027
Figure 1664: DNA324621, NM_014035, gen.NM_014035
Figure 1665: PRO1285
Figure 1666: DNA324622, XM_003830, gen.XM_003830
Figure 1667: PRO81269
Figure 1668: DNA324623, XM_037002, gen.XM_037002
Figure 1669: DNA324624, XM_166026, gen.XM_166026
Figure 1670: DNA324625, XM_041059, gen.XM_041059
Figure 1671: DNA83020, NM_000358, gen.NM_000358
Figure 1672: PRO2561
Figure 1673: DNA324626, NM_003687, gen.NM_003687
Figure 1674: PRO81272
Figure 1675: DNA324627, XM_034862, gen.XM_034862
Figure 1676: PRO34544
Figure 1677: DNA103380, NM_003374, gen.NM_003374
Figure 1678: PRO4710
Figure 1679: DNA324628, XM_017474, gen.XM_017474
Figure 1680: PRO63082
Figure 1681A-B: DNA324629, NM_014829, gen.NM_014829
Figure 1682: PRO81273
Figure 1683A-B: DNA324630, XM_114482, gen.XM_114482
Figure 1684: PRO81274
Figure 1685: DNA324631, NM_004893, gen.NM_004893
Figure 1686: PRO81275
Figure 1687: DNA269809, NM_006805, gen.NM_006805
Figure 1688: PRO58213
Figure 1689: DNA226872, NM_001964, gen.NM_001964
Figure 1690: PRO37335
Figure 1691: DNA324632, XM_116307, gen.XM_116307
Figure 1692: PRO81276
Figure 1693: DNA324633, NM_004134, gen.NM_004134
Figure 1694: PRO81277
Figure 1695: DNA324634, XM_038221, gen.XM_038221
Figure 1696: PRO81278
Figure 1697: DNA271931, NM_005754, gen.NM_005754
Figure 1698: PRO60207
Figure 1699: DNA324635, XM_003841, gen.XM_003841
Figure 1700: DNA324636, XM_032759, gen.XM_032759
Figure 1701: DNA324637, XM_017591,

gen.XM_017591
Figure 1702: DNA324638, NM_006058, gen.NM_006058
Figure 1703: PRO81280
Figure 1704: DNA324639, NM_002084, gen.NM_002084
Figure 1705: PRO81281
Figure 1706: DNA324640, NM_018047, gen.NM_018047
Figure 1707: PRO81282
Figure 1708: DNA324641, NM_005617, gen.NM_005617
Figure 1709: PRO10849
Figure 1710: DNA324642, XM_003937, gen.XM_003937
Figure 1711: DNA324643, XM_087621, gen.XM_087621
Figure 1712A-B: DNA324644, XM_003789, gen.XM_003789
Figure 1713: DNA324645, XM_087652, gen.XM_087652
Figure 1714: DNA324646, XM_068853, gen.XM_068853
Figure 1715: PRO81286
Figure 1716: DNA324647, XM_116465, gen.XM_116465
Figure 1717: PRO81287
Figure 1718: DNA302020, NM_005573, gen.NM_005573
Figure 1719: PRO70993
Figure 1720: DNA324648, XM_113467, gen.XM_113467
Figure 1721: DNA271626, NM_014773, gen.NM_014773
Figure 1722: PRO59913
Figure 1723A-B: DNA324649, XM_056315, gen.XM_056315
Figure 1724: DNA324650, NM_024668, gen.NM_024668
Figure 1725: PRO81289
Figure 1726: DNA324651, NM_080670, gen.NM_080670
Figure 1727: PRO81290
Figure 1728A-B: DNA324652, NM_002588, gen.NM_002588
Figure 1729: PRO81291
Figure 1730A-B: DNA324653, NM_003735, gen.NM_003735
Figure 1731: PRO81292
Figure 1732A-B: DNA150679, NM_003736, gen.NM_003736
Figure 1733: PRO12416
Figure 1734A-B: DNA324654, NM_018912, gen.NM_018912
Figure 1735: PRO36058
Figure 1736A-B: DNA324655, NM_018913, gen.NM_018913
Figure 1737: PRO81293
Figure 1738A-B: DNA324656, NM_018914, gen.NM_018914
Figure 1739: PRO81294
Figure 1740A-B: DNA324657, NM_018915, gen.NM_018915
Figure 1741: PRO36020
Figure 1742A-B: DNA324658, NM_018916, gen.NM_018916
Figure 1743: PRO81295
Figure 1744A-B: DNA324659, NM_018917, gen.NM_018917
Figure 1745: PRO81296
Figure 1746A-B: DNA324660, NM_018918, gen.NM_018918
Figure 1747: PRO81297
Figure 1748A-B: DNA324661, NM_018919, gen.NM_018919
Figure 1749: PRO81298
Figure 1750A-B: DNA324662, NM_018920, gen.NM_018920
Figure 1751: PRO81299
Figure 1752A-B: DNA324663, NM_018921, gen.NM_018921
Figure 1753: PRO81300
Figure 1754A-B: DNA324664, NM_018922, gen.NM_018922
Figure 1755: PRO81301
Figure 1756A-B: DNA324665, NM_018923, gen.NM_018923
Figure 1757: PRO81302
Figure 1758A-B: DNA324666, NM_018924, gen.NM_018924
Figure 1759: PRO81303
Figure 1760A-B: DNA324667, NM_018925, gen.NM_018925
Figure 1761: PRO81304
Figure 1762A-B: DNA324668, NM_018926, gen.NM_018926
Figure 1763: PRO81305
Figure 1764A-B: DNA324669, NM_018927, gen.NM_018927
Figure 1765: PRO37091
Figure 1766A-B: DNA324670, NM_018928, gen.NM_018928
Figure 1767: PRO81306
Figure 1768A-B: DNA324671, NM_018929, gen.NM_018929
Figure 1769: PRO81307
Figure 1770A-B: DNA324672, NM_032088, gen.NM_032088
Figure 1771: PRO81308
Figure 1772A-B: DNA324673, NM_032092, gen.NM_032092
Figure 1773: PRO81309

Figure 1774: DNA324674, NM_032403, gen.NM_032403
Figure 1775: PRO81310
Figure 1776: DNA324675, NM_032402, gen.NM_032402
Figure 1777: PRO81311
Figure 1778: DNA324676, XM_098387, gen.XM_098387
Figure 1779: DNA324677, NM_002109, gen.NM_002109
Figure 1780: PRO4908
Figure 1781: DNA324678, XM_084180, gen.XM_084180
Figure 1782: PRO81313
Figure 1783: DNA324679, XM_039975, gen.XM_039975
Figure 1784: PRO81314
Figure 1785: DNA324680, NM_033551, gen.NM_033551
Figure 1786: PRO81315
Figure 1787: DNA324681, NM_004821, gen.NM_004821
Figure 1788: PRO81316
Figure 1789: DNA324682, XM_068395, gen.XM_068395
Figure 1790: PRO81317
Figure 1791: DNA226418, NM_004060, gen.NM_004060
Figure 1792: PRO36881
Figure 1793A-B: DNA324683, XM_056963, gen.XM_056963
Figure 1794: PRO81318
Figure 1795: DNA324684, NM_004219, gen.NM_004219
Figure 1796: PRO81319
Figure 1797: DNA324685, XM_094243, gen.XM_094243
Figure 1798A-B: DNA324686, XM_047964, gen.XM_047964
Figure 1799: DNA324687, XM_016345, gen.XM_016345
Figure 1800: DNA324688, NM_002887, gen.NM_002887
Figure 1801: PRO81323
Figure 1802: DNA324689, XM_166029, gen.XM_166029
Figure 1803: DNA324690, NM_002520, gen.NM_002520
Figure 1804: PRO58993
Figure 1805: DNA324691, XM_043340, gen.XM_043340
Figure 1806: PRO81325
Figure 1807: DNA324692, XM_116340, gen.XM_116340
Figure 1808A-B: DNA324693, XM_043388, gen.XM_043388
Figure 1809: PRO81327
Figure 1810: DNA324694, XM_116856, gen.XM_116856
Figure 1811: DNA324695, XM_003716, gen.XM_003716
Figure 1812: DNA227320, NM_003714, gen.NM_003714
Figure 1813: PRO37783
Figure 1814: DNA324696, NM_032361, gen.NM_032361
Figure 1815: PRO81330
Figure 1816: DNA324697, XM_087773, gen.XM_087773
Figure 1817: DNA324698, XM_114457, gen.XM_114457
Figure 1818: DNA324699, XM_165483, gen.XM_165483
Figure 1819: DNA324700, XM_114453, gen.XM_114453
Figure 1820: DNA324701, XM_165484, gen.XM_165484
Figure 1821: DNA324702, XM_030771, gen.XM_030771
Figure 1822: PRO19615
Figure 1823: DNA324703, XM_030777, gen.XM_030777
Figure 1824: DNA324704, XM_030782, gen.XM_030782
Figure 1825: PRO81336
Figure 1826: DNA324705, NM_030567, gen.NM_030567
Figure 1827: PRO81337
Figure 1828: DNA225909, NM_000505, gen.NM_000505
Figure 1829: PRO36372
Figure 1830: DNA274206, NM_006816, gen.NM_006816
Figure 1831: PRO62135
Figure 1832: DNA324706, NM_031300, gen.NM_031300
Figure 1833: PRO81338
Figure 1834: DNA324707, NM_013237, gen.NM_013237
Figure 1835: PRO81339
Figure 1836: DNA324708, NM_002011, gen.NM_002011
Figure 1837: PRO81340
Figure 1838: DNA324709, NM_022963, gen.NM_022963
Figure 1839: PRO81341
Figure 1840: DNA324710, XM_038946, gen.XM_038946
Figure 1841: DNA324711, XM_113454, gen.XM_113454
Figure 1842: DNA324712, XM_166028, gen.XM_166028

Figure 1843: DNA324713, NM_015043, gen.NM_015043
Figure 1844: PRO81345
Figure 1845: DNA324714, XM_113468, gen.XM_113468
Figure 1846: DNA324715, NM_014275, gen.NM_014275
Figure 1847: PRO1927
Figure 1848: DNA324716, NM_054013, gen.NM_054013
Figure 1849: PRO81347
Figure 1850: DNA270675, NM_005520, gen.NM_005520
Figure 1851: PRO59040
Figure 1852: DNA324717, NM_006098, gen.NM_006098
Figure 1853: PRO25849
Figure 1854: DNA269593, NM_005110, gen.NM_005110
Figure 1855: PRO58006
Figure 1856: DNA324718, XM_116365, gen.XM_116365
Figure 1857: DNA324719, XM_116511, gen.XM_116511
Figure 1858: DNA324720, XM_087823, gen.XM_087823
Figure 1859A-C: DNA324721, XM_053955, gen.XM_053955
Figure 1860: DNA324722, XM_113476, gen.XM_113476
Figure 1861: DNA324723, XM_116514, gen.XM_116514
Figure 1862: DNA324724, XM_094741, gen.XM_094741
Figure 1863: DNA324725, NM_025168, gen.NM_025168
Figure 1864: PRO81354
Figure 1865A-B: DNA324726, XM_165740, gen.XM_165740
Figure 1866: DNA272171, NM_002388, gen.NM_002388
Figure 1867: PRO60438
Figure 1868: DNA324727, XM_167169, gen.XM_167169
Figure 1869: PRO81355
Figure 1870: DNA324728, NM_014452, gen.NM_014452
Figure 1871: PRO868
Figure 1872: DNA324729, XM_166349, gen.XM_166349
Figure 1873: PRO81356
Figure 1874: DNA304680, NM_007355, gen.NM_007355
Figure 1875: PRO71106
Figure 1876: DNA324730, XM_165772, gen.XM_165772
Figure 1877: DNA324731, XM_168123, gen.XM_168123
Figure 1878: DNA324732, XM_166457, gen.XM_166457
Figure 1879: DNA324733, XM_166469, gen.XM_166469
Figure 1880: DNA324734, NM_018135, gen.NM_018135
Figure 1881: PRO81359
Figure 1882A-B: DNA324735, XM_166340, gen.XM_166340
Figure 1883: DNA324736, XM_087960, gen.XM_087960
Figure 1884: DNA324737, XM_166362, gen.XM_166362
Figure 1885: PRO81362
Figure 1886: DNA227204, NM_015388, gen.NM_015388
Figure 1887: PRO37667
Figure 1888: DNA324738, XM_166425, gen.XM_166425
Figure 1889: PRO81363
Figure 1890: DNA324739, NM_057161, gen.NM_057161
Figure 1891: PRO81364
Figure 1892: DNA270613, NM_006245, gen.NM_006245
Figure 1893: PRO58984
Figure 1894: DNA324740, NM_006586, gen.NM_006586
Figure 1895: PRO81365
Figure 1896: DNA324741, XM_166402, gen.XM_166402
Figure 1897: PRO81366
Figure 1898: DNA324742, NM_001760, gen.NM_001760
Figure 1899: PRO81367
Figure 1900: DNA287246, NM_004053, gen.NM_004053
Figure 1901: PRO69521
Figure 1902: DNA324743, NM_017601, gen.NM_017601
Figure 1903: PRO81368
Figure 1904: DNA275630, NM_006708, gen.NM_006708
Figure 1905: PRO63253
Figure 1906: DNA324744, NM_014341, gen.NM_014341
Figure 1907: PRO81369
Figure 1908: DNA304460, NM_016059, gen.NM_016059
Figure 1909: PRO4984
Figure 1910: DNA324745, XM_166412, gen.XM_166412
Figure 1911: PRO81370
Figure 1912: DNA304716, NM_078467,

gen.NM_078467
Figure 1913: PRO71142
Figure 1914: DNA324746, XM_166417, gen.XM_166417
Figure 1915: PRO81371
Figure 1916A-B: DNA324747, NM_003137, gen.NM_003137
Figure 1917: PRO81372
Figure 1918A-B: DNA324748, NM_004117, gen.NM_004117
Figure 1919: PRO36841
Figure 1920: DNA324749, XM_166419, gen.XM_166419
Figure 1921: DNA324750, XM_165794, gen.XM_165794
Figure 1922: DNA324751, NM_007104, gen.NM_007104
Figure 1923: PRO10360
Figure 1924: DNA324752, NM_024294, gen.NM_024294
Figure 1925: PRO81375
Figure 1926: DNA324753, NM_022758, gen.NM_022758
Figure 1927: PRO50582
Figure 1928: DNA324754, XM_168070, gen.XM_168070
Figure 1929: DNA324755, NM_012391, gen.NM_012391
Figure 1930: PRO81377
Figure 1931: DNA324756, XM_166459, gen.XM_166459
Figure 1932: DNA324757, XM_166333, gen.XM_166333
Figure 1933: PRO81379
Figure 1934: DNA324758, XM_058039, gen.XM_058039
Figure 1935: PRO81380
Figure 1936: DNA324759, XM_087990, gen.XM_087990
Figure 1937: DNA324760, XM_165743, gen.XM_165743
Figure 1938: DNA324761, XM_166360, gen.XM_166360
Figure 1939: DNA324763, XM_059801, gen.XM_059801
Figure 1940: DNA324764, XM_166363, gen.XM_166363
Figure 1941: DNA324765, XM_016857, gen.XM_016857
Figure 1942: DNA227442, NM_001350, gen.NM_001350
Figure 1943: PRO37905
Figure 1944: DNA324766, NM_005452, gen.NM_005452
Figure 1945: PRO81387
Figure 1946: DNA304661, NM_022551, gen.NM_022551
Figure 1947: PRO71088
Figure 1948: DNA324767, XM_165747, gen.XM_165747
Figure 1949: DNA324768, XM_165698, gen.XM_165698
Figure 1950: PRO4884
Figure 1951A-B: DNA324769, XM_165770, gen.XM_165770
Figure 1952: DNA287227, NM_004159, gen.NM_004159
Figure 1953: PRO69506
Figure 1954: DNA324770, XM_165717, gen.XM_165717
Figure 1955: DNA324771, XM_166480, gen.XM_166480
Figure 1956: DNA324772, XM_165801, gen.XM_165801
Figure 1957A-B: DNA324773, NM_000592, gen.NM_000592
Figure 1958: PRO36316
Figure 1959: DNA324774, NM_001710, gen.NM_001710
Figure 1960: PRO36305
Figure 1961: DNA227607, NM_005346, gen.NM_005346
Figure 1962: PRO38070
Figure 1963: DNA304668, NM_005345, gen.NM_005345
Figure 1964: PRO71095
Figure 1965: DNA324775, NM_021177, gen.NM_021177
Figure 1966: PRO81394
Figure 1967A-B: DNA272263, NM_006295, gen.NM_006295
Figure 1968: PRO70138
Figure 1969: DNA287319, NM_001288, gen.NM_001288
Figure 1970: PRO69584
Figure 1971: DNA324776, NM_001320, gen.NM_001320
Figure 1972: PRO63052
Figure 1973A-B: DNA324777, NM_004639, gen.NM_004639
Figure 1974: PRO81395
Figure 1975A-B: DNA324778, NM_080703, gen.NM_080703
Figure 1976: PRO81396
Figure 1977A-B: DNA324779, NM_080702, gen.NM_080702
Figure 1978: PRO81397
Figure 1979A-B: DNA324780, NM_004638, gen.NM_004638
Figure 1980: PRO81398
Figure 1981A-B: DNA324781, NM_080686, gen.NM_080686

Figure 1982: PRO81399
Figure 1983: DNA324782, XM_165771, gen.XM_165771
Figure 1984: DNA324783, NM_080598, gen.NM_080598
Figure 1985: PRO71125
Figure 1986: DNA304699, NM_004640, gen.NM_004640
Figure 1987: PRO71125
Figure 1988: DNA324784, XM_165765, gen.XM_165765
Figure 1989: PRO81400
Figure 1990: DNA324785, XM_087945, gen.XM_087945
Figure 1991: PRO81401
Figure 1992: DNA324786, XM_166381, gen.XM_166381
Figure 1993: PRO81402
Figure 1994: DNA324787, XM_168104, gen.XM_168104
Figure 1995: DNA324788, XM_166401, gen.XM_166401
Figure 1996: PRO81404
Figure 1997: DNA271040, NM_001517, gen.NM_001517
Figure 1998: PRO59365
Figure 1999A-B: DNA324789, XM_165738, gen.XM_165738
Figure 2000: DNA324790, XM_087939, gen.XM_087939
Figure 2001: PRO81406
Figure 2002: DNA324791, XM_166353, gen.XM_166353
Figure 2003: PRO1112
Figure 2004A-B: DNA324792, XM_166376, gen.XM_166376
Figure 2005: PRO81407
Figure 2006A-B: DNA324793, XM_165799, gen.XM_165799
Figure 2007: DNA290264, NM_025263, gen.NM_025263
Figure 2008: PRO70393
Figure 2009: DNA324794, XM_166361, gen.XM_166361
Figure 2010: PRO81409
Figure 2011: DNA324795, XM_165764, gen.XM_165764
Figure 2012: PRO81410
Figure 2013: DNA324796, XM_165758, gen.XM_165758
Figure 2014: PRO81411
Figure 2015: DNA324797, XM_166406, gen.XM_166406
Figure 2016: DNA324798, XM_165809, gen.XM_165809
Figure 2017: DNA324799, NM_018950, gen.NM_018950
Figure 2018: PRO81414
Figure 2019: DNA324800, XM_166392, gen.XM_166392
Figure 2020: PRO81415
Figure 2021: DNA324801, XM_166336, gen.XM_166336
Figure 2022: PRO81416
Figure 2023: DNA324802, XM_167128, gen.XM_167128
Figure 2024: PRO23797
Figure 2025: DNA324803, XM_167161, gen.XM_167161
Figure 2026: PRO81417
Figure 2027: DNA324804, NM_013375, gen.NM_013375
Figure 2028: PRO81418
Figure 2029: DNA324805, NM_007047, gen.NM_007047
Figure 2030: PRO81419
Figure 2031: DNA324806, XM_167179, gen.XM_167179
Figure 2032: DNA290785, NM_003107, gen.NM_003107
Figure 2033: PRO70544
Figure 2034: DNA150772, NM_003472, gen.NM_003472
Figure 2035: PRO12797
Figure 2036A-B: DNA324807, XM_165728, gen.XM_165728
Figure 2037: DNA324808, XM_165749, gen.XM_165749
Figure 2038: PRO81421
Figure 2039A-B: DNA324809, NM_004973, gen.NM_004973
Figure 2040: PRO81422
Figure 2041: DNA324810, XM_167196, gen.XM_167196
Figure 2042: DNA324811, XM_166446, gen.XM_166446
Figure 2043: PRO81424
Figure 2044A-C: DNA324812, XM_165777, gen.XM_165777
Figure 2045: DNA324813, XM_037875, gen.XM_037875
Figure 2046: PRO81426
Figure 2047: DNA324814, XM_167225, gen.XM_167225
Figure 2048: PRO81427
Figure 2049: DNA324815, XM_166357, gen.XM_166357
Figure 2050: DNA324816, NM_001069, gen.NM_001069
Figure 2051: PRO81429
Figure 2052: DNA324817, NM_001500, gen.NM_001500

Figure 2053: PRO81430
Figure 2054A-B: DNA324818, XM_166042, gen.XM_166042
Figure 2055: PRO51389
Figure 2056: DNA324819, XM_052721, gen.XM_052721
Figure 2057: DNA324820, XM_165499, gen.XM_165499
Figure 2058: DNA324821, XM_114497, gen.XM_114497
Figure 2059: DNA324822, XM_011117, gen.XM_011117
Figure 2060: DNA324823, XM_094855, gen.XM_094855
Figure 2061: PRO81435
Figure 2062: DNA324824, XM_059776, gen.XM_059776
Figure 2063: PRO81436
Figure 2064: DNA324825, XM_055641, gen.XM_055641
Figure 2065: DNA324826, XM_004151, gen.XM_004151
Figure 2066: DNA324827, NM_133645, gen.NM_133645
Figure 2067: PRO81439
Figure 2068: DNA324828, XM_097453, gen.XM_097453
Figure 2069: DNA324829, XM_029228, gen.XM_029228
Figure 2070: DNA103471, NM_006670, gen.NM_006670
Figure 2071: PRO4798
Figure 2072: DNA324830, XM_068963, gen.XM_068963
Figure 2073: PRO81441
Figure 2074: DNA324831, XM_040623, gen.XM_040623
Figure 2075: DNA324832, NM_020320, gen.NM_020320
Figure 2076: PRO81443
Figure 2077: DNA324833, NM_014107, gen.NM_014107
Figure 2078: PRO81444
Figure 2079A-B: DNA324834, XM_084204, gen.XM_084204
Figure 2080: DNA324835, XM_017517, gen.XM_017517
Figure 2081: DNA324836, NM_032929, gen.NM_032929
Figure 2082: PRO81446
Figure 2083: DNA324837, XM_003611, gen.XM_003611
Figure 2084: PRO81447
Figure 2085: DNA324838, XM_068919, gen.XM_068919
Figure 2086: PRO81448
Figure 2087: DNA324839, XM_167016, gen.XM_167016
Figure 2088: PRO81449
Figure 2089: DNA324840, XM_087855, gen.XM_087855
Figure 2090: DNA324841, XM_087853, gen.XM_087853
Figure 2091: DNA324842, XM_165669, gen.XM_165669
Figure 2092: DNA324843, XM_166303, gen.XM_166303
Figure 2093: PRO81453
Figure 2094: DNA324844, XM_167027, gen.XM_167027
Figure 2095: PRO81454
Figure 2096: DNA324845, XM_167037, gen.XM_167037
Figure 2097: PRO81455
Figure 2098: DNA324846, XM_018182, gen.XM_018182
Figure 2099: DNA227924, NM_000165, gen.NM_000165
Figure 2100: PRO38387
Figure 2101: DNA324847, XM_166310, gen.XM_166310
Figure 2102: PRO81457
Figure 2103: DNA324848, XM_168054, gen.XM_168054
Figure 2104: DNA271418, NM_003287, gen.NM_003287
Figure 2105: PRO59717
Figure 2106: DNA324849, XM_114492, gen.XM_114492
Figure 2107: DNA324850, XM_037056, gen.XM_037056
Figure 2108: DNA324851, XM_098468, gen.XM_098468
Figure 2109: PRO19933
Figure 2110: DNA324852, XM_004526, gen.XM_004526
Figure 2111: DNA324853, NM_001016, gen.NM_001016
Figure 2112: PRO81462
Figure 2113: DNA324854, XM_004297, gen.XM_004297
Figure 2114: DNA324855, XM_004256, gen.XM_004256
Figure 2115: PRO81464
Figure 2116: DNA324856, NM_014320, gen.NM_014320
Figure 2117: PRO81465
Figure 2118: DNA324857, XM_059741, gen.XM_059741
Figure 2119: DNA324858, XM_017831, gen.XM_017831
Figure 2120: PRO81467

Figure 2121: DNA324859, XM_049899, gen.XM_049899
Figure 2122: DNA324860, XM_004379, gen.XM_004379
Figure 2123A-C: DNA324861, XM_087834, gen.XM_087834
Figure 2124A-B: DNA324862, XM_087836, gen.XM_087836
Figure 2125: PRO81471
Figure 2126: DNA324863, NM_005389, gen.NM_005389
Figure 2127: PRO66279
Figure 2128A-C: DNA324864, XM_029746, gen.XM_029746
Figure 2129: PRO66282
Figure 2130: DNA324865, XM_004383, gen.XM_004383
Figure 2131: DNA324866, XM_059745, gen.XM_059745
Figure 2132: DNA324867, XM_033912, gen.XM_033912
Figure 2133: PRO81474
Figure 2134: DNA324868, XM_033910, gen.XM_033910
Figure 2135: DNA324870, NM_003181, gen.NM_003181
Figure 2136: PRO81476
Figure 2137: DNA324871, NM_002793, gen.NM_002793
Figure 2138: PRO81477
Figure 2139: DNA324872, XM_044866, gen.XM_044866
Figure 2140: DNA324873, XM_116524, gen.XM_116524
Figure 2141: DNA324874, XM_059773, gen.XM_059773
Figure 2142: DNA324875, XM_084998, gen.XM_084998
Figure 2143: PRO81481
Figure 2144: DNA324876, XM_058266, gen.XM_058266
Figure 2145: DNA324877, XM_042422, gen.XM_042422
Figure 2146A-B: DNA324878, XM_054706, gen.XM_054706
Figure 2147: DNA324879, XM_166049, gen.XM_166049
Figure 2148: DNA324880, XM_042473, gen.XM_042473
Figure 2149: PRO81486
Figure 2150: DNA324881, XM_167046, gen.XM_167046
Figure 2151: PRO23797
Figure 2152: DNA324882, XM_071937, gen.XM_071937
Figure 2153: PRO81487
Figure 2154: DNA324883, XM_087991, gen.XM_087991
Figure 2155: DNA324884, NM_005514, gen.NM_005514
Figure 2156: PRO81490
Figure 2157: DNA324885, XM_166327, gen.XM_166327
Figure 2158: PRO81491
Figure 2159: DNA324886, XM_165692, gen.XM_165692
Figure 2160: DNA324887, XM_117449, gen.XM_117449
Figure 2161: DNA324888, XM_086428, gen.XM_086428
Figure 2162: PRO81494
Figure 2163: DNA324889, NM_032350, gen.NM_032350
Figure 2164: PRO81495
Figure 2165: DNA324890, NM_013393, gen.NM_013393
Figure 2166: PRO81496
Figure 2167: DNA324891, XM_165860, gen.XM_165860
Figure 2168: DNA324892, XM_166541, gen.XM_166541
Figure 2169: PRO81498
Figure 2170A-B: DNA324893, XM_166523, gen.XM_166523
Figure 2171: PRO81499
Figure 2172: DNA324894, NM_016003, gen.NM_016003
Figure 2173: PRO81500
Figure 2174: DNA225631, NM_001101, gen.NM_001101
Figure 2175: PRO36094
Figure 2176: DNA274326, NM_003088, gen.NM_003088
Figure 2177: PRO62244
Figure 2178: DNA324895, NM_006303, gen.NM_006303
Figure 2179: PRO81501
Figure 2180: DNA324896, NM_014413, gen.NM_014413
Figure 2181: PRO60579
Figure 2182: DNA247595, NM_006908, gen.NM_006908
Figure 2183: PRO45014
Figure 2184: DNA324897, NM_006854, gen.NM_006854
Figure 2185: PRO12468
Figure 2186: DNA324898, NM_024067, gen.NM_024067
Figure 2187: PRO81502
Figure 2188: DNA324899, NM_002947, gen.NM_002947
Figure 2189: PRO81503

Figure 2190: DNA324900, XM_166531, gen.XM_166531
Figure 2191: DNA324901, XM_166540, gen.XM_166540
Figure 2192: PRO81505
Figure 2193: DNA193955, NM_002489, gen.NM_002489
Figure 2194: PRO23362
Figure 2195: DNA324902, XM_088264, gen.XM_088264
Figure 2196: PRO81506
Figure 2197: DNA324903, XM_165841, gen.XM_165841
Figure 2198: DNA324904, XM_166521, gen.XM_166521
Figure 2199: PRO81508
Figure 2200: DNA324905, XM_166506, gen.XM_166506
Figure 2201: PRO81509
Figure 2202: DNA324906, XM_166505, gen.XM_166505
Figure 2203: DNA324907, XM_166514, gen.XM_166514
Figure 2204: DNA324908, XM_166515, gen.XM_166515
Figure 2205: DNA324909, XM_166512, gen.XM_166512
Figure 2206: DNA227929, NM_019059, gen.NM_019059
Figure 2207: PRO38392
Figure 2208A-B: DNA324910, NM_018947, gen.NM_018947
Figure 2209: PRO81514
Figure 2210: DNA324911, NM_002137, gen.NM_002137
Figure 2211: PRO81515
Figure 2212: DNA324912, NM_031243, gen.NM_031243
Figure 2213: PRO6373
Figure 2214: DNA324913, NM_007276, gen.NM_007276
Figure 2215: PRO81516
Figure 2216: DNA324914, NM_016587, gen.NM_016587
Figure 2217: PRO81517
Figure 2218: DNA324915, XM_040853, gen.XM_040853
Figure 2219: DNA324916, XM_166509, gen.XM_166509
Figure 2220: DNA324917, XM_166513, gen.XM_166513
Figure 2221: PRO81520
Figure 2222: DNA324918, XM_166504, gen.XM_166504
Figure 2223: PRO81521
Figure 2224: DNA324919, XM_166494, gen.XM_166494
Figure 2225: DNA324920, XM_107825, gen.XM_107825
Figure 2226A-B: DNA324921, NM_022748, gen.NM_022748
Figure 2227: PRO81523
Figure 2228: DNA324922, NM_000598, gen.NM_000598
Figure 2229: PRO119
Figure 2230A-B: DNA324923, XM_166594, gen.XM_166594
Figure 2231: PRO81524
Figure 2232A-B: DNA275334, NM_030900, gen.NM_030900
Figure 2233: PRO63009
Figure 2234: DNA324924, NM_031443, gen.NM_031443
Figure 2235: PRO81525
Figure 2236: DNA324925, NM_012412, gen.NM_012412
Figure 2237: PRO61812
Figure 2238: DNA324926, NM_021130, gen.NM_021130
Figure 2239: PRO7427
Figure 2240A-B: DNA324927, XM_165877, gen.XM_165877
Figure 2241: PRO81526
Figure 2242: DNA227268, NM_019082, gen.NM_019082
Figure 2243: PRO37731
Figure 2244: DNA324928, XM_015258, gen.XM_015258
Figure 2245: DNA324929, XM_165870, gen.XM_165870
Figure 2246: DNA273865, NM_006230, gen.NM_006230
Figure 2247: PRO61824
Figure 2248A-B: DNA324930, XM_165882, gen.XM_165882
Figure 2249: DNA324931, XM_165867, gen.XM_165867
Figure 2250: PRO61688
Figure 2251: DNA324932, NM_014063, gen.NM_014063
Figure 2252: PRO81529
Figure 2253: DNA324933, XM_165872, gen.XM_165872
Figure 2254: DNA304707, NM_002787, gen.NM_002787
Figure 2255: PRO71133
Figure 2256: DNA324934, XM_016733, gen.XM_016733
Figure 2257: PRO81531
Figure 2258: DNA324935, XM_165876, gen.XM_165876
Figure 2259A-B: DNA324936, NM_014800,

gen.NM_014800
Figure 2260: DNA324937, NM_130442, gen.NM_130442
Figure 2261: PRO81534
Figure 2262: DNA226416, NM_000385, gen.NM_000385
Figure 2263: PRO36879
Figure 2264A-B: DNA324938, XM_167339, gen.XM_167339
Figure 2265: DNA287189, NM_002047, gen.NM_002047
Figure 2266: PRO69475
Figure 2267: DNA324939, XM_170195, gen.XM_170195
Figure 2268: PRO81536
Figure 2269: DNA324940, XM_168378, gen.XM_168378
Figure 2270: PRO81537
Figure 2271: DNA324941, XM_168354, gen.XM_168354
Figure 2272: PRO81538
Figure 2273: DNA324942, XM_167494, gen.XM_167494
Figure 2274: DNA103588, NM_001762, gen.NM_001762
Figure 2275: PRO4912
Figure 2276: DNA324943, XM_037741, gen.XM_037741
Figure 2277: PRO81540
Figure 2278: DNA324944, XM_050265, gen.XM_050265
Figure 2279: PRO81541
Figure 2280: DNA324945, XM_017483, gen.XM_017483
Figure 2281A-B: DNA324946, XM_018359, gen.XM_018359
Figure 2282: DNA324947, XM_059876, gen.XM_059876
Figure 2283: PRO81544
Figure 2284: DNA324948, NM_032951, gen.NM_032951
Figure 2285: PRO81545
Figure 2286: DNA324949, NM_032953, gen.NM_032953
Figure 2287: PRO81546
Figure 2288: DNA324950, NM_022170, gen.NM_022170
Figure 2289: PRO81547
Figure 2290: DNA324951, NM_031992, gen.NM_031992
Figure 2291: PRO81548
Figure 2292: DNA324952, XM_004901, gen.XM_004901
Figure 2293: DNA324953, NM_016328, gen.NM_016328
Figure 2294: PRO81550
Figure 2295A-B: DNA324954, NM_032999, gen.NM_032999
Figure 2296: PRO81551
Figure 2297: DNA324955, XM_088239, gen.XM_088239
Figure 2298: PRO81552
Figure 2299A-B: DNA324956, XM_167500, gen.XM_167500
Figure 2300A-B: DNA324957, XM_167504, gen.XM_167504
Figure 2301: DNA324958, XM_167498, gen.XM_167498
Figure 2302: DNA324959, XM_168454, gen.XM_168454
Figure 2303: PRO81556
Figure 2304: DNA324960, NM_031925, gen.NM_031925
Figure 2305: PRO81557
Figure 2306: DNA324961, NM_005918, gen.NM_005918
Figure 2307: PRO81558
Figure 2308: DNA304710, NM_001540, gen.NM_001540
Figure 2309: PRO71136
Figure 2310: DNA324962, XM_168470, gen.XM_168470
Figure 2311: DNA324963, XM_168461, gen.XM_168461
Figure 2312A-B: DNA324964, XM_167502, gen.XM_167502
Figure 2313: DNA324965, XM_017442, gen.XM_017442
Figure 2314: PRO81561
Figure 2315: DNA324966, XM_168450, gen.XM_168450
Figure 2316: DNA324967, XM_168435, gen.XM_168435
Figure 2317: DNA324968, XM_168464, gen.XM_168464
Figure 2318: DNA324969, XM_170427, gen.XM_170427
Figure 2319A-B: DNA324971, NM_015068, gen.NM_015068
Figure 2320: PRO81566
Figure 2321A-B: DNA324972, XM_167476, gen.XM_167476
Figure 2322: DNA324973, XM_168181, gen.XM_168181
Figure 2323: DNA324974, XM_168251, gen.XM_168251
Figure 2324: PRO81569
Figure 2325: DNA324975, XM_167477, gen.XM_167477
Figure 2326: DNA324976, NM_005837, gen.NM_005837
Figure 2327: PRO81571

Figure 2328: DNA324977, XM_167483, gen.XM_167483
Figure 2329: DNA324978, XM_167484, gen.XM_167484
Figure 2330: PRO81572
Figure 2331: DNA324979, NM_030935, gen.NM_030935
Figure 2332: PRO81573
Figure 2333: DNA324980, NM_019606, gen.NM_019606
Figure 2334: PRO81574
Figure 2335: DNA324981, NM_024070, gen.NM_024070
Figure 2336: PRO81575
Figure 2337: DNA324982, XM_084241, gen.XM_084241
Figure 2338: DNA324983, NM_006833, gen.NM_006833
Figure 2339: PRO22897
Figure 2340: DNA324984, NM_032164, gen.NM_032164
Figure 2341: PRO81578
Figure 2342: DNA304801, NM_004889, gen.NM_004889
Figure 2343: PRO71211
Figure 2344: DNA324985, NM_006693, gen.NM_006693
Figure 2345: PRO81579
Figure 2346: DNA324986, XM_165839, gen.XM_165839
Figure 2347: PRO81580
Figure 2348: DNA272090, NM_005720, gen.NM_005720
Figure 2349: PRO60360
Figure 2350: DNA324987, XM_165836, gen.XM_165836
Figure 2351A-B: DNA324988, XM_166482, gen.XM_166482
Figure 2352: DNA324989, XM_088180, gen.XM_088180
Figure 2353A-B: DNA324990, XM_166485, gen.XM_166485
Figure 2354: PRO81584
Figure 2355: DNA324991, NM_001673, gen.NM_001673
Figure 2356: PRO81585
Figure 2357: DNA324992, NM_133436, gen.NM_133436
Figure 2358: PRO81586
Figure 2359: DNA324993, XM_168586, gen.XM_168586
Figure 2360: PRO81587
Figure 2361: DNA83141, NM_000602, gen.NM_000602
Figure 2362: PRO2604
Figure 2363: DNA324994, NM_057089, gen.NM_057089
Figure 2364: PRO81588
Figure 2365: DNA324995, NM_001283, gen.NM_001283
Figure 2366: PRO41882
Figure 2367: DNA324996, NM_003378, gen.NM_003378
Figure 2368: PRO81589
Figure 2369: DNA324997, NM_001084, gen.NM_001084
Figure 2370: PRO58437
Figure 2371: DNA270711, NM_006349, gen.NM_006349
Figure 2372: PRO59074
Figure 2373: DNA324998, NM_024653, gen.NM_024653
Figure 2374: PRO81590
Figure 2375: DNA324999, XM_168548, gen.XM_168548
Figure 2376: DNA325000, NM_032958, gen.NM_032958
Figure 2377: PRO81591
Figure 2378: DNA325001, NM_002803, gen.NM_002803
Figure 2379: PRO81592
Figure 2380: DNA325002, XM_168572, gen.XM_168572
Figure 2381: DNA325003, XM_071605, gen.XM_071605
Figure 2382: PRO81594
Figure 2383: DNA325004, XM_033876, gen.XM_033876
Figure 2384: PRO81595
Figure 2385A-B: DNA325005, XM_027214, gen.XM_027214
Figure 2386: DNA325006, XM_088073, gen.XM_088073
Figure 2387: DNA325007, XM_072430, gen.XM_072430
Figure 2388: PRO81598
Figure 2389: DNA325008, XM_050430, gen.XM_050430
Figure 2390: PRO81599
Figure 2391: DNA325009, NM_001753, gen.NM_001753
Figure 2392: PRO81600
Figure 2393: DNA226560, NM_006136, gen.NM_006136
Figure 2394: PRO37023
Figure 2395: DNA325010, XM_012284, gen.XM_012284
Figure 2396: DNA325011, NM_005000, gen.NM_005000
Figure 2397: PRO59380
Figure 2398: DNA325012, NM_001662, gen.NM_001662

Figure 2399: PRO39773
Figure 2400: DNA325013, XM_011618, gen.XM_011618
Figure 2401: PRO81602
Figure 2402: DNA325014, XM_004627, gen.XM_004627
Figure 2403: DNA325015, XM_045401, gen.XM_045401
Figure 2404: DNA325016, XM_114602, gen.XM_114602
Figure 2405: PRO81605
Figure 2406: DNA325017, XM_117481, gen.XM_117481
Figure 2407A-C: DNA325018, XM_045856, gen.XM_045856
Figure 2408: PRO81607
Figure 2409A-B: DNA325019, XM_088105, gen.XM_088105
Figure 2410: PRO81608
Figure 2411: DNA325020, XM_011548, gen.XM_011548
Figure 2412: PRO81609
Figure 2413: DNA325021, XM_045952, gen.XM_045952
Figure 2414: DNA325022, XM_046001, gen.XM_046001
Figure 2415: PRO81611
Figure 2416: DNA325023, XM_088099, gen.XM_088099
Figure 2417: DNA325024, XM_040498, gen.XM_040498
Figure 2418: DNA325025, XM_088103, gen.XM_088103
Figure 2419: PRO81614
Figure 2420: DNA325026, XM_088122, gen.XM_088122
Figure 2421: PRO81615
Figure 2422: DNA325027, XM_088119, gen.XM_088119
Figure 2423: DNA325028, NM_001628, gen.NM_001628
Figure 2424: PRO81617
Figure 2425: DNA325029, NM_020299, gen.NM_020299
Figure 2426: PRO81618
Figure 2427: DNA325030, NM_024033, gen.NM_024033
Figure 2428: PRO81619
Figure 2429: DNA325031, XM_114555, gen.XM_114555
Figure 2430: DNA325032, XM_059839, gen.XM_059839
Figure 2431: PRO81621
Figure 2432: DNA325033, XM_095146, gen.XM_095146
Figure 2433: DNA325034, XM_016700, gen.XM_016700
Figure 2434: DNA325035, XM_042781, gen.XM_042781
Figure 2435: DNA304685, NM_003143, gen.NM_003143
Figure 2436: PRO71111
Figure 2437: DNA325036, NM_018238, gen.NM_018238
Figure 2438: PRO81625
Figure 2439: DNA325037, XM_035107, gen.XM_035107
Figure 2440: DNA325038, NM_003461, gen.NM_003461
Figure 2441: PRO10194
Figure 2442: DNA325039, NM_004911, gen.NM_004911
Figure 2443: PRO2733
Figure 2444A-B: DNA325040, XM_114578, gen.XM_114578
Figure 2445: PRO81627
Figure 2446: DNA325041, XM_088135, gen.XM_088135
Figure 2447: DNA325042, XM_098654, gen.XM_098654
Figure 2448: PRO81629
Figure 2449: DNA325043, NM_023942, gen.NM_023942
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Figure 2451: DNA325044, NM_138434, gen.NM_138434
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Figure 2453: DNA325045, XM_084238, gen.XM_084238
Figure 2454A-B: DNA325046, XM_032216, gen.XM_032216
Figure 2455A-B: DNA325047, XM_032121, gen.XM_032121
Figure 2456: DNA325048, NM_031434, gen.NM_031434
Figure 2457: PRO1555
Figure 2458: DNA226337, NM_005692, gen.NM_005692
Figure 2459: PRO36800
Figure 2460: DNA325049, NM_005614, gen.NM_005614
Figure 2461: PRO37938
Figure 2462A-B: DNA325050, NM_053043, gen.NM_053043
Figure 2463: PRO81634
Figure 2464: DNA325051, NM_022458, gen.NM_022458
Figure 2465: PRO81635
Figure 2466: DNA325052, XM_098669, gen.XM_098669
Figure 2467: DNA325053, NM_017760, gen.NM_017760

Figure 2468: PRO81637
Figure 2469: DNA325054, XM_036413, gen.XM_036413
Figure 2470A-B: DNA325055, XM_032944, gen.XM_032944
Figure 2471: DNA325056, XM_117444, gen.XM_117444
Figure 2472: DNA325057, XM_117452, gen.XM_117452
Figure 2473: DNA325058, XM_070203, gen.XM_070203
Figure 2474: PRO81641
Figure 2475: DNA325059, XM_095371, gen.XM_095371
Figure 2476: DNA325060, NM_004084, gen.NM_004084
Figure 2477: PRO2570
Figure 2478: DNA325061, NM_005217, gen.NM_005217
Figure 2479: PRO9980
Figure 2480: DNA325062, XM_070188, gen.XM_070188
Figure 2481: PRO81643
Figure 2482: DNA325063, XM_035680, gen.XM_035680
Figure 2483: DNA325064, XM_035662, gen.XM_035662
Figure 2484: PRO3344
Figure 2485: DNA325065, XM_005305, gen.XM_005305
Figure 2486: PRO81645
Figure 2487: DNA325066, XM_050293, gen.XM_050293
Figure 2488A-B: DNA325067, XM_027679, gen.XM_027679
Figure 2489: PRO81647
Figure 2490A-B: DNA325068, XM_027651, gen.XM_027651
Figure 2491: DNA274178, NM_005775, gen.NM_005775
Figure 2492: PRO62108
Figure 2493: DNA325069, XM_113557, gen.XM_113557
Figure 2494: PRO81649
Figure 2495: DNA83022, NM_001199, gen.NM_001199
Figure 2496: PRO2042
Figure 2497: DNA325070, NM_006128, gen.NM_006128
Figure 2498: PRO81650
Figure 2499: DNA325071, NM_006131, gen.NM_006131
Figure 2500: PRO81651
Figure 2501: DNA325072, NM_006132, gen.NM_006132
Figure 2502: PRO81652
Figure 2503: DNA325073, NM_025232, gen.NM_025232
Figure 2504: PRO81653
Figure 2505: DNA325074, XM_027440, gen.XM_027440
Figure 2506: DNA225671, NM_001831, gen.NM_001831
Figure 2507: PRO36134
Figure 2508: DNA325075, NM_024567, gen.NM_024567
Figure 2509: PRO81654
Figure 2510: DNA325076, NM_018250, gen.NM_018250
Figure 2511: PRO81655
Figure 2512: DNA227267, NM_018660, gen.NM_018660
Figure 2513: PRO37730
Figure 2514A-B: DNA325077, XM_095545, gen.XM_095545
Figure 2515: DNA325078, XM_088338, gen.XM_088338
Figure 2516: PRO81657
Figure 2517: DNA325079, XM_114617, gen.XM_114617
Figure 2518: PRO81658
Figure 2519: DNA325080, XM_088336, gen.XM_088336
Figure 2520: PRO81659
Figure 2521: DNA325081, XM_047083, gen.XM_047083
Figure 2522: PRO81660
Figure 2523: DNA325082, XM_114618, gen.XM_114618
Figure 2524: PRO81661
Figure 2525: DNA325083, XM_050215, gen.XM_050215
Figure 2526: DNA325084, XM_113531, gen.XM_113531
Figure 2527: DNA325085, NM_018310, gen.NM_018310
Figure 2528: PRO81664
Figure 2529: DNA325086, XM_088294, gen.XM_088294
Figure 2530: DNA325087, XM_013112, gen.XM_013112
Figure 2531: DNA325088, XM_059933, gen.XM_059933
Figure 2532: PRO1108
Figure 2533: DNA325089, XM_011629, gen.XM_011629
Figure 2534: DNA325090, NM_000930, gen.NM_000930
Figure 2535: PRO4
Figure 2536: DNA325091, NM_000931, gen.NM_000931
Figure 2537: PRO81668

Figure 2538: DNA325092, NM_033011, gen.NM_033011
Figure 2539: PRO81669
Figure 2540: DNA325093, XM_166063, gen.XM_166063
Figure 2541: DNA325094, NM_025070, gen.NM_025070
Figure 2542: PRO81671
Figure 2543A-B: DNA325095, XM_030268, gen.XM_030268
Figure 2544: DNA325096, XM_030274, gen.XM_030274
Figure 2545: PRO81673
Figure 2546: DNA151010, NM_003350, gen.NM_003350
Figure 2547: PRO12838
Figure 2548: DNA325097, XM_113540, gen.XM_113540
Figure 2549: PRO81674
Figure 2550: DNA325098, NM_006330, gen.NM_006330
Figure 2551: PRO59230
Figure 2552: DNA325099, NM_001023, gen.NM_001023
Figure 2553: PRO58263
Figure 2554: DNA325100, XM_095667, gen.XM_095667
Figure 2555: PRO81675
Figure 2556: DNA325101, XM_114640, gen.XM_114640
Figure 2557: DNA325102, XM_057780, gen.XM_057780
Figure 2558: DNA325103, XM_166064, gen.XM_166064
Figure 2559: DNA325104, XM_088399, gen.XM_088399
Figure 2560: DNA325105, XM_088401, gen.XM_088401
Figure 2561: DNA325106, XM_042658, gen.XM_042658
Figure 2562: DNA325107, XM_011769, gen.XM_011769
Figure 2563: DNA325108, XM_044627, gen.XM_044627
Figure 2564: DNA325109, XM_098761, gen.XM_098761
Figure 2565: DNA226496, NM_006837, gen.NM_006837
Figure 2566: PRO36959
Figure 2567: DNA325110, NM_014294, gen.NM_014294
Figure 2568: PRO23248
Figure 2569: DNA325111, NM_000971, gen.NM_000971
Figure 2570: PRO81685
Figure 2571: DNA325112, XM_050731, gen.XM_050731
Figure 2572: DNA325113, XM_088325, gen.XM_088325
Figure 2573: PRO81687
Figure 2574: DNA325114, XM_088323, gen.XM_088323
Figure 2575: DNA325115, NM_001444, gen.NM_001444
Figure 2576: PRO81689
Figure 2577: DNA325116, XM_013127, gen.XM_013127
Figure 2578: PRO81690
Figure 2579: DNA325117, XM_165514, gen.XM_165514
Figure 2580: PRO81691
Figure 2581: DNA325118, XM_017816, gen.XM_017816
Figure 2582: DNA325119, XM_098747, gen.XM_098747
Figure 2583: DNA325120, XM_050506, gen.XM_050506
Figure 2584: DNA325121, NM_024613, gen.NM_024613
Figure 2585: PRO81695
Figure 2586: DNA325122, XM_011642, gen.XM_011642
Figure 2587: PRO81696
Figure 2588: DNA325123, NM_000989, gen.NM_000989
Figure 2589: PRO11265
Figure 2590: DNA325124, NM_003406, gen.NM_003406
Figure 2591: PRO71091
Figure 2592: DNA325125, XM_011657, gen.XM_011657
Figure 2593: DNA131588, NM_002568, gen.NM_002568
Figure 2594: PRO7445
Figure 2595: DNA325126, XM_018287, gen.XM_018287
Figure 2596: DNA325127, NM_001568, gen.NM_001568
Figure 2597: PRO81699
Figure 2598: DNA325128, NM_003756, gen.NM_003756
Figure 2599: PRO81700
Figure 2600A-B: DNA272050, NM_006265, gen.NM_006265
Figure 2601: PRO60321
Figure 2602: DNA325129, NM_052886, gen.NM_052886
Figure 2603: PRO81701
Figure 2604: DNA325130, XM_016047, gen.XM_016047
Figure 2605: DNA325131, XM_005060, gen.XM_005060

Figure 2606: DNA325132, NM_005005, gen.NM_005005
Figure 2607: PRO81704
Figure 2608: DNA325133, XM_037657, gen.XM_037657
Figure 2609: DNA325134, XM_029567, gen.XM_029567
Figure 2610: PRO81705
Figure 2611: DNA325135, XM_088316, gen.XM_088316
Figure 2612: DNA325136, XM_051298, gen.XM_051298
Figure 2613: DNA325137, XM_088370, gen.XM_088370
Figure 2614: DNA325138, NM_016647, gen.NM_016647
Figure 2615: PRO23201
Figure 2616: DNA325139, NM_052963, gen.NM_052963
Figure 2617: PRO81708
Figure 2618: DNA325140, XM_049247, gen.XM_049247
Figure 2619: DNA325141, XM_058968, gen.XM_058968
Figure 2620: DNA325143, NM_023078, gen.NM_023078
Figure 2621: PRO81711
Figure 2622: DNA325144, XM_117487, gen.XM_117487
Figure 2623: DNA325145, XM_049226, gen.XM_049226
Figure 2624: PRO81714
Figure 2625: DNA325146, XM_114613, gen.XM_114613
Figure 2626: DNA325147, XM_035368, gen.XM_035368
Figure 2627: DNA325148, XM_113532, gen.XM_113532
Figure 2628: DNA325149, XM_088321, gen.XM_088321
Figure 2629: DNA325150, XM_035373, gen.XM_035373
Figure 2630: PRO81719
Figure 2631: DNA325151, XM_035370, gen.XM_035370
Figure 2632: PRO81720
Figure 2633: DNA325152, NM_000973, gen.NM_000973
Figure 2634: PRO22907
Figure 2635: DNA325153, NM_033301, gen.NM_033301
Figure 2636: PRO22907
Figure 2637: DNA325154, XM_049421, gen.XM_049421
Figure 2638: DNA325155, XM_034640, gen.XM_034640
Figure 2639: PRO81722
Figure 2640: DNA325156, XM_088550, gen.XM_088550
Figure 2641: DNA325157, XM_088552, gen.XM_088552
Figure 2642: DNA325158, XM_088553, gen.XM_088553
Figure 2643: PRO81725
Figure 2644: DNA325159, XM_059979, gen.XM_059979
Figure 2645: DNA325160, XM_167558, gen.XM_167558
Figure 2646: DNA325161, XM_039654, gen.XM_039654
Figure 2647: DNA325162, XM_060006, gen.XM_060006
Figure 2648: PRO81729
Figure 2649: DNA325163, NM_001122, gen.NM_001122
Figure 2650: PRO81730
Figure 2651: DNA325164, NM_001010, gen.NM_001010
Figure 2652: PRO10824
Figure 2653: DNA325165, NM_058195, gen.NM_058195
Figure 2654: PRO81731
Figure 2655: DNA325166, NM_000077, gen.NM_000077
Figure 2656: PRO36693
Figure 2657: DNA325167, NM_058196, gen.NM_058196
Figure 2658: PRO81732
Figure 2659: DNA325168, XM_017931, gen.XM_017931
Figure 2660: DNA271847, NM_001539, gen.NM_001539
Figure 2661: PRO60127
Figure 2662: DNA270991, NM_004323, gen.NM_004323
Figure 2663: PRO59321
Figure 2664: DNA325169, NM_016410, gen.NM_016410
Figure 2665: PRO81734
Figure 2666: DNA325170, XM_005543, gen.XM_005543
Figure 2667: PRO38028
Figure 2668: DNA325171, NM_001842, gen.NM_001842
Figure 2669: PRO21481
Figure 2670: DNA226345, NM_005866, gen.NM_005866
Figure 2671: PRO36808
Figure 2672: DNA325172, XM_088563, gen.XM_088563
Figure 2673: DNA325173, XM_059998, gen.XM_059998

Figure 2674: PRO59579
Figure 2675: DNA325174, NM_013442, gen.NM_013442
Figure 2676: PRO9819
Figure 2677: DNA325175, XM_114661, gen.XM_114661
Figure 2678: PRO81736
Figure 2679: DNA325176, XM_048479, gen.XM_048479
Figure 2680: DNA290319, NM_003289, gen.NM_003289
Figure 2681: PRO70595
Figure 2682A-C: DNA325177, NM_006289, gen.NM_006289
Figure 2683: PRO81738
Figure 2684: DNA325178, XM_048518, gen.XM_048518
Figure 2685: PRO81739
Figure 2686: DNA325179, XM_048539, gen.XM_048539
Figure 2687: PRO81740
Figure 2688: DNA325180, XM_114662, gen.XM_114662
Figure 2689: DNA325181, NM_001833, gen.NM_001833
Figure 2690: PRO81742
Figure 2691: DNA227491, NM_007096, gen.NM_007096
Figure 2692: PRO37954
Figure 2693: DNA254771, NM_012203, gen.NM_012203
Figure 2694: PRO49869
Figure 2695: DNA89242, NM_000700, gen.NM_000700
Figure 2696: PRO2907
Figure 2697: DNA325182, XM_041020, gen.XM_041020
Figure 2698: PRO81743
Figure 2699: DNA325183, XM_114686, gen.XM_114686
Figure 2700: DNA325184, XM_088637, gen.XM_088637
Figure 2701: DNA287216, NM_021154, gen.NM_021154
Figure 2702: PRO69496
Figure 2703: DNA288247, NM_058179, gen.NM_058179
Figure 2704: PRO70011
Figure 2705: DNA325185, XM_071178, gen.XM_071178
Figure 2706: PRO81746
Figure 2707: DNA325186, XM_005490, gen.XM_005490
Figure 2708: DNA325187, NM_031263, gen.NM_031263
Figure 2709: PRO81748
Figure 2710: DNA325188, XM_018006, gen.XM_018006
Figure 2711: DNA325189, XM_017996, gen.XM_017996
Figure 2712: DNA325190, XM_016113, gen.XM_016113
Figure 2713: PRO81751
Figure 2714: DNA272655, NM_001827, gen.NM_001827
Figure 2715: PRO60781
Figure 2716A-B: DNA325191, NM_002161, gen.NM_002161
Figure 2717: PRO81752
Figure 2718A-B: DNA325192, NM_013417, gen.NM_013417
Figure 2719: PRO81753
Figure 2720A-B: DNA325193, XM_046863, gen.XM_046863
Figure 2721: PRO81754
Figure 2722: DNA325194, XM_046836, gen.XM_046836
Figure 2723: DNA275322, NM_003837, gen.NM_003837
Figure 2724: PRO63000
Figure 2725A-B: DNA325195, XM_098943, gen.XM_098943
Figure 2726: DNA325196, XM_016308, gen.XM_016308
Figure 2727: DNA325197, XM_005525, gen.XM_005525
Figure 2728: DNA325198, NM_003389, gen.NM_003389
Figure 2729: PRO81759
Figure 2730: DNA325199, NM_033219, gen.NM_033219
Figure 2731: PRO81760
Figure 2732: DNA325200, NM_006401, gen.NM_006401
Figure 2733: PRO81761
Figure 2734: DNA272213, NM_002486, gen.NM_002486
Figure 2735: PRO60475
Figure 2736: DNA325201, NM_001333, gen.NM_001333
Figure 2737: PRO81762
Figure 2738: DNA325202, XM_116818, gen.XM_116818
Figure 2739: PRO81763
Figure 2740: DNA254543, NM_006808, gen.NM_006808
Figure 2741: PRO49648
Figure 2742: DNA325203, XM_070873, gen.XM_070873
Figure 2743: PRO81764
Figure 2744: DNA325204, XM_042788, gen.XM_042788

Figure 2745: PRO81765
Figure 2746: DNA257309, NM_032342, gen.NM_032342
Figure 2747: PRO51901
Figure 2748: DNA325205, XM_088569, gen.XM_088569
Figure 2749: PRO81766
Figure 2750: DNA325206, XM_088571, gen.XM_088571
Figure 2751: DNA271722, NM_004697, gen.NM_004697
Figure 2752: PRO60006
Figure 2753: DNA325207, NM_017443, gen.NM_017443
Figure 2754: PRO81768
Figure 2755A-C: DNA325208, XM_005348, gen.XM_005348
Figure 2756: DNA325209, XM_114646, gen.XM_114646
Figure 2757: DNA325210, XM_038391, gen.XM_038391
Figure 2758: PRO81771
Figure 2759A-B: DNA325211, XM_045296, gen.XM_045296
Figure 2760: DNA325212, XM_005365, gen.XM_005365
Figure 2761: DNA289530, NM_004435, gen.NM_004435
Figure 2762: PRO70290
Figure 2763: DNA287271, NM_032799, gen.NM_032799
Figure 2764: PRO69542
Figure 2765: DNA325213, XM_026987, gen.XM_026987
Figure 2766: DNA325214, XM_026985, gen.XM_026985
Figure 2767: DNA225630, NM_016174, gen.NM_016174
Figure 2768: PRO36093
Figure 2769: DNA325215, XM_026968, gen.XM_026968
Figure 2770: PRO81775
Figure 2771: DNA325216, XM_026951, gen.XM_026951
Figure 2772: DNA325217, NM_025072, gen.NM_025072
Figure 2773: PRO33818
Figure 2774: DNA325218, XM_033424, gen.XM_033424
Figure 2775: DNA325219, NM_004957, gen.NM_004957
Figure 2776: PRO81778
Figure 2777: DNA325220, XM_033457, gen.XM_033457
Figure 2778A-B: DNA325221, XM_033460, gen.XM_033460
Figure 2779: PRO81780
Figure 2780: DNA325222, NM_000976, gen.NM_000976
Figure 2781: PRO62236
Figure 2782: DNA218841, NM_012098, gen.NM_012098
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Figure 2787: DNA325225, XM_026944, gen.XM_026944
Figure 2788: PRO81783
Figure 2789: DNA325226, XM_116806, gen.XM_116806
Figure 2790A-B: DNA325227, NM_005347, gen.NM_005347
Figure 2791: PRO81785
Figure 2792: DNA325228, NM_005833, gen.NM_005833
Figure 2793: PRO81786
Figure 2794: DNA325229, NM_007209, gen.NM_007209
Figure 2795: PRO61897
Figure 2796: DNA88350, NM_000177, gen.NM_000177
Figure 2797: PRO2758
Figure 2798A-B: DNA325230, XM_011749, gen.XM_011749
Figure 2799: DNA325231, XM_114679, gen.XM_114679
Figure 2800: DNA325232, XM_087041, gen.XM_087041
Figure 2801: DNA325233, XM_114678, gen.XM_114678
Figure 2802: DNA325234, XM_114677, gen.XM_114677
Figure 2803: DNA325235, XM_087038, gen.XM_087038
Figure 2804: DNA325236, XM_059637, gen.XM_059637
Figure 2805: PRO81792
Figure 2806: DNA325237, NM_000368, gen.NM_000368
Figure 2807: PRO60115
Figure 2808: DNA325238, XM_033385, gen.XM_033385
Figure 2809A-B: DNA325239, XM_033380, gen.XM_033380
Figure 2810: PRO81794
Figure 2811: DNA325240, XM_033362, gen.XM_033362
Figure 2812: PRO81795
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gen.XM_059986
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Figure 2816: PRO81797
Figure 2817A-B: DNA325243, XM_033360, gen.XM_033360
Figure 2818: DNA325244, XM_033359, gen.XM_033359
Figure 2819A-B: DNA325245, XM_033355, gen.XM_033355
Figure 2820: DNA325246, NM_014285, gen.NM_014285
Figure 2821: PRO81800
Figure 2822: DNA325247, NM_054012, gen.NM_054012
Figure 2823: PRO81801
Figure 2824: DNA325248, XM_035103, gen.XM_035103
Figure 2825: DNA325249, XM_035109, gen.XM_035109
Figure 2826: DNA325250, NM_000972, gen.NM_000972
Figure 2827: PRO81804
Figure 2828: DNA325251, NM_033161, gen.NM_033161
Figure 2829: PRO81805
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Figure 2831: PRO81806
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Figure 2833: DNA325254, XM_088426, gen.XM_088426
Figure 2834: DNA325255, NM_002003, gen.NM_002003
Figure 2835: PRO1910
Figure 2836: DNA325256, NM_058199, gen.NM_058199
Figure 2837: PRO81809
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Figure 2839: DNA325258, XM_088422, gen.XM_088422
Figure 2840: PRO81811
Figure 2841: DNA325259, XM_029168, gen.XM_029168
Figure 2842: PRO81812
Figure 2843: DNA325260, XM_098913, gen.XM_098913
Figure 2844: PRO81813
Figure 2845: DNA325261, XM_114669, gen.XM_114669
Figure 2846: DNA325262, XM_113564, gen.XM_113564
Figure 2847A-B: DNA325263, XM_088459, gen.XM_088459
Figure 2848: PRO81815
Figure 2849: DNA325264, XM_054752, gen.XM_054752
Figure 2850: PRO81816
Figure 2851: DNA325265, XM_084270, gen.XM_084270
Figure 2852: DNA325266, XM_054763, gen.XM_054763
Figure 2853: PRO81817
Figure 2854: DNA325267, XM_114655, gen.XM_114655
Figure 2855: DNA325268, XM_038030, gen.XM_038030
Figure 2856: PRO59351
Figure 2857: DNA325269, XM_072526, gen.XM_072526
Figure 2858: PRO81819
Figure 2859: DNA325270, XM_059961, gen.XM_059961
Figure 2860: DNA325271, NM_032928, gen.NM_032928
Figure 2861: PRO81821
Figure 2862: DNA325272, NM_014172, gen.NM_014172
Figure 2863: PRO81822
Figure 2864: DNA325273, XM_038049, gen.XM_038049
Figure 2865: PRO62069
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Figure 2867: PRO81823
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Figure 2870: DNA325276, XM_088461, gen.XM_088461
Figure 2871: DNA325277, XM_059966, gen.XM_059966
Figure 2872: PRO81826
Figure 2873: DNA325278, XM_114649, gen.XM_114649
Figure 2874: DNA325279, XM_117519, gen.XM_117519
Figure 2875: DNA325280, XM_053206, gen.XM_053206
Figure 2876: DNA325281, XM_040272, gen.XM_040272
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Figure 2879: DNA325283, XM_040267, gen.XM_040267
Figure 2880: PRO81831
Figure 2881: DNA325284, XM_048859, gen.XM_048859

Figure 2882: PRO62617
Figure 2883: DNA325285, NM_003739, gen.NM_003739
Figure 2884: PRO81832
Figure 2885: DNA325286, XM_060976, gen.XM_060976
Figure 2886: PRO81833
Figure 2887: DNA325287, XM_167626, gen.XM_167626
Figure 2888: PRO81834
Figure 2889: DNA325288, XM_165555, gen.XM_165555
Figure 2890: PRO81835
Figure 2891: DNA325289, NM_001494, gen.NM_001494
Figure 2892: PRO81836
Figure 2893: DNA325290, NM_032905, gen.NM_032905
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Figure 2895: DNA325291, NM_005174, gen.NM_005174
Figure 2896: PRO81838
Figure 2897: DNA325292, XM_165557, gen.XM_165557
Figure 2898: DNA325293, XM_167374, gen.XM_167374
Figure 2899: DNA273759, NM_006023, gen.NM_006023
Figure 2900: PRO61721
Figure 2901: DNA325294, XM_167411, gen.XM_167411
Figure 2902: DNA325295, NM_031453, gen.NM_031453
Figure 2903: PRO81841
Figure 2904: DNA325296, XM_167414, gen.XM_167414
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Figure 2922: DNA325308, XM_166157, gen.XM_166157
Figure 2923: DNA325309, NM_032023, gen.NM_032023
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Figure 2925: DNA325310, XM_165560, gen.XM_165560
Figure 2926: DNA325311, XM_165563, gen.XM_165563
Figure 2927: DNA325312, XM_113615, gen.XM_113615
Figure 2928: PRO81855
Figure 2929: DNA325313, XM_165890, gen.XM_165890
Figure 2930: DNA325314, XM_061126, gen.XM_061126
Figure 2931: DNA325315, XM_061125, gen.XM_061125
Figure 2932: PRO81858
Figure 2933: DNA325316, XM_054474, gen.XM_054474
Figure 2934: DNA325317, XM_165888, gen.XM_165888
Figure 2935: DNA325318, XM_054475, gen.XM_054475
Figure 2936: PRO81861
Figure 2937: DNA325319, XM_015652, gen.XM_015652
Figure 2938: PRO81862
Figure 2939: DNA325320, XM_036593, gen.XM_036593
Figure 2940: PRO81863
Figure 2941: DNA325321, XM_165891, gen.XM_165891
Figure 2942: DNA325322, XM_084450, gen.XM_084450
Figure 2943: PRO81865
Figure 2944: DNA325323, XM_084385, gen.XM_084385
Figure 2945: DNA325324, NM_021226, gen.NM_021226
Figure 2946: PRO81867
Figure 2947: DNA193957, NM_003055, gen.NM_003055
Figure 2948: PRO23364
Figure 2949: DNA325325, NM_032997, gen.NM_032997
Figure 2950: PRO81868

Figure 2951: DNA287642, NM_018464, gen.NM_018464
Figure 2952: PRO9902
Figure 2953: DNA325326, XM_084451, gen.XM_084451
Figure 2954: PRO81869
Figure 2955: DNA325327, NM_012207, gen.NM_012207
Figure 2956: PRO81870
Figure 2957: DNA325328, NM_024045, gen.NM_024045
Figure 2958: PRO81871
Figure 2959: DNA325329, NM_004728, gen.NM_004728
Figure 2960: PRO81872
Figure 2961: DNA88562, NM_002727, gen.NM_002727
Figure 2962: PRO2842
Figure 2963: DNA325330, XM_167395, gen.XM_167395
Figure 2964: DNA227172, NM_021129, gen.NM_021129
Figure 2965: PRO37635
Figure 2966A-B: DNA325331, XM_166125, gen.XM_166125
Figure 2967: PRO81874
Figure 2968: DNA325332, XM_044354, gen.XM_044354
Figure 2969: PRO81875
Figure 2970: DNA325333, XM_032520, gen.XM_032520
Figure 2971: DNA325334, NM_019058, gen.NM_019058
Figure 2972: PRO81877
Figure 2973: DNA325335, XM_045140, gen.XM_045140
Figure 2974: PRO2875
Figure 2975: DNA325336, XM_116863, gen.XM_116863
Figure 2976: DNA325337, XM_032476, gen.XM_032476
Figure 2977: DNA325338, XM_114894, gen.XM_114894
Figure 2978: DNA325339, NM_033022, gen.NM_033022
Figure 2979: PRO81881
Figure 2980: DNA325340, NM_001026, gen.NM_001026
Figure 2981: PRO11139
Figure 2982: DNA103421, NM_003375, gen.NM_003375
Figure 2983: PRO4749
Figure 2984A-B: DNA325341, XM_166093, gen.XM_166093
Figure 2985: PRO81882
Figure 2986: DNA304459, NM_005729, gen.NM_005729
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Figure 2988: DNA325342, XM_166629, gen.XM_166629
Figure 2989: PRO81883
Figure 2990: DNA103506, NM_001157, gen.NM_001157
Figure 2991: PRO4833
Figure 2992: DNA325343, XM_016093, gen.XM_016093
Figure 2993: PRO81884
Figure 2994: DNA325344, XM_084467, gen.XM_084467
Figure 2995: PRO81885
Figure 2996: DNA304488, NM_032333, gen.NM_032333
Figure 2997: PRO71057
Figure 2998: DNA325345, XM_043589, gen.XM_043589
Figure 2999: DNA325346, XM_043605, gen.XM_043605
Figure 3000: DNA325347, XM_087480, gen.XM_087480
Figure 3001: PRO81887
Figure 3002: DNA325348, NM_002921, gen.NM_002921
Figure 3003: PRO81888
Figure 3004: DNA226217, NM_005271, gen.NM_005271
Figure 3005: PRO36680
Figure 3006: DNA325349, XM_089551, gen.XM_089551
Figure 3007: PRO81889
Figure 3008: DNA287237, NM_001613, gen.NM_001613
Figure 3009: PRO39648
Figure 3010: DNA325350, XM_084477, gen.XM_084477
Figure 3011: PRO69523
Figure 3012: DNA325351, XM_084480, gen.XM_084480
Figure 3013A-B: DNA325352, NM_013451, gen.NM_013451
Figure 3014: PRO12813
Figure 3015: DNA325353, XM_018167, gen.XM_018167
Figure 3016: DNA325354, XM_084372, gen.XM_084372
Figure 3017: DNA325355, NM_020992, gen.NM_020992
Figure 3018: PRO81893
Figure 3019: DNA325356, XM_089514, gen.XM_089514
Figure 3020A-B: DNA325357, XM_058343, gen.XM_058343
Figure 3021: PRO81895

Figure 3022: DNA325358, XM_058602, gen.XM_058602
Figure 3023: PRO81896
Figure 3024A-B: DNA325359, NM_015179, gen.NM_015179
Figure 3025: PRO81897
Figure 3026: DNA325360, XM_083842, gen.XM_083842
Figure 3027: PRO69473
Figure 3028: DNA325361, XM_084413, gen.XM_084413
Figure 3029: DNA325362, NM_022362, gen.NM_022362
Figure 3030: PRO81899
Figure 3031: DNA325363, NM_032112, gen.NM_032112
Figure 3032: PRO81900
Figure 3033: DNA325364, NM_021830, gen.NM_021830
Figure 3034: PRO81901
Figure 3035A-B: DNA325365, XM_046743, gen.XM_046743
Figure 3036: PRO81902
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Figure 3038: PRO81903
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Figure 3040: PRO81904
Figure 3041A-B: DNA325368, XM_031866, gen.XM_031866
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Figure 3043: PRO81905
Figure 3044A-B: DNA325370, XM_031890, gen.XM_031890
Figure 3045A-B: DNA325371, NM_004193, gen.NM_004193
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Figure 3050: PRO4900
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Figure 3052: PRO34073
Figure 3053: DNA325374, XM_005698, gen.XM_005698
Figure 3054: PRO81909
Figure 3055: DNA325375, NM_006523, gen.NM_006523
Figure 3056: PRO59043
Figure 3057: DNA325376, XM_018279, gen.XM_018279
Figure 3058A-B: DNA325377, XM_005938, gen.XM_005938
Figure 3059A-B: DNA325378, XM_031992, gen.XM_031992
Figure 3060: PRO81912
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Figure 3063: DNA325380, NM_005004, gen.NM_005004
Figure 3064: PRO81914
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Figure 3066: DNA273521, NM_002079, gen.NM_002079
Figure 3067: PRO61502
Figure 3068A-B: DNA325382, NM_032211, gen.NM_032211
Figure 3069: PRO81916
Figure 3070: DNA325383, NM_031484, gen.NM_031484
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Figure 3074A-D: DNA325386, XM_045667, gen.XM_045667
Figure 3075: DNA325387, XM_109162, gen.XM_109162
Figure 3076: DNA227509, NM_000274, gen.NM_000274
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Figure 3080: DNA325389, XM_084505, gen.XM_084505
Figure 3081: PRO81923
Figure 3082A-B: DNA325390, XM_049795, gen.XM_049795
Figure 3083: PRO81924
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Figure 3085: PRO81925
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Figure 3089: DNA325394, NM_007190, gen.NM_007190
Figure 3090: PRO81926
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Figure 3092: PRO81927

Figure 3093: DNA269952, NM_004725, gen.NM_004725
Figure 3094: PRO58348
Figure 3095: DNA325396, NM_024942, gen.NM_024942
Figure 3096: PRO81928
Figure 3097: DNA325397, NM_016567, gen.NM_016567
Figure 3098: PRO81929
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Figure 3100: PRO81930
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Figure 3102: PRO57854
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Figure 3104: DNA325400, XM_114862, gen.XM_114862
Figure 3105: PRO81932
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Figure 3107: DNA325402, NM_016526, gen.NM_016526
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Figure 3126: PRO81941
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Figure 3128: PRO81942
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Figure 3132: PRO81944
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Figure 3138: PRO69635
Figure 3139: DNA325418, XM_114981, gen.XM_114981
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Figure 3143: PRO81946
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Figure 3147: PRO81948
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Figure 3150: PRO81950
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Figure 3152: DNA325426, XM_113238, gen.XM_113238
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Figure 3159: DNA325430, XM_058414, gen.XM_058414
Figure 3160: PRO81955
Figure 3161A-B: DNA325431, XM_049197, gen.XM_049197
Figure 3162: PRO81956
Figure 3163A-B: DNA325432, NM_001418, gen.NM_001418

Figure 3164: PRO81957
Figure 3165: DNA325433, XM_096520, gen.XM_096520
Figure 3166: PRO81958
Figure 3167: DNA325434, XM_006212, gen.XM_006212
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Figure 3178: DNA325440, XM_036339, gen.XM_036339
Figure 3179: PRO81964
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Figure 3181: PRO81965
Figure 3182: DNA325442, XM_084516, gen.XM_084516
Figure 3183: DNA325443, XM_084515, gen.XM_084515
Figure 3184: DNA325444, XM_084517, gen.XM_084517
Figure 3185: DNA325445, XM_034431, gen.XM_034431
Figure 3186: PRO11691
Figure 3187: DNA325446, XM_030326, gen.XM_030326
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Figure 3189: PRO81970
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Figure 3191: PRO81971
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Figure 3193: DNA325450, XM_054856, gen.XM_054856
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Figure 3195: DNA325452, XM_084681, gen.XM_084681
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Figure 3197: DNA325454, NM_003646, gen.NM_003646
Figure 3198: PRO81977
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Figure 3223A-B: DNA325463, XM_165612, gen.XM_165612
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Figure 3233: PRO81992
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Figure 3248: DNA325476, XM_167726, gen.XM_167726
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Figure 3255: DNA325480, XM_048286, gen.XM_048286
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Figure 3295: DNA270721, NM_006842, gen.NM_006842
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Figure 3309: PRO82024
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Figure 3323: PRO61238
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Figure 3330: PRO49298
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Figure 3342A-B: DNA325529, NM_080491, gen.NM_080491
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Figure 3344A-B: DNA325530, NM_012296, gen.NM_012296
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Figure 3347: PRO82038
Figure 3348: DNA325532, NM_007173, gen.NM_007173
Figure 3349: DNA325533, XM_166239, gen.XM_166239
Figure 3350: DNA325534, XM_084610, gen.XM_084610
Figure 3351: PRO82040
Figure 3352: DNA325535, XM_058450, gen.XM_058450
Figure 3353: DNA325536, XM_084601, gen.XM_084601
Figure 3354: PRO82042
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Figure 3365: DNA325544, XM_115063, gen.XM_115063
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Figure 3374: DNA325550, NM_025164, gen.NM_025164
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Figure 3381: PRO59629
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Figure 3383: PRO82056
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Figure 3387: PRO82057
Figure 3388: DNA325555, XM_084654, gen.XM_084654
Figure 3389: PRO82058
Figure 3390: DNA272413, NM_003002, gen.NM_003002
Figure 3391: PRO60666
Figure 3392: DNA271843, NM_004398, gen.NM_004398
Figure 3393: PRO60123
Figure 3394: DNA325556, XM_017369, gen.XM_017369
Figure 3395: DNA325557, NM_032299, gen.NM_032299
Figure 3396: PRO82060
Figure 3397: DNA325558, XM_055369, gen.XM_055369
Figure 3398: DNA325559, XM_051430, gen.XM_051430
Figure 3399: DNA325560, XM_006467, gen.XM_006467
Figure 3400: DNA325561, XM_113226, gen.XM_113226
Figure 3401: DNA325562, XM_165592, gen.XM_165592
Figure 3402: PRO82064
Figure 3403: DNA325563, XM_166181, gen.XM_166181
Figure 3404: DNA325564, XM_052862, gen.XM_052862
Figure 3405: PRO82066
Figure 3406: DNA325565, XM_166177, gen.XM_166177
Figure 3407: DNA325566, XM_165571, gen.XM_165571
Figure 3408: PRO82068
Figure 3409: DNA325567, XM_166174, gen.XM_166174
Figure 3410: PRO82069
Figure 3411: DNA325568, NM_001274, gen.NM_001274
Figure 3412: PRO12187
Figure 3413: DNA325569, XM_165586, gen.XM_165586
Figure 3414: DNA325570, XM_165584, gen.XM_165584
Figure 3415: DNA257965, NM_032873, gen.NM_032873
Figure 3416: PRO52492
Figure 3417: DNA325571, XM_167780, gen.XM_167780
Figure 3418: DNA325572, XM_166743, gen.XM_166743
Figure 3419: PRO82072
Figure 3420: DNA325573, NM_012101, gen.NM_012101
Figure 3421: PRO82073
Figure 3422: DNA325574, NM_058193, gen.NM_058193
Figure 3423: PRO82074
Figure 3424: DNA325575, XM_084522, gen.XM_084522
Figure 3425: PRO82075
Figure 3426: DNA325576, XM_091786, gen.XM_091786
Figure 3427: DNA325577, XM_165390, gen.XM_165390
Figure 3428: DNA325578, XM_084525, gen.XM_084525
Figure 3429A-B: DNA325579, XM_010494, gen.XM_010494
Figure 3430A-B: DNA325580, NM_015064, gen.NM_015064
Figure 3431: PRO82078
Figure 3432: DNA325581, NM_030775, gen.NM_030775
Figure 3433: PRO71031
Figure 3434: DNA297398, NM_032642, gen.NM_032642
Figure 3435: PRO71031
Figure 3436: DNA325582, XM_017080, gen.XM_017080
Figure 3437: DNA325583, XM_113739, gen.XM_113739
Figure 3438: PRO82080
Figure 3439: DNA325584, NM_002014,

gen.NM_002014
Figure 3440: PRO59262
Figure 3441: DNA325585, XM_096661, gen.XM_096661
Figure 3442: DNA325586, NM_018463, gen.NM_018463
Figure 3443: PRO82082
Figure 3444: DNA325587, NM_021953, gen.NM_021953
Figure 3445: PRO82083
Figure 3446: DNA325588, NM_031465, gen.NM_031465
Figure 3447: PRO82084
Figure 3448: DNA325589, NM_005002, gen.NM_005002
Figure 3449: PRO82085
Figure 3450: DNA325590, XM_033227, gen.XM_033227
Figure 3451: DNA325591, XM_116926, gen.XM_116926
Figure 3452: DNA88114, NM_001734, gen.NM_001734
Figure 3453: PRO2660
Figure 3454: DNA325592, XM_058574, gen.XM_058574
Figure 3455: DNA325593, NM_007273, gen.NM_007273
Figure 3456: PRO36970
Figure 3457A-B: DNA325594, XM_032588, gen.XM_032588
Figure 3458: DNA325595, NM_001975, gen.NM_001975
Figure 3459: PRO38010
Figure 3460: DNA325596, NM_000365, gen.NM_000365
Figure 3461: PRO69549
Figure 3462: DNA325597, XM_032614, gen.XM_032614
Figure 3463: DNA325598, NM_002075, gen.NM_002075
Figure 3464: PRO82091
Figure 3465: DNA325599, XM_165910, gen.XM_165910
Figure 3466: DNA151827, NM_005439, gen.NM_005439
Figure 3467: PRO12902
Figure 3468A-B: DNA254624, NM_001273, gen.NM_001273
Figure 3469: PRO49726
Figure 3470: DNA325600, NM_015438, gen.NM_015438
Figure 3471: PRO82093
Figure 3472: DNA325601, XM_033263, gen.XM_033263
Figure 3473: DNA225632, NM_002046, gen.NM_002046
Figure 3474: PRO36095
Figure 3475A-B: DNA325602, XM_006958, gen.XM_006958
Figure 3476: DNA83180, NM_002342, gen.NM_002342
Figure 3477: PRO2622
Figure 3478: DNA103514, NM_001038, gen.NM_001038
Figure 3479: PRO4841
Figure 3480: DNA188396, NM_001065, gen.NM_001065
Figure 3481: PRO21924
Figure 3482A-C: DNA325603, XM_006947, gen.XM_006947
Figure 3483A-B: DNA325604, XM_006936, gen.XM_006936
Figure 3484: PRO82097
Figure 3485A-B: DNA325605, XM_006925, gen.XM_006925
Figure 3486: DNA325606, XM_096630, gen.XM_096630
Figure 3487: PRO82099
Figure 3488: DNA325607, XM_084901, gen.XM_084901
Figure 3489: DNA226028, NM_002355, gen.NM_002355
Figure 3490: PRO36491
Figure 3491: DNA325608, XM_031807, gen.XM_031807
Figure 3492: PRO82101
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Figure 3494: DNA325610, XM_012159, gen.XM_012159
Figure 3495: DNA325611, XM_084922, gen.XM_084922
Figure 3496: DNA325612, NM_031289, gen.NM_031289
Figure 3497: PRO82104
Figure 3498: DNA226771, NM_003979, gen.NM_003979
Figure 3499: PRO37234
Figure 3500: DNA325613, XM_084918, gen.XM_084918
Figure 3501: DNA325614, NM_007178, gen.NM_007178
Figure 3502: PRO82106
Figure 3503: DNA325615, XM_041100, gen.XM_041100
Figure 3504A-B: DNA325616, XM_058567, gen.XM_058567
Figure 3505: PRO82107
Figure 3506A-B: DNA325617, XM_166605, gen.XM_166605
Figure 3507: DNA325618, XM_029805, gen.XM_029805

Figure 3508: PRO82109
Figure 3509: DNA325619, NM_005889, gen.NM_005889
Figure 3510: PRO82110
Figure 3511: DNA256072, NM_001644, gen.NM_001644
Figure 3512: PRO51121
Figure 3513: DNA325620, NM_018686, gen.NM_018686
Figure 3514: PRO82111
Figure 3515: DNA325621, XM_084770, gen.XM_084770
Figure 3516: PRO82112
Figure 3517: DNA325622, NM_018048, gen.NM_018048
Figure 3518: PRO82113
Figure 3519: DNA325623, XM_113730, gen.XM_113730
Figure 3520: DNA150978, NM_007244, gen.NM_007244
Figure 3521: PRO11601
Figure 3522: DNA325624, NM_006250, gen.NM_006250
Figure 3523: PRO82115
Figure 3524: DNA79313, NM_005042, gen.NM_005042
Figure 3525: PRO2555
Figure 3526: DNA150997, NM_004982, gen.NM_004982
Figure 3527: PRO12573
Figure 3528: DNA325625, XM_050074, gen.XM_050074
Figure 3529: DNA325626, NM_024854, gen.NM_024854
Figure 3530: PRO82117
Figure 3531: DNA325627, XM_084807, gen.XM_084807
Figure 3532: DNA325628, XM_165906, gen.XM_165906
Figure 3533A-B: DNA325629, XM_038659, gen.XM_038659
Figure 3534: PRO82120
Figure 3535: DNA325630, XM_006694, gen.XM_006694
Figure 3536: DNA325631, XM_006748, gen.XM_006748
Figure 3537: PRO82122
Figure 3538: DNA325632, XM_016640, gen.XM_016640
Figure 3539: DNA325633, XM_096146, gen.XM_096146
Figure 3540A-B: DNA325634, XM_084841, gen.XM_084841
Figure 3541: PRO82125
Figure 3542: DNA325635, XM_090218, gen.XM_090218
Figure 3543: DNA325636, XM_012272, gen.XM_012272
Figure 3544: PRO82127
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Figure 3546: DNA325638, NM_006262, gen.NM_006262
Figure 3547: PRO82129
Figure 3548: DNA325639, NM_018113, gen.NM_018113
Figure 3549: PRO82130
Figure 3550: DNA271344, NM_001659, gen.NM_001659
Figure 3551: PRO59647
Figure 3552: DNA325640, NM_017822, gen.NM_017822
Figure 3553: PRO82131
Figure 3554A-E: DNA325641, XM_028760, gen.XM_028760
Figure 3555: DNA272379, NM_002733, gen.NM_002733
Figure 3556: PRO60634
Figure 3557: DNA325642, XM_084866, gen.XM_084866
Figure 3558: PRO82133
Figure 3559: DNA325643, XM_006826, gen.XM_006826
Figure 3560: DNA325644, XM_113719, gen.XM_113719
Figure 3561: DNA325645, XM_028662, gen.XM_028662
Figure 3562: DNA325646, XM_035497, gen.XM_035497
Figure 3563: PRO82137
Figure 3564: DNA325647, XM_035490, gen.XM_035490
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Figure 3566: DNA325648, NM_013277, gen.NM_013277
Figure 3567: PRO82139
Figure 3568: DNA325649, NM_003076, gen.NM_003076
Figure 3569: PRO82140
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Figure 3571: DNA325651, XM_035485, gen.XM_035485
Figure 3572A-B: DNA325652, NM_016357, gen.NM_016357
Figure 3573: PRO82143
Figure 3574: DNA325653, NM_005171, gen.NM_005171
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Figure 3576: DNA325654, NM_014033, gen.NM_014033
Figure 3577: PRO4348

Figure 3578: DNA325655, XM_096620, gen.XM_096620
Figure 3579: DNA325656, XM_165905, gen.XM_165905
Figure 3580: DNA325657, XM_015481, gen.XM_015481
Figure 3581: DNA325658, XM_049148, gen.XM_049148
Figure 3582: DNA325659, XM_084885, gen.XM_084885
Figure 3583: DNA325660, XM_084884, gen.XM_084884
Figure 3584: DNA325661, XM_113726, gen.XM_113726
Figure 3585: DNA325662, XM_015476, gen.XM_015476
Figure 3586: DNA325663, XM_049141, gen.XM_049141
Figure 3587: PRO82152
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Figure 3589: PRO37654
Figure 3590: DNA325664, XM_083868, gen.XM_083868
Figure 3591: DNA270458, NM_002273, gen.NM_002273
Figure 3592: PRO58837
Figure 3593: DNA227092, NM_000224, gen.NM_000224
Figure 3594: PRO37555
Figure 3595: DNA325665, XM_029728, gen.XM_029728
Figure 3596: DNA325666, XM_015468, gen.XM_015468
Figure 3597: PRO82155
Figure 3598: DNA325667, XM_012162, gen.XM_012162
Figure 3599: DNA325668, XM_084789, gen.XM_084789
Figure 3600: DNA196351, NM_002178, gen.NM_002178
Figure 3601: PRO3449
Figure 3602A-B: DNA325669, XM_029631, gen.XM_029631
Figure 3603: PRO82158
Figure 3604: DNA325670, NM_015665, gen.NM_015665
Figure 3605: PRO82159
Figure 3606: DNA325671, NM_014311, gen.NM_014311
Figure 3607: PRO82160
Figure 3608: DNA325672, XM_096606, gen.XM_096606
Figure 3609: PRO82161
Figure 3610: DNA325673, NM_018457, gen.NM_018457
Figure 3611: PRO82162
Figure 3612: DNA325674, NM_031157, gen.NM_031157
Figure 3613: PRO82163
Figure 3614: DNA325675, NM_004178, gen.NM_004178
Figure 3615: PRO82164
Figure 3616: DNA325676, NM_134323, gen.NM_134323
Figure 3617: PRO82165
Figure 3618: DNA325677, NM_134324, gen.NM_134324
Figure 3619: PRO82166
Figure 3620: DNA290294, NM_005016, gen.NM_005016
Figure 3621: PRO70453
Figure 3622: DNA325678, NM_031989, gen.NM_031989
Figure 3623: PRO82167
Figure 3624: DNA325679, XM_028643, gen.XM_028643
Figure 3625: PRO82168
Figure 3626: DNA325680, XM_006710, gen.XM_006710
Figure 3627: PRO82169
Figure 3628: DNA227094, NM_005594, gen.NM_005594
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Figure 3630: DNA325681, XM_084824, gen.XM_084824
Figure 3631: DNA304783, NM_014255, gen.NM_014255
Figure 3632: PRO4426
Figure 3633: DNA325682, XM_165903, gen.XM_165903
Figure 3634: DNA325683, XM_115140, gen.XM_115140
Figure 3635: DNA325684, XM_113712, gen.XM_113712
Figure 3636: DNA325685, NM_006601, gen.NM_006601
Figure 3637: PRO82174
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Figure 3639: PRO82175
Figure 3640: DNA325687, XM_048943, gen.XM_048943
Figure 3641: DNA325688, XM_053164, gen.XM_053164
Figure 3642: DNA325689, XM_048991, gen.XM_048991
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Figure 3649: PRO82182
Figure 3650: DNA325694, NM_079425, gen.NM_079425
Figure 3651: PRO82183
Figure 3652: DNA325695, XM_049048, gen.XM_049048
Figure 3653: PRO82184
Figure 3654: DNA325696, NM_021104, gen.NM_021104
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Figure 3660: DNA325700, NM_006928, gen.NM_006928
Figure 3661: PRO2846
Figure 3662: DNA325701, XM_056353, gen.XM_056353
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Figure 3672: DNA325706, XM_084801, gen.XM_084801
Figure 3673: PRO82190
Figure 3674: DNA325707, XM_048603, gen.XM_048603
Figure 3675: PRO82191
Figure 3676: DNA325708, NM_133483, gen.NM_133483
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Figure 3678: DNA79101, NM_006812, gen.NM_006812
Figure 3679: PRO2549
Figure 3680: DNA325709, XM_096566, gen.XM_096566
Figure 3681: DNA325710, NM_005981, gen.NM_005981
Figure 3682: PRO4666
Figure 3683: DNA325711, NM_000075, gen.NM_000075
Figure 3684: PRO4873
Figure 3685: DNA325712, NM_052984, gen.NM_052984
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Figure 3687: DNA325713, NM_000785, gen.NM_000785
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Figure 3689: DNA325714, NM_005371, gen.NM_005371
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Figure 3691: DNA325715, NM_023032, gen.NM_023032
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Figure 3693: DNA325716, NM_023033, gen.NM_023033
Figure 3694: PRO82197
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Figure 3696: PRO82198
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Figure 3698: PRO82199
Figure 3699A-B: DNA325719, XM_096038, gen.XM_096038
Figure 3700: DNA325720, XM_056681, gen.XM_056681
Figure 3701: PRO82201
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Figure 3703: PRO82202
Figure 3704: DNA325722, XM_004098, gen.XM_004098
Figure 3705: DNA325723, XM_084912, gen.XM_084912
Figure 3706: PRO82204
Figure 3707: DNA325724, XM_040221, gen.XM_040221
Figure 3708: DNA325725, XM_016605, gen.XM_016605
Figure 3709: PRO82206
Figure 3710: DNA325726, XM_017508, gen.XM_017508
Figure 3711: PRO82207
Figure 3712: DNA325727, NM_032338, gen.NM_032338
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Figure 3714A-B: DNA325728, XM_052460, gen.XM_052460
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Figure 3716: PRO82210
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Figure 3718: PRO71120
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Figure 3720: DNA227474, NM_015646, gen.NM_015646
Figure 3721: PRO37937
Figure 3722: DNA325731, XM_053952, gen.XM_053952
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Figure 3724: DNA227171, NM_014515, gen.NM_014515
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Figure 3727: DNA271492, NM_006530, gen.NM_006530
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Figure 3737: DNA325738, XM_038308, gen.XM_038308
Figure 3738: PRO82215
Figure 3739: DNA325739, XM_096597, gen.XM_096597
Figure 3740: DNA325740, NM_001920, gen.NM_001920
Figure 3741: PRO2841
Figure 3742: DNA325741, NM_133503, gen.NM_133503
Figure 3743: PRO2841
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Figure 3756: PRO82223
Figure 3757: DNA325749, NM_003877, gen.NM_003877
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Figure 3770: PRO82228
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Figure 3772: DNA325757, XM_049201, gen.XM_049201
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Figure 3775: DNA325760, XM_062437, gen.XM_062437
Figure 3776: PRO82232
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Figure 3783: DNA325763, XM_084800, gen.XM_084800
Figure 3784: PRO82235
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Figure 3788A-B: DNA325766, XM_084941, gen.XM_084941
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Figure 3797: DNA325771, XM_007002, gen.XM_007002
Figure 3798: DNA325772, XM_056996, gen.XM_056996
Figure 3799: PRO82243
Figure 3800: DNA325773, XM_084946, gen.XM_084946
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Figure 3806: PRO82247
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Figure 3810: DNA325780, NM_017901, gen.NM_017901
Figure 3811: PRO82250
Figure 3812: DNA325781, NM_032814, gen.NM_032814
Figure 3813: PRO82252
Figure 3814: DNA325782, XM_084889, gen.XM_084889
Figure 3815: PRO82253
Figure 3816: DNA325783, NM_002567, gen.NM_002567
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Figure 3818: DNA325784, XM_084808, gen.XM_084808
Figure 3819: DNA325785, XM_096572, gen.XM_096572
Figure 3820: PRO82255
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Figure 3827: DNA302016, NM_001002, gen.NM_001002
Figure 3828: PRO70989
Figure 3829: DNA325789, NM_053275, gen.NM_053275
Figure 3830: PRO70989
Figure 3831: DNA325790, NM_006253, gen.NM_006253
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Figure 3834: DNA325792, XM_045963, gen.XM_045963
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Figure 3837: DNA325795, NM_002813, gen.NM_002813
Figure 3838: PRO82263
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Figure 3842: PRO82264
Figure 3843: DNA325798, NM_016638, gen.NM_016638
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Figure 3845: DNA325799, XM_116913, gen.XM_116913
Figure 3846: PRO82266
Figure 3847: DNA325800, NM_006815, gen.NM_006815
Figure 3848: PRO4793
Figure 3849: DNA325801, XM_006566, gen.XM_006566
Figure 3850: PRO82267
Figure 3851: DNA325802, NM_032656, gen.NM_032656
Figure 3852: PRO82268
Figure 3853: DNA325803, XM_055013, gen.XM_055013
Figure 3854: PRO82269
Figure 3855: DNA325804, XM_113737, gen.XM_113737
Figure 3856A-C: DNA325805, XM_045602, gen.XM_045602
Figure 3857: DNA325806, XM_087955, gen.XM_087955

Figure 3858: PRO82272
Figure 3859A-B: DNA325807, XM_044334, gen.XM_044334
Figure 3860: PRO82273
Figure 3861: DNA325808, XM_012184, gen.XM_012184
Figure 3862: DNA325809, XM_113702, gen.XM_113702
Figure 3863: PRO82275
Figure 3864A-B: DNA270015, NM_003453, gen.NM_003453
Figure 3865: PRO58410
Figure 3866: DNA226853, NM_004004, gen.NM_004004
Figure 3867: PRO37316
Figure 3868: DNA325810, XM_167911, gen.XM_167911
Figure 3869: DNA325811, XM_167918, gen.XM_167918
Figure 3870: DNA325812, XM_084982, gen.XM_084982
Figure 3871: PRO82278
Figure 3872: DNA325813, NM_024026, gen.NM_024026
Figure 3873: PRO82279
Figure 3874: DNA325814, XM_012638, gen.XM_012638
Figure 3875: PRO82280
Figure 3876: DNA325815, XM_167439, gen.XM_167439
Figure 3877: DNA325816, XM_167906, gen.XM_167906
Figure 3878A-B: DNA325817, NM_014778, gen.NM_014778
Figure 3879: PRO82283
Figure 3880: DNA325818, XM_169414, gen.XM_169414
Figure 3881A-B: DNA325819, NM_006646, gen.NM_006646
Figure 3882: PRO82285
Figure 3883: DNA325820, XM_167892, gen.XM_167892
Figure 3884: DNA325821, NM_015932, gen.NM_015932
Figure 3885: PRO82287
Figure 3886: DNA325822, XM_166273, gen.XM_166273
Figure 3887: DNA304669, NM_002128, gen.NM_002128
Figure 3888: PRO71096
Figure 3889: DNA325823, NM_014887, gen.NM_014887
Figure 3890: PRO82289
Figure 3891: DNA325824, NM_002915, gen.NM_002915
Figure 3892: PRO82290
Figure 3893: DNA325825, XM_085017, gen.XM_085017
Figure 3894: PRO82291
Figure 3895: DNA325826, XM_017432, gen.XM_017432
Figure 3896A-B: DNA270254, NM_002015, gen.NM_002015
Figure 3897: PRO58642
Figure 3898: DNA325827, NM_005830, gen.NM_005830
Figure 3899: PRO58092
Figure 3900: DNA281436, NM_003295, gen.NM_003295
Figure 3901: PRO66275
Figure 3902: DNA325828, XM_038371, gen.XM_038371
Figure 3903A-B: DNA325829, XM_165636, gen.XM_165636
Figure 3904: DNA325830, XM_166266, gen.XM_166266
Figure 3905: PRO82295
Figure 3906: DNA325831, NM_014166, gen.NM_014166
Figure 3907: PRO82296
Figure 3908: DNA325832, NM_021999, gen.NM_021999
Figure 3909: PRO1869
Figure 3910: DNA325833, NM_030925, gen.NM_030925
Figure 3911: PRO82297
Figure 3912: DNA274058, NM_016119, gen.NM_016119
Figure 3913: PRO61999
Figure 3914: DNA325834, NM_032565, gen.NM_032565
Figure 3915: PRO11982
Figure 3916: DNA325835, XM_085044, gen.XM_085044
Figure 3917: DNA325836, XM_165639, gen.XM_165639
Figure 3918: DNA325837, XM_018399, gen.XM_018399
Figure 3919: PRO82300
Figure 3920: DNA325838, XM_058977, gen.XM_058977
Figure 3921: DNA325839, XM_015840, gen.XM_015840
Figure 3922: PRO82302
Figure 3923: DNA325840, XM_007199, gen.XM_007199
Figure 3924: DNA325841, XM_016351, gen.XM_016351
Figure 3925: DNA325842, XM_041209, gen.XM_041209
Figure 3926: DNA325843, XM_058611, gen.XM_058611

Figure 3927: PRO82305
Figure 3928: DNA325844, XM_041473, gen.XM_041473
Figure 3929: PRO82306
Figure 3930: DNA325845, XM_032443, gen.XM_032443
Figure 3931: DNA325847, XM_048957, gen.XM_048957
Figure 3932: DNA325848, XM_015842, gen.XM_015842
Figure 3933: DNA325849, XM_084997, gen.XM_084997
Figure 3934: PRO82311
Figure 3935: DNA325850, NM_024089, gen.NM_024089
Figure 3936: PRO82312
Figure 3937A-B: DNA325851, XM_049904, gen.XM_049904
Figure 3938: DNA325852, NM_024537, gen.NM_024537
Figure 3939: PRO82314
Figure 3940: DNA325853, NM_023011, gen.NM_023011
Figure 3941: PRO82315
Figure 3942: DNA325854, NM_080687, gen.NM_080687
Figure 3943: PRO82316
Figure 3944: DNA325855, XM_041484, gen.XM_041484
Figure 3945: PRO82317
Figure 3946A-B: DNA325856, XM_113752, gen.XM_113752
Figure 3947: PRO82318
Figure 3948: DNA325857, XM_115215, gen.XM_115215
Figure 3949: DNA325858, XM_046651, gen.XM_046651
Figure 3950: DNA325859, XM_046648, gen.XM_046648
Figure 3951: DNA325860, XM_046642, gen.XM_046642
Figure 3952: PRO10404
Figure 3953: DNA325861, XM_017914, gen.XM_017914
Figure 3954: PRO82321
Figure 3955: DNA325862, XM_085166, gen.XM_085166
Figure 3956: PRO82322
Figure 3957: DNA325863, XM_007316, gen.XM_007316
Figure 3958: DNA325864, XM_007315, gen.XM_007315
Figure 3959: DNA325865, XM_033251, gen.XM_033251
Figure 3960: DNA325866, NM_024658, gen.NM_024658
Figure 3961: PRO82325
Figure 3962: DNA210180, NM_005132, gen.NM_005132
Figure 3963: PRO33717
Figure 3964: DNA325867, XM_033337, gen.XM_033337
Figure 3965: PRO82326
Figure 3966: DNA325868, XM_096772, gen.XM_096772
Figure 3967: DNA325869, XM_007293, gen.XM_007293
Figure 3968: DNA325870, XM_007288, gen.XM_007288
Figure 3969A-B: DNA325871, XM_033391, gen.XM_033391
Figure 3970: PRO82329
Figure 3971: DNA325872, NM_017815, gen.NM_017815
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Figure 3975: DNA325874, XM_033435, gen.XM_033435
Figure 3976: DNA225865, NM_004995, gen.NM_004995
Figure 3977: PRO36328
Figure 3978: DNA325875, XM_058647, gen.XM_058647
Figure 3979: PRO82333
Figure 3980: DNA325876, XM_033445, gen.XM_033445
Figure 3981: DNA325877, NM_005015, gen.NM_005015
Figure 3982: PRO82334
Figure 3983: DNA325878, XM_012377, gen.XM_012377
Figure 3984: DNA227321, NM_001344, gen.NM_001344
Figure 3985: PRO37784
Figure 3986: DNA325879, XM_058646, gen.XM_058646
Figure 3987: DNA325880, XM_085106, gen.XM_085106
Figure 3988: DNA325881, NM_019852, gen.NM_019852
Figure 3989: PRO82338
Figure 3990: DNA325882, XM_012376, gen.XM_012376
Figure 3991: DNA325883, XM_033553, gen.XM_033553
Figure 3992: DNA226105, NM_002934, gen.NM_002934
Figure 3993: PRO36568
Figure 3994: DNA325884, XM_033595, gen.XM_033595

Figure 3995: PRO2871
Figure 3996: DNA325885, XM_007491, gen.XM_007491
Figure 3997: DNA325886, NM_001641, gen.NM_001641
Figure 3998: PRO82342
Figure 3999: DNA325887, NM_080648, gen.NM_080648
Figure 4000: PRO82343
Figure 4001: DNA325888, NM_080649, gen.NM_080649
Figure 4002: PRO82344
Figure 4003: DNA325889, NM_017807, gen.NM_017807
Figure 4004: PRO82345
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Figure 4006: DNA325891, NM_021178, gen.NM_021178
Figure 4007: PRO82347
Figure 4008: DNA325892, XM_041235, gen.XM_041235
Figure 4009: PRO82348
Figure 4010: DNA325893, NM_002028, gen.NM_002028
Figure 4011: PRO82349
Figure 4012: DNA325894, NM_002083, gen.NM_002083
Figure 4013: PRO82350
Figure 4014A-B: DNA325895, XM_085127, gen.XM_085127
Figure 4015: PRO82351
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Figure 4019: DNA325898, XM_085141, gen.XM_085141
Figure 4020: DNA325899, NM_021728, gen.NM_021728
Figure 4021: PRO82355
Figure 4022: DNA325900, NM_002306, gen.NM_002306
Figure 4023: PRO82356
Figure 4024: DNA325901, XM_007328, gen.XM_007328
Figure 4025A-B: DNA325902, XM_051712, gen.XM_051712
Figure 4026: PRO82357
Figure 4027: DNA325903, XM_007324, gen.XM_007324
Figure 4028: PRO82358
Figure 4029: DNA325904, NM_002863, gen.NM_002863
Figure 4030: PRO82359
Figure 4031: DNA325905, XM_085125, gen.XM_085125
Figure 4032: DNA325906, XM_031025, gen.XM_031025
Figure 4033: DNA325907, XM_085066, gen.XM_085066
Figure 4034: DNA325908, XM_096744, gen.XM_096744
Figure 4035: DNA325909, NM_016445, gen.NM_016445
Figure 4036: PRO82364
Figure 4037: DNA325910, NM_016026, gen.NM_016026
Figure 4038: PRO82365
Figure 4039: DNA325911, XM_031074, gen.XM_031074
Figure 4040: DNA325912, NM_001102, gen.NM_001102
Figure 4041: PRO82367
Figure 4042: DNA225649, NM_022137, gen.NM_022137
Figure 4043: PRO36112
Figure 4044: DNA325913, XM_085065, gen.XM_085065
Figure 4045: DNA325914, XM_007441, gen.XM_007441
Figure 4046: DNA325915, NM_006821, gen.NM_006821
Figure 4047: PRO82369
Figure 4048: DNA325916, NM_006432, gen.NM_006432
Figure 4049: PRO2066
Figure 4050A-B: DNA325917, XM_085151, gen.XM_085151
Figure 4051: PRO82370
Figure 4052: DNA325918, NM_002632, gen.NM_002632
Figure 4053: PRO82371
Figure 4054: DNA325919, XM_085162, gen.XM_085162
Figure 4055: DNA325920, NM_012111, gen.NM_012111
Figure 4056: PRO82373
Figure 4057: DNA325921, NM_024824, gen.NM_024824
Figure 4058: PRO82374
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Figure 4063: DNA325923, NM_006888, gen.NM_006888
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Figure 4067: DNA325925, XM_029288, gen.XM_029288
Figure 4068A-B: DNA325926, XM_016487, gen.XM_016487
Figure 4069: DNA325927, NM_020414, gen.NM_020414
Figure 4070: PRO62099
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Figure 4072: DNA325929, XM_007483, gen.XM_007483
Figure 4073: DNA325930, XM_028358, gen.XM_028358
Figure 4074: DNA325931, XM_028347, gen.XM_028347
Figure 4075: DNA325932, XM_028322, gen.XM_028322
Figure 4076: PRO82381
Figure 4077: DNA325933, XM_056317, gen.XM_056317
Figure 4078: PRO82382
Figure 4079: DNA151893, NM_021966, gen.NM_021966
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Figure 4081: DNA325934, XM_007272, gen.XM_007272
Figure 4082: DNA325935, XM_090914, gen.XM_090914
Figure 4083: PRO82383
Figure 4084: DNA325936, NM_022747, gen.NM_022747
Figure 4085: PRO82384
Figure 4086: DNA325937, XM_041014, gen.XM_041014
Figure 4087: PRO60575
Figure 4088: DNA325938, NM_003836, gen.NM_003836
Figure 4089: PRO82385
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Figure 4091: DNA325940, XM_058618, gen.XM_058618
Figure 4092: DNA325941, NM_005348, gen.NM_005348
Figure 4093: PRO82388
Figure 4094: DNA325942, XM_040942, gen.XM_040942
Figure 4095: DNA226324, NM_014226, gen.NM_014226
Figure 4096: PRO36787
Figure 4097A-B: DNA325943, XM_007254, gen.XM_007254
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Figure 4099: PRO82391
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Figure 4101: DNA325946, NM_005432, gen.NM_005432
Figure 4102: PRO60070
Figure 4103A-B: DNA325947, XM_050278, gen.XM_050278
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Figure 4105: DNA325948, XM_113759, gen.XM_113759
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Figure 4109: PRO82396
Figure 4110: DNA103509, NM_005163, gen.NM_005163
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Figure 4112: DNA325951, NM_017955, gen.NM_017955
Figure 4113: PRO82397
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Figure 4115: DNA325953, XM_060012, gen.XM_060012
Figure 4116: DNA325954, XM_034953, gen.XM_034953
Figure 4117: PRO82400
Figure 4118: DNA325955, XM_058636, gen.XM_058636
Figure 4119: DNA325956, XM_035014, gen.XM_035014
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Figure 4123: DNA325960, XM_018054, gen.XM_018054
Figure 4124: DNA325961, XM_091108, gen.XM_091108
Figure 4125A-B: DNA325962, XM_039225, gen.XM_039225
Figure 4126: PRO82408
Figure 4127: DNA325963, XM_165921, gen.XM_165921
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Figure 4130: DNA325965, XM_085203, gen.XM_085203
Figure 4131: PRO82411
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Figure 4133: DNA325967, XM_012398, gen.XM_012398
Figure 4134A-B: DNA325968, XM_036727, gen.XM_036727
Figure 4135: DNA325969, XM_017240, gen.XM_017240
Figure 4136: DNA325970, NM_020149, gen.NM_020149
Figure 4137: PRO82415
Figure 4138A-B: DNA325971, XM_031617, gen.XM_031617
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Figure 4148: DNA325976, NM_024111, gen.NM_024111
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Figure 4150: DNA325977, NM_032196, gen.NM_032196
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Figure 4152: DNA325978, NM_016359, gen.NM_016359
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Figure 4154: DNA325979, NM_018454, gen.NM_018454
Figure 4155: PRO82424
Figure 4156A-B: DNA325980, XM_007545, gen.XM_007545
Figure 4157: DNA325981, XM_091159, gen.XM_091159
Figure 4158: PRO82425
Figure 4159: DNA325982, XM_031718, gen.XM_031718
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Figure 4165: DNA325985, XM_016713, gen.XM_016713
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Figure 4167A-B: DNA325986, XM_007531, gen.XM_007531
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Figure 4188: PRO82437
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Figure 4191: DNA325997, XM_090991, gen.XM_090991
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Figure 4198: PRO82442
Figure 4199A-B: DNA326001, XM_012418, gen.XM_012418
Figure 4200: DNA326002, XM_039702, gen.XM_039702
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Figure 4236: DNA326020, XM_085249, gen.XM_085249
Figure 4237: DNA326021, XM_016076, gen.XM_016076
Figure 4238: PRO82460
Figure 4239: DNA326022, XM_015366, gen.XM_015366
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Figure 4242: DNA287331, NM_002654, gen.NM_002654
Figure 4243: PRO69595
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Figure 4245: DNA326025, XM_096842, gen.XM_096842
Figure 4246: DNA326026, NM_022369, gen.NM_022369
Figure 4247: PRO82465
Figure 4248: DNA326027, NM_032907, gen.NM_032907
Figure 4249: PRO82466
Figure 4250: DNA326028, XM_058699, gen.XM_058699
Figure 4251: DNA326029, XM_118637, gen.XM_118637
Figure 4252: DNA326030, XM_053585, gen.XM_053585
Figure 4253: PRO82469
Figure 4254: DNA326031, XM_085239, gen.XM_085239
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Figure 4256: DNA326032, XM_034897, gen.XM_034897
Figure 4257A-B: DNA326033, XM_057020, gen.XM_057020
Figure 4258: PRO82472
Figure 4259: DNA326034, NM_000743, gen.NM_000743
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Figure 4261: DNA326035, NM_002789, gen.NM_002789
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Figure 4270: DNA326038, NM_025234, gen.NM_025234
Figure 4271: PRO82475
Figure 4272: DNA326039, XM_044569, gen.XM_044569

Figure 4273: DNA326040, NM_005724, gen.NM_005724
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Figure 4279: DNA326044, NM_006791, gen.NM_006791
Figure 4280: PRO82479
Figure 4281: DNA326045, XM_060042, gen.XM_060042
Figure 4282: DNA326046, XM_085215, gen.XM_085215
Figure 4283: DNA326047, NM_001021, gen.NM_001021
Figure 4284: PRO82482
Figure 4285: DNA326048, XM_031404, gen.XM_031404
Figure 4286: DNA326049, XM_096844, gen.XM_096844
Figure 4287: DNA326050, XM_045681, gen.XM_045681
Figure 4288: PRO82485
Figure 4289: DNA326051, XM_085280, gen.XM_085280
Figure 4290: DNA326052, NM_022839, gen.NM_022839
Figure 4291: PRO82487
Figure 4292: DNA326053, XM_031354, gen.XM_031354
Figure 4293: DNA326054, NM_002168, gen.NM_002168
Figure 4294: PRO82489
Figure 4295: DNA326055, XM_031292, gen.XM_031292
Figure 4296: DNA326056, NM_022566, gen.NM_022566
Figure 4297: PRO82491
Figure 4298A-B: DNA326057, XM_051860, gen.XM_051860
Figure 4299: PRO82492
Figure 4300: DNA275144, NM_000137, gen.NM_000137
Figure 4301: PRO62852
Figure 4302: DNA326058, NM_016645, gen.NM_016645
Figure 4303: PRO82493
Figure 4304: DNA326059, XM_044523, gen.XM_044523
Figure 4305: DNA150485, NM_006384, gen.NM_006384
Figure 4306: PRO12774
Figure 4307A-B: DNA326060, XM_044533, gen.XM_044533
Figure 4308: PRO82495
Figure 4309A-C: DNA326061, XM_054900, gen.XM_054900
Figure 4310: DNA326062, NM_032162, gen.NM_032162
Figure 4311A-B: DNA326063, XM_015835, gen.XM_015835
Figure 4312: DNA326064, NM_018668, gen.NM_018668
Figure 4313: PRO82499
Figure 4314: DNA326065, XM_085262, gen.XM_085262
Figure 4315: DNA326066, NM_033544, gen.NM_033544
Figure 4316: PRO82501
Figure 4317: DNA326067, XM_049372, gen.XM_049372
Figure 4318: PRO82502
Figure 4319: DNA326068, XM_017971, gen.XM_017971
Figure 4320: DNA275181, NM_003090, gen.NM_003090
Figure 4321: PRO62882
Figure 4322: DNA326069, XM_012462, gen.XM_012462
Figure 4323A-B: DNA326070, XM_085525, gen.XM_085525
Figure 4324: PRO82505
Figure 4325: DNA326071, XM_165923, gen.XM_165923
Figure 4326: DNA326072, XM_113836, gen.XM_113836
Figure 4327: DNA326073, NM_017668, gen.NM_017668
Figure 4328: PRO82508
Figure 4329: DNA326074, XM_027309, gen.XM_027309
Figure 4330: PRO82509
Figure 4331: DNA326075, XM_018432, gen.XM_018432
Figure 4332: PRO82510
Figure 4333: DNA326076, XM_115352, gen.XM_115352
Figure 4334: DNA326077, XM_027365, gen.XM_027365
Figure 4335: DNA326078, NM_016641, gen.NM_016641
Figure 4336: PRO38464
Figure 4337: DNA326079, XM_058796, gen.XM_058796
Figure 4338: DNA326080, XM_017984, gen.XM_017984
Figure 4339: PRO82513
Figure 4340: DNA326081, NM_020677,

gen.NM_020677
Figure 4341: PRO82514
Figure 4342: DNA326082, XM_036680, gen.XM_036680
Figure 4343: PRO37961
Figure 4344A-B: DNA326083, XM_048119, gen.XM_048119
Figure 4345: PRO82515
Figure 4346: DNA326084, NM_024589, gen.NM_024589
Figure 4347: PRO82516
Figure 4348: DNA326085, XM_050534, gen.XM_050534
Figure 4349: PRO82517
Figure 4350: DNA326086, NM_024571, gen.NM_024571
Figure 4351: PRO82518
Figure 4352: DNA326087, XM_027558, gen.XM_027558
Figure 4353: DNA326088, XM_008126, gen.XM_008126
Figure 4354: DNA326089, NM_000517, gen.NM_000517
Figure 4355: PRO3629
Figure 4356: DNA326090, NM_000558, gen.NM_000558
Figure 4357: PRO3629
Figure 4358: DNA326091, NM_018032, gen.NM_018032
Figure 4359: PRO38311
Figure 4360: DNA273839, NM_006428, gen.NM_006428
Figure 4361: PRO61799
Figure 4362A-B: DNA256844, NM_005632, gen.NM_005632
Figure 4363: PRO51775
Figure 4364: DNA326092, XM_083939, gen.XM_083939
Figure 4365: PRO82521
Figure 4366: DNA326093, NM_058192, gen.NM_058192
Figure 4367: PRO82522
Figure 4368: DNA326094, XM_027412, gen.XM_027412
Figure 4369: PRO82523
Figure 4370: DNA256886, NM_014587, gen.NM_014587
Figure 4371: PRO51815
Figure 4372A-B: DNA326095, NM_001287, gen.NM_001287
Figure 4373: PRO38480
Figure 4374: DNA254781, NM_016111, gen.NM_016111
Figure 4375: PRO49879
Figure 4376: DNA326096, XM_034586, gen.XM_034586
Figure 4377: PRO82524
Figure 4378: DNA326097, NM_023936, gen.NM_023936
Figure 4379: PRO82525
Figure 4380: DNA326098, XM_034590, gen.XM_034590
Figure 4381: PRO82526
Figure 4382: DNA326099, NM_002952, gen.NM_002952
Figure 4383: PRO82527
Figure 4384: DNA326100, NM_006453, gen.NM_006453
Figure 4385: PRO82528
Figure 4386: DNA326101, NM_014353, gen.NM_014353
Figure 4387: PRO82529
Figure 4388: DNA326102, NM_032271, gen.NM_032271
Figure 4389: PRO82530
Figure 4390: DNA326103, XM_028848, gen.XM_028848
Figure 4391: PRO82531
Figure 4392: DNA326104, NM_006711, gen.NM_006711
Figure 4393: PRO82532
Figure 4394: DNA326105, NM_080594, gen.NM_080594
Figure 4395: PRO82533
Figure 4396: DNA326106, NM_024339, gen.NM_024339
Figure 4397: PRO82534
Figure 4398: DNA326107, NM_016639, gen.NM_016639
Figure 4399: PRO12683
Figure 4400: DNA326108, NM_021195, gen.NM_021195
Figure 4401: PRO82535
Figure 4402: DNA326109, NM_004203, gen.NM_004203
Figure 4403: PRO82536
Figure 4404: DNA326110, XM_058784, gen.XM_058784
Figure 4405: PRO82537
Figure 4406: DNA326111, NM_024507, gen.NM_024507
Figure 4407: PRO82538
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Figure 4409: PRO303
Figure 4410A-C: DNA326113, XM_036528, gen.XM_036528
Figure 4411: DNA326114, NM_025108, gen.NM_025108
Figure 4412: PRO82540
Figure 4413A-C: DNA326115, XM_165411, gen.XM_165411

Figure 4414: DNA326116, NM_016292, gen.NM_016292
Figure 4415: PRO82542
Figure 4416: DNA326117, NM_002484, gen.NM_002484
Figure 4417: PRO82543
Figure 4418: DNA326118, XM_113845, gen.XM_113845
Figure 4419: PRO82544
Figure 4420: DNA326119, XM_113843, gen.XM_113843
Figure 4421: DNA97293, NM_003366, gen.NM_003366
Figure 4422: PRO3640
Figure 4423: DNA326120, NM_006110, gen.NM_006110
Figure 4424: PRO82546
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Figure 4426: DNA326122, XM_113876, gen.XM_113876
Figure 4427A-B: DNA326123, XM_055195, gen.XM_055195
Figure 4428: PRO82548
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Figure 4430A-B: DNA326125, XM_007988, gen.XM_007988
Figure 4431: DNA326126, XM_113874, gen.XM_113874
Figure 4432: DNA326127, XM_102377, gen.XM_102377
Figure 4433: PRO82551
Figure 4434: DNA326128, XM_086278, gen.XM_086278
Figure 4435: DNA326129, XM_085452, gen.XM_085452
Figure 4436: DNA326130, NM_018054, gen.NM_018054
Figure 4437: PRO82554
Figure 4438A-B: DNA326131, XM_056260, gen.XM_056260
Figure 4439: PRO82555
Figure 4440: DNA326132, NM_032626, gen.NM_032626
Figure 4441: PRO82556
Figure 4442: DNA326133, NM_005030, gen.NM_005030
Figure 4443: PRO82557
Figure 4444: DNA326134, NM_032486, gen.NM_032486
Figure 4445: PRO82558
Figure 4446: DNA289522, NM_005003, gen.NM_005003
Figure 4447: PRO70276
Figure 4448: DNA326135, XM_085340, gen.XM_085340
Figure 4449: DNA326136, NM_003752, gen.NM_003752
Figure 4450: PRO60325
Figure 4451: DNA326137, NM_012248, gen.NM_012248
Figure 4452: PRO82560
Figure 4453A-B: DNA326138, XM_046035, gen.XM_046035
Figure 4454: DNA326139, NM_024671, gen.NM_024671
Figure 4455: PRO82562
Figure 4456: DNA326140, NM_033410, gen.NM_033410
Figure 4457: PRO82563
Figure 4458: DNA326141, NM_024031, gen.NM_024031
Figure 4459: PRO82564
Figure 4460A-B: DNA326142, XM_034375, gen.XM_034375
Figure 4461: DNA326143, XM_012569, gen.XM_012569
Figure 4462: DNA326144, XM_050194, gen.XM_050194
Figure 4463: DNA326145, XM_008106, gen.XM_008106
Figure 4464: PRO82567
Figure 4465: DNA326146, NM_004960, gen.NM_004960
Figure 4466: PRO82568
Figure 4467: DNA326147, XM_113293, gen.XM_113293
Figure 4468: DNA326148, NM_022744, gen.NM_022744
Figure 4469: PRO82570
Figure 4470: DNA326149, NM_024048, gen.NM_024048
Figure 4471: PRO82571
Figure 4472: DNA326150, XM_018088, gen.XM_018088
Figure 4473: PRO82572
Figure 4474: DNA326151, XM_007963, gen.XM_007963
Figure 4475: PRO82573
Figure 4476: DNA274002, NM_014321, gen.NM_014321
Figure 4477: PRO61948
Figure 4478: DNA326152, XM_015700, gen.XM_015700
Figure 4479: DNA326153, XM_051219, gen.XM_051219
Figure 4480: DNA326154, XM_085393, gen.XM_085393
Figure 4481: PRO82576
Figure 4482: DNA326155, XM_085395, gen.XM_085395

Figure 4483: DNA326156, XM_091270, gen.XM_091270
Figure 4484: DNA326157, XM_165656, gen.XM_165656
Figure 4485: DNA326158, NM_032330, gen.NM_032330
Figure 4486: PRO82579
Figure 4487: DNA254532, NM_001043, gen.NM_001043
Figure 4488: PRO49639
Figure 4489: DNA326159, XM_165658, gen.XM_165658
Figure 4490: DNA326160, XM_166285, gen.XM_166285
Figure 4491: DNA326161, XM_166282, gen.XM_166282
Figure 4492: PRO82582
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Figure 4494: PRO82583
Figure 4495: DNA326163, NM_032038, gen.NM_032038
Figure 4496: PRO82584
Figure 4497: DNA326164, XM_008065, gen.XM_008065
Figure 4498: DNA326165, NM_017458, gen.NM_017458
Figure 4499: PRO82585
Figure 4500: DNA326166, NM_005115, gen.NM_005115
Figure 4501: PRO82586
Figure 4502: DNA326167, NM_024516, gen.NM_024516
Figure 4503: PRO82587
Figure 4504: DNA326168, XM_113299, gen.XM_113299
Figure 4505: DNA326169, XM_055771, gen.XM_055771
Figure 4506: PRO82589
Figure 4507: DNA271171, NM_007317, gen.NM_007317
Figure 4508: PRO59491
Figure 4509: DNA326170, XM_008064, gen.XM_008064
Figure 4510: PRO82590
Figure 4511: DNA326171, NM_003123, gen.NM_003123
Figure 4512: PRO2355
Figure 4513: DNA326172, XM_085442, gen.XM_085442
Figure 4514: DNA326173, XM_055132, gen.XM_055132
Figure 4515: PRO82592
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Figure 4517: PRO62110
Figure 4518: DNA326174, NM_002720, gen.NM_002720
Figure 4519: PRO42208
Figure 4520: DNA287355, NM_000034, gen.NM_000034
Figure 4521: PRO69617
Figure 4522: DNA326175, NM_031478, gen.NM_031478
Figure 4523: PRO82593
Figure 4524: DNA326176, XM_085434, gen.XM_085434
Figure 4525: PRO82594
Figure 4526: DNA326177, XM_058116, gen.XM_058116
Figure 4527: DNA326178, XM_165649, gen.XM_165649
Figure 4528: DNA326179, XM_165647, gen.XM_165647
Figure 4529: PRO82597
Figure 4530: DNA194805, NM_014685, gen.NM_014685
Figure 4531: PRO24075
Figure 4532: DNA326180, XM_166277, gen.XM_166277
Figure 4533: PRO82598
Figure 4534: DNA326181, XM_165645, gen.XM_165645
Figure 4535: DNA326182, NM_018110, gen.NM_018110
Figure 4536: PRO82599
Figure 4537: DNA326183, XM_165648, gen.XM_165648
Figure 4538: DNA326184, XM_167453, gen.XM_167453
Figure 4539: DNA326185, NM_022770, gen.NM_022770
Figure 4540: PRO82602
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Figure 4542: PRO82603
Figure 4543: DNA326187, XM_058745, gen.XM_058745
Figure 4544: DNA326188, XM_091420, gen.XM_091420
Figure 4545: DNA326189, NM_004691, gen.NM_004691
Figure 4546: PRO82606
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Figure 4551: DNA326192, XM_039306, gen.XM_039306
Figure 4552: PRO82608

Figure 4553: DNA326193, NM_030579, gen.NM_030579
Figure 4554: PRO82609
Figure 4555: DNA326194, XM_012487, gen.XM_012487
Figure 4556: DNA326195, NM_014062, gen.NM_014062
Figure 4557: PRO82611
Figure 4558: DNA326196, XM_085471, gen.XM_085471
Figure 4559: PRO82612
Figure 4560: DNA326197, XM_113855, gen.XM_113855
Figure 4561: DNA326198, XM_085475, gen.XM_085475
Figure 4562: DNA326199, XM_028151, gen.XM_028151
Figure 4563: PRO82615
Figure 4564: DNA275408, NM_001605, gen.NM_001605
Figure 4565: PRO63068
Figure 4566: DNA326200, NM_007242, gen.NM_007242
Figure 4567: PRO82616
Figure 4568: DNA189703, NM_005548, gen.NM_005548
Figure 4569: PRO22637
Figure 4570: DNA326201, XM_113853, gen.XM_113853
Figure 4571: DNA326202, NM_032140, gen.NM_032140
Figure 4572: PRO82618
Figure 4573: DNA326203, NM_030819, gen.NM_030819
Figure 4574: PRO82619
Figure 4575: DNA304704, NM_005796, gen.NM_005796
Figure 4576: PRO71130
Figure 4577: DNA326204, XM_043047, gen.XM_043047
Figure 4578: PRO49967
Figure 4579: DNA88261, NM_001907, gen.NM_001907
Figure 4580: PRO2719
Figure 4581A-B: DNA326205, NM_005072, gen.NM_005072
Figure 4582: PRO4814
Figure 4583: DNA326206, XM_165410, gen.XM_165410
Figure 4584: DNA326207, NM_017803, gen.NM_017803
Figure 4585: PRO82621
Figure 4586A-B: DNA326208, NM_004555, gen.NM_004555
Figure 4587: PRO82622
Figure 4588A-B: DNA326209, NM_018124, gen.NM_018124
Figure 4589: PRO82623
Figure 4590: DNA326210, XM_091399, gen.XM_091399
Figure 4591: PRO82624
Figure 4592A-B: DNA326211, NM_014003, gen.NM_014003
Figure 4593: PRO82625
Figure 4594: DNA326212, NM_017853, gen.NM_017853
Figure 4595: PRO82626
Figure 4596: DNA326213, XM_042621, gen.XM_042621
Figure 4597: DNA326214, XM_064091, gen.XM_064091
Figure 4598: PRO82627
Figure 4599: DNA326215, XM_085981, gen.XM_085981
Figure 4600A-B: DNA326216, XM_051778, gen.XM_051778
Figure 4601: PRO82629
Figure 4602: DNA326217, NM_004483, gen.NM_004483
Figure 4603: PRO82630
Figure 4604: DNA326218, NM_020188, gen.NM_020188
Figure 4605: PRO82631
Figure 4606: DNA326219, XM_033922, gen.XM_033922
Figure 4607: PRO82632
Figure 4608: DNA326220, XM_113840, gen.XM_113840
Figure 4609: PRO82633
Figure 4610: DNA326221, NM_016095, gen.NM_016095
Figure 4611: PRO82634
Figure 4612: DNA326222, NM_006067, gen.NM_006067
Figure 4613: PRO50658
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Figure 4615: PRO82635
Figure 4616A-B: DNA326224, XM_085483, gen.XM_085483
Figure 4617: DNA326225, NM_017566, gen.NM_017566
Figure 4618: PRO82637
Figure 4619: DNA326226, XM_057150, gen.XM_057150
Figure 4620: PRO82638
Figure 4621: DNA326227, XM_058739, gen.XM_058739
Figure 4622: DNA326228, XM_085327, gen.XM_085327
Figure 4623: PRO82640
Figure 4624: DNA326229, XM_047436,

gen.XM_047436
Figure 4625: PRO82641
Figure 4626: DNA227234, NM_002386, gen.NM_002386
Figure 4627: PRO37697
Figure 4628: DNA326230, NM_014972, gen.NM_014972
Figure 4629: PRO82642
Figure 4630: DNA326231, XM_071873, gen.XM_071873
Figure 4631: PRO82643
Figure 4632: DNA326232, XM_047525, gen.XM_047525
Figure 4633: DNA326233, NM_000977, gen.NM_000977
Figure 4634: PRO82645
Figure 4635: DNA326234, NM_033251, gen.NM_033251
Figure 4636: PRO82646
Figure 4637: DNA326235, XM_085408, gen.XM_085408
Figure 4638: DNA326236, NM_004933, gen.NM_004933
Figure 4639: PRO2198
Figure 4640: DNA326237, XM_113882, gen.XM_113882
Figure 4641: DNA326238, XM_010938, gen.XM_010938
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Figure 4643: PRO39530
Figure 4644A-B: DNA326240, XM_017096, gen.XM_017096
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Figure 4646A-B: DNA326242, XM_033689, gen.XM_033689
Figure 4647: DNA326243, NM_002615, gen.NM_002615
Figure 4648: DNA326244, XM_056082, gen.XM_056082
Figure 4649: PRO82654
Figure 4650: DNA326245, XM_008557, gen.XM_008557
Figure 4651: DNA326246, XM_045183, gen.XM_045183
Figure 4652: PRO82656
Figure 4653: DNA326247, XM_113901, gen.XM_113901
Figure 4654: DNA326248, NM_080822, gen.NM_080822
Figure 4655: PRO82658
Figure 4656A-B: DNA326249, XM_029438, gen.XM_029438
Figure 4657: PRO82659
Figure 4658: DNA326250, XM_008509, gen.XM_008509
Figure 4659: DNA326251, XM_085687, gen.XM_085687
Figure 4660: PRO82661
Figure 4661: DNA326252, XM_027825, gen.XM_027825
Figure 4662: PRO82662
Figure 4663: DNA326253, XM_053717, gen.XM_053717
Figure 4664: PRO82663
Figure 4665: DNA326254, NM_005022, gen.NM_005022
Figure 4666: PRO62780
Figure 4667A-B: DNA326255, XM_028398, gen.XM_028398
Figure 4668: PRO82664
Figure 4669: DNA326256, NM_000018, gen.NM_000018
Figure 4670: PRO66265
Figure 4671: DNA326257, XM_008334, gen.XM_008334
Figure 4672: DNA326258, NM_024297, gen.NM_024297
Figure 4673: PRO82665
Figure 4674: DNA326259, XM_113324, gen.XM_113324
Figure 4675: DNA326260, XM_012676, gen.XM_012676
Figure 4676: PRO82667
Figure 4677: DNA326261, XM_085691, gen.XM_085691
Figure 4678: DNA326262, XM_028417, gen.XM_028417
Figure 4679: PRO82669
Figure 4680A-B: DNA326263, XM_041964, gen.XM_041964
Figure 4681: PRO82670
Figure 4682: DNA326264, NM_019013, gen.NM_019013
Figure 4683: PRO82671
Figure 4684: DNA326265, XM_008538, gen.XM_008538
Figure 4685: PRO82672
Figure 4686: DNA326266, XM_008441, gen.XM_008441
Figure 4687: DNA97300, NM_001416, gen.NM_001416
Figure 4688: PRO3647
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Figure 4690: PRO82674
Figure 4691: DNA326268, NM_006942, gen.NM_006942
Figure 4692: PRO82675
Figure 4693: DNA326269, XM_008679, gen.XM_008679

Figure 4694: DNA326270, XM_008231, gen.XM_008231
Figure 4695: DNA326271, XM_113328, gen.XM_113328
Figure 4696: DNA326272, XM_113929, gen.XM_113929
Figure 4697: DNA326273, NM_001970, gen.NM_001970
Figure 4698: PRO82678
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Figure 4700: PRO70812
Figure 4701: DNA326274, XM_165421, gen.XM_165421
Figure 4702: PRO82679
Figure 4703: DNA326275, XM_113325, gen.XM_113325
Figure 4704: DNA326276, XM_165422, gen.XM_165422
Figure 4705: PRO49182
Figure 4706: DNA326277, XM_113931, gen.XM_113931
Figure 4707: DNA326278, XM_036659, gen.XM_036659
Figure 4708: DNA103401, NM_003876, gen.NM_003876
Figure 4709: PRO4729
Figure 4710A-B: DNA326279, XM_042698, gen.XM_042698
Figure 4711: PRO82683
Figure 4712A-B: DNA326280, XM_017234, gen.XM_017234
Figure 4713: DNA326281, XM_165418, gen.XM_165418
Figure 4714: DNA304715, NM_000987, gen.NM_000987
Figure 4715: PRO71141
Figure 4716A-B: DNA326282, NM_004618, gen.NM_004618
Figure 4717: PRO62981
Figure 4718: DNA326283, XM_085743, gen.XM_085743
Figure 4719A-B: DNA254198, NM_002018, gen.NM_002018
Figure 4720: PRO49310
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Figure 4722: PRO82687
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Figure 4724: DNA326286, XM_085613, gen.XM_085613
Figure 4725: DNA326287, NM_006470, gen.NM_006470
Figure 4726: PRO82689
Figure 4727: DNA326288, XM_051763, gen.XM_051763
Figure 4728: DNA290292, NM_018955, gen.NM_018955
Figure 4729: PRO70449
Figure 4730: DNA326289, XM_058900, gen.XM_058900
Figure 4731: PRO82691
Figure 4732: DNA326290, XM_039921, gen.XM_039921
Figure 4733: PRO82692
Figure 4734: DNA326291, XM_012549, gen.XM_012549
Figure 4735: DNA326292, XM_085548, gen.XM_085548
Figure 4736: PRO82694
Figure 4737: DNA326293, NM_018019, gen.NM_018019
Figure 4738: PRO82695
Figure 4739: DNA326294, NM_138427, gen.NM_138427
Figure 4740: PRO82696
Figure 4741: DNA326295, XM_085545, gen.XM_085545
Figure 4742A-B: DNA227084, NM_004176, gen.NM_004176
Figure 4743: PRO37547
Figure 4744: DNA326296, XM_012615, gen.XM_012615
Figure 4745: DNA326297, XM_085722, gen.XM_085722
Figure 4746: PRO82699
Figure 4747: DNA255414, NM_018242, gen.NM_018242
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Figure 4751: DNA326300, XM_045535, gen.XM_045535
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Figure 4753: PRO82702
Figure 4754: DNA326302, XM_097204, gen.XM_097204
Figure 4755: DNA326303, XM_058867, gen.XM_058867
Figure 4756: PRO82704
Figure 4757: DNA326304, XM_085672, gen.XM_085672
Figure 4758: DNA326305, XM_031536, gen.XM_031536
Figure 4759: PRO82706
Figure 4760: DNA326306, XM_008486, gen.XM_008486
Figure 4761: DNA326307, NM_015584,

gen.NM_015584
Figure 4762: PRO82707
Figure 4763: DNA326308, NM_000638, gen.NM_000638
Figure 4764: PRO82708
Figure 4765A-B: DNA326309, XM_031466, gen.XM_031466
Figure 4766: PRO82709
Figure 4767: DNA326310, XM_031415, gen.XM_031415
Figure 4768: DNA326311, XM_117066, gen.XM_117066
Figure 4769: DNA326312, XM_031427, gen.XM_031427
Figure 4770: PRO82712
Figure 4771: DNA326313, NM_032322, gen.NM_032322
Figure 4772: PRO82713
Figure 4773A-B: DNA326314, XM_050101, gen.XM_050101
Figure 4774: PRO82714
Figure 4775: DNA326315, XM_056730, gen.XM_056730
Figure 4776: PRO82715
Figure 4777: DNA326316, XM_008462, gen.XM_008462
Figure 4778: DNA287427, NM_002815, gen.NM_002815
Figure 4779: PRO69684
Figure 4780: DNA326317, NM_015544, gen.NM_015544
Figure 4781: PRO82717
Figure 4782: DNA188351, NM_005623, gen.NM_005623
Figure 4783: PRO21887
Figure 4784: DNA326318, NM_002878, gen.NM_002878
Figure 4785: PRO82718
Figure 4786: DNA326319, NM_133627, gen.NM_133627
Figure 4787: PRO82719
Figure 4788: DNA326320, NM_133630, gen.NM_133630
Figure 4789: PRO82720
Figure 4790: DNA326321, NM_133629, gen.NM_133629
Figure 4791: PRO82721
Figure 4792: DNA326322, NM_018096, gen.NM_018096
Figure 4793: PRO37791
Figure 4794A-B: DNA326323, XM_039474, gen.XM_039474
Figure 4795: PRO82722
Figure 4796A-B: DNA66475, NM_004448, gen.NM_004448
Figure 4797: PRO1204
Figure 4798: DNA326324, NM_000981, gen.NM_000981
Figure 4799: PRO4738
Figure 4800A-B: DNA326325, XM_008150, gen.XM_008150
Figure 4801: DNA326326, NM_000978, gen.NM_000978
Figure 4802: PRO82724
Figure 4803: DNA326327, XM_058830, gen.XM_058830
Figure 4804: PRO82725
Figure 4805: DNA270979, NM_002809, gen.NM_002809
Figure 4806: PRO59309
Figure 4807: DNA326328, NM_000422, gen.NM_000422
Figure 4808: PRO82726
Figure 4809: DNA326329, XM_008579, gen.XM_008579
Figure 4810: DNA326330, NM_002276, gen.NM_002276
Figure 4811: PRO82728
Figure 4812: DNA272889, NM_002275, gen.NM_002275
Figure 4813: PRO60979
Figure 4814: DNA326331, NM_002274, gen.NM_002274
Figure 4815: PRO82729
Figure 4816: DNA326332, NM_000526, gen.NM_000526
Figure 4817: PRO82730
Figure 4818: DNA326333, XM_049937, gen.XM_049937
Figure 4819A-B: DNA326334, XM_113334, gen.XM_113334
Figure 4820: DNA226389, NM_000964, gen.NM_000964
Figure 4821: PRO36852
Figure 4822: DNA326335, NM_006455, gen.NM_006455
Figure 4823: PRO82732
Figure 4824: DNA326336, XM_113938, gen.XM_113938
Figure 4825: DNA326337, XM_036465, gen.XM_036465
Figure 4826: DNA326338, XM_055061, gen.XM_055061
Figure 4827A-B: DNA326339, XM_036462, gen.XM_036462
Figure 4828: PRO82736
Figure 4829: DNA326340, XM_048654, gen.XM_048654
Figure 4830: DNA326341, NM_025197, gen.NM_025197
Figure 4831: PRO82737
Figure 4832: DNA326342, XM_054038,

gen.XM_054038
Figure 4833: PRO82738
Figure 4834: DNA326343, NM_002265, gen.NM_002265
Figure 4835: PRO82739
Figure 4836: DNA326344, XM_032201, gen.XM_032201
Figure 4837: PRO82740
Figure 4838: DNA326345, NM_012138, gen.NM_012138
Figure 4839: PRO82741
Figure 4840: DNA326346, XM_018534, gen.XM_018534
Figure 4841: DNA227873, NM_001050, gen.NM_001050
Figure 4842: PRO38336
Figure 4843: DNA270975, NM_000386, gen.NM_000386
Figure 4844: PRO59305
Figure 4845: DNA88378, NM_002087, gen.NM_002087
Figure 4846: PRO2769
Figure 4847: DNA326347, NM_016016, gen.NM_016016
Figure 4848: PRO82743
Figure 4849: DNA326348, XM_012642, gen.XM_012642
Figure 4850A-B: DNA326349, NM_005474, gen.NM_005474
Figure 4851: PRO82745
Figure 4852: DNA326350, XM_045901, gen.XM_045901
Figure 4853: PRO82746
Figure 4854: DNA257428, NM_032376, gen.NM_032376
Figure 4855: PRO52010
Figure 4856: DNA326351, XM_008351, gen.XM_008351
Figure 4857: DNA326352, XM_032852, gen.XM_032852
Figure 4858: PRO82748
Figure 4859: DNA326353, NM_025233, gen.NM_025233
Figure 4860: PRO82749
Figure 4861: DNA326354, XM_032817, gen.XM_032817
Figure 4862: PRO82750
Figure 4863: DNA326355, XM_032813, gen.XM_032813
Figure 4864: DNA326356, XM_032766, gen.XM_032766
Figure 4865: DNA326357, NM_003766, gen.NM_003766
Figure 4866: PRO82753
Figure 4867: DNA326358, XM_008401, gen.XM_008401
Figure 4868: PRO82754
Figure 4869: DNA326359, XM_008402, gen.XM_008402
Figure 4870: PRO82755
Figure 4871: DNA326360, NM_017595, gen.NM_017595
Figure 4872: PRO82756
Figure 4873: DNA326361, XM_085636, gen.XM_085636
Figure 4874: PRO82757
Figure 4875: DNA326362, NM_006373, gen.NM_006373
Figure 4876: PRO82758
Figure 4877: DNA196642, NM_005440, gen.NM_005440
Figure 4878: PRO25115
Figure 4879A-B: DNA270901, NM_004247, gen.NM_004247
Figure 4880: DNA326363, XM_050159, gen.XM_050159
Figure 4881: DNA326364, XM_083983, gen.XM_083983
Figure 4882: PRO82760
Figure 4883A-B: DNA326365, NM_021079, gen.NM_021079
Figure 4884: PRO82761
Figure 4885: DNA326366, NM_133373, gen.NM_133373
Figure 4886: PRO82762
Figure 4887: DNA97290, NM_002512, gen.NM_002512
Figure 4888: PRO3637
Figure 4889: DNA227071, NM_000269, gen.NM_000269
Figure 4890: PRO37534
Figure 4891: DNA227764, NM_003971, gen.NM_003971
Figure 4892: PRO38227
Figure 4893A-B: DNA326367, NM_020038, gen.NM_020038
Figure 4894: PRO82763
Figure 4895A-B: DNA326368, NM_020037, gen.NM_020037
Figure 4896: PRO82764
Figure 4897: DNA326369, XM_037971, gen.XM_037971
Figure 4898: DNA254791, NM_018346, gen.NM_018346
Figure 4899: PRO49888
Figure 4900: DNA287425, NM_018509, gen.NM_018509
Figure 4901: PRO69682
Figure 4902A-B: DNA326370, XM_008432, gen.XM_008432
Figure 4903: DNA88554, NM_000250, gen.NM_000250

Figure 4904: PRO2839
Figure 4905: DNA326371, XM_113919, gen.XM_113919
Figure 4906: DNA326372, NM_017777, gen.NM_017777
Figure 4907: PRO82768
Figure 4908: DNA326373, NM_006924, gen.NM_006924
Figure 4909: PRO82769
Figure 4910: DNA326374, XM_115480, gen.XM_115480
Figure 4911: DNA326375, NM_005831, gen.NM_005831
Figure 4912: PRO59328
Figure 4913: DNA326376, XM_117061, gen.XM_117061
Figure 4914: PRO82771
Figure 4915: DNA326377, XM_008459, gen.XM_008459
Figure 4916A-B: DNA326378, XM_012651, gen.XM_012651
Figure 4917: DNA326379, NM_021626, gen.NM_021626
Figure 4918: PRO302
Figure 4919: DNA287291, NM_021213, gen.NM_021213
Figure 4920: PRO69561
Figure 4921A-B: DNA326380, NM_004859, gen.NM_004859
Figure 4922: PRO82774
Figure 4923: DNA326381, XM_083966, gen.XM_083966
Figure 4924: DNA326382, XM_044426, gen.XM_044426
Figure 4925: PRO82776
Figure 4926: DNA326383, XM_008253, gen.XM_008253
Figure 4927: DNA326384, XM_044394, gen.XM_044394
Figure 4928: PRO10400
Figure 4929: DNA326385, NM_017647, gen.NM_017647
Figure 4930: PRO82778
Figure 4931: DNA326386, NM_007372, gen.NM_007372
Figure 4932: PRO82779
Figure 4933: DNA326387, NM_002401, gen.NM_002401
Figure 4934: PRO37764
Figure 4935: DNA326388, XM_044376, gen.XM_044376
Figure 4936A-B: DNA150457, NM_006039, gen.NM_006039
Figure 4937: PRO12265
Figure 4938: DNA326389, XM_044367, gen.XM_044367
Figure 4939: DNA227055, NM_002634, gen.NM_002634
Figure 4940: PRO37518
Figure 4941: DNA326390, XM_011118, gen.XM_011118
Figure 4942: DNA326391, XM_055199, gen.XM_055199
Figure 4943A-B: DNA326392, XM_044372, gen.XM_044372
Figure 4944: DNA326393, XM_113315, gen.XM_113315
Figure 4945: DNA326394, XM_012609, gen.XM_012609
Figure 4946: DNA326395, NM_005220, gen.NM_005220
Figure 4947: PRO82787
Figure 4948: DNA326396, XM_085589, gen.XM_085589
Figure 4949: PRO82788
Figure 4950: DNA326397, XM_012634, gen.XM_012634
Figure 4951: DNA326398, XM_085627, gen.XM_085627
Figure 4952: PRO82790
Figure 4953: DNA150814, NM_002086, gen.NM_002086
Figure 4954: PRO12806
Figure 4955: DNA326399, NM_024844, gen.NM_024844
Figure 4956: PRO82791
Figure 4957: DNA326400, XM_041583, gen.XM_041583
Figure 4958: DNA326401, XM_046932, gen.XM_046932
Figure 4959: PRO82792
Figure 4960: DNA326402, NM_004524, gen.NM_004524
Figure 4961: PRO82793
Figure 4962A-B: DNA326403, XM_113951, gen.XM_113951
Figure 4963A-B: DNA88430, NM_000213, gen.NM_000213
Figure 4964: PRO2788
Figure 4965A-B: DNA326404, XM_036104, gen.XM_036104
Figure 4966: PRO82794
Figure 4967: DNA326405, NM_000154, gen.NM_000154
Figure 4968: PRO82795
Figure 4969: DNA326406, NM_005324, gen.NM_005324
Figure 4970: PRO11403
Figure 4971A-B: DNA326407, XM_036115, gen.XM_036115
Figure 4972: PRO82796
Figure 4973: DNA326408, XM_054344,

gen.XM_054344
Figure 4974: PRO82797
Figure 4975: DNA274755, NM_002766, gen.NM_002766
Figure 4976: PRO70703
Figure 4977A-B: DNA326409, XM_085531, gen.XM_085531
Figure 4978: DNA326410, XM_113892, gen.XM_113892
Figure 4979: PRO82799
Figure 4980: DNA326411, XM_017578, gen.XM_017578
Figure 4981: PRO82800
Figure 4982: DNA326412, XM_036785, gen.XM_036785
Figure 4983: PRO39201
Figure 4984: DNA326413, XM_097043, gen.XM_097043
Figure 4985: DNA129504, NM_001168, gen.NM_001168
Figure 4986: PRO7143
Figure 4987: DNA326414, XM_037196, gen.XM_037196
Figure 4988: DNA326415, XM_037195, gen.XM_037195
Figure 4989: DNA326416, XM_045104, gen.XM_045104
Figure 4990: PRO37540
Figure 4991: DNA326417, XM_085563, gen.XM_085563
Figure 4992A-B: DNA326418, XM_085716, gen.XM_085716
Figure 4993: PRO82805
Figure 4994A-B: DNA326419, XM_049934, gen.XM_049934
Figure 4995: DNA326420, XM_049931, gen.XM_049931
Figure 4996A-B: DNA326421, XM_045581, gen.XM_045581
Figure 4997: PRO82807
Figure 4998: DNA326422, XM_113945, gen.XM_113945
Figure 4999: DNA326423, XM_046481, gen.XM_046481
Figure 5000: DNA326424, XM_097195, gen.XM_097195
Figure 5001: DNA326425, XM_097193, gen.XM_097193
Figure 5002: DNA326426, NM_004309, gen.NM_004309
Figure 5003: PRO61246
Figure 5004: DNA326427, XM_046472, gen.XM_046472
Figure 5005: PRO82812
Figure 5006: DNA326428, NM_016286, gen.NM_016286
Figure 5007: PRO82813
Figure 5008: DNA326429, NM_004127, gen.NM_004127
Figure 5009: PRO82814
Figure 5010A-C: DNA326430, XM_113943, gen.XM_113943
Figure 5011: DNA326431, XM_113330, gen.XM_113330
Figure 5012: PRO82816
Figure 5013: DNA326432, XM_113303, gen.XM_113303
Figure 5014: DNA287234, NM_031968, gen.NM_031968
Figure 5015: PRO69513
Figure 5016: DNA326433, NM_022158, gen.NM_022158
Figure 5017: PRO82818
Figure 5018: DNA326434, XM_038424, gen.XM_038424
Figure 5019: DNA326435, XM_085735, gen.XM_085735
Figure 5020: DNA326436, XM_046765, gen.XM_046765
Figure 5021: DNA326437, XM_046769, gen.XM_046769
Figure 5022: DNA326438, XM_046767, gen.XM_046767
Figure 5023: DNA273694, NM_006101, gen.NM_006101
Figure 5024: PRO61661
Figure 5025A-B: DNA326439, XM_028744, gen.XM_028744
Figure 5026: DNA326440, XM_165954, gen.XM_165954
Figure 5027: DNA326441, XM_041678, gen.XM_041678
Figure 5028: DNA326442, XM_113343, gen.XM_113343
Figure 5029: PRO82825
Figure 5030: DNA326443, XM_067325, gen.XM_067325
Figure 5031: DNA326444, XM_012741, gen.XM_012741
Figure 5032: DNA326445, NM_014214, gen.NM_014214
Figure 5033: PRO82828
Figure 5034A-B: DNA326446, XM_035640, gen.XM_035640
Figure 5035: PRO82829
Figure 5036: DNA326447, XM_016382, gen.XM_016382
Figure 5037: DNA326448, NM_032933, gen.NM_032933
Figure 5038: PRO82831
Figure 5039: DNA274690, NM_006938, gen.NM_006938

Figure 5040A-B: DNA88457, NM_000227, gen.NM_000227
Figure 5041: PRO2799
Figure 5042: DNA326449, XM_085791, gen.XM_085791
Figure 5043: DNA326450, XM_085789, gen.XM_085789
Figure 5044: PRO82833
Figure 5045: DNA326451, XM_085790, gen.XM_085790
Figure 5046: DNA326452, XM_015755, gen.XM_015755
Figure 5047: PRO82835
Figure 5048: DNA326453, XM_097232, gen.XM_097232
Figure 5049: DNA326454, XM_085788, gen.XM_085788
Figure 5050: DNA88281, NM_001944, gen.NM_001944
Figure 5051: PRO2267
Figure 5052: DNA271841, NM_003787, gen.NM_003787
Figure 5053: PRO60121
Figure 5054: DNA326455, XM_008723, gen.XM_008723
Figure 5055: DNA326456, XM_084007, gen.XM_084007
Figure 5056: DNA256813, NM_018255, gen.NM_018255
Figure 5057: PRO51744
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Figure 5059: PRO82840
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Figure 5061: PRO82841
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Figure 5063: PRO82842
Figure 5064: DNA326460, XM_086779, gen.XM_086779
Figure 5065: DNA326461, XM_167363, gen.XM_167363
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Figure 5067: DNA326463, NM_000985, gen.NM_000985
Figure 5068: PRO82846
Figure 5069: DNA326464, NM_002396, gen.NM_002396
Figure 5070: PRO61113
Figure 5071: DNA326465, XM_166288, gen.XM_166288
Figure 5072: DNA326466, NM_004539, gen.NM_004539
Figure 5073: PRO60800
Figure 5074: DNA326467, XM_006937, gen.XM_006937
Figure 5075: DNA326468, XM_085779, gen.XM_085779
Figure 5076: DNA326469, XM_011089, gen.XM_011089
Figure 5077: PRO82850
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Figure 5079: PRO82851
Figure 5080: DNA326471, XM_167008, gen.XM_167008
Figure 5081: PRO82852
Figure 5082: DNA326472, XM_048471, gen.XM_048471
Figure 5083A-B: DNA326473, XM_008812, gen.XM_008812
Figure 5084A-B: DNA326474, XM_117096, gen.XM_117096
Figure 5085: PRO82855
Figure 5086: DNA326475, NM_002385, gen.NM_002385
Figure 5087: PRO82856
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Figure 5089A-B: DNA326477, XM_008695, gen.XM_008695
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Figure 5091: PRO82859
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Figure 5093: DNA326480, NM_003712, gen.NM_003712
Figure 5094: PRO1077
Figure 5095: DNA326481, XM_042018, gen.XM_042018
Figure 5096: PRO2560
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Figure 5098: DNA326483, NM_017876, gen.NM_017876
Figure 5099: PRO82861
Figure 5100: DNA326484, NM_031990, gen.NM_031990
Figure 5101: PRO82862
Figure 5102: DNA326485, NM_002819, gen.NM_002819
Figure 5103: PRO62899
Figure 5104: DNA326486, NM_005224, gen.NM_005224
Figure 5105: PRO82863
Figure 5106: DNA326487, XM_037565, gen.XM_037565
Figure 5107: PRO82864
Figure 5108: DNA326488, XM_092042,

gen.XM_092042
Figure 5109: DNA326489, XM_037572, gen.XM_037572
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Figure 5111: PRO82867
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Figure 5113A-B: DNA326492, XM_009277, gen.XM_009277
Figure 5114: DNA326493, XM_012913, gen.XM_012913
Figure 5115: DNA274101, NM_001687, gen.NM_001687
Figure 5116: PRO62039
Figure 5117: DNA326494, XM_028067, gen.XM_028067
Figure 5118: PRO82871
Figure 5119: DNA326495, XM_028064, gen.XM_028064
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Figure 5121: PRO82872
Figure 5122: DNA326497, NM_000156, gen.NM_000156
Figure 5123: PRO58046
Figure 5124: DNA326498, NM_138924, gen.NM_138924
Figure 5125: PRO82873
Figure 5126: DNA326499, NM_001018, gen.NM_001018
Figure 5127: PRO10485
Figure 5128: DNA326500, XM_086101, gen.XM_086101
Figure 5129: PRO82874
Figure 5130: DNA326501, XM_086102, gen.XM_086102
Figure 5131: DNA326502, XM_047584, gen.XM_047584
Figure 5132A-B: DNA326503, XM_047600, gen.XM_047600
Figure 5133: PRO38496
Figure 5134: DNA326504, XM_097420, gen.XM_097420
Figure 5135A-B: DNA326505, XM_030721, gen.XM_030721
Figure 5136: PRO82877
Figure 5137: DNA326506, XM_030720, gen.XM_030720
Figure 5138: DNA326507, NM_031213, gen.NM_031213
Figure 5139: PRO82879
Figure 5140: DNA326508, XM_039723, gen.XM_039723
Figure 5141: DNA326509, NM_001319, gen.NM_001319
Figure 5142: PRO82881
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Figure 5144: PRO82882
Figure 5145: DNA326511, XM_030714, gen.XM_030714
Figure 5146: DNA256555, NM_017572, gen.NM_017572
Figure 5147: PRO51586
Figure 5148A-B: DNA326512, NM_003938, gen.NM_003938
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Figure 5151: PRO82885
Figure 5152: DNA326514, NM_007165, gen.NM_007165
Figure 5153: PRO82886
Figure 5154: DNA287636, NM_004152, gen.NM_004152
Figure 5155: DNA326515, NM_012458, gen.NM_012458
Figure 5156: PRO82887
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Figure 5158: PRO82888
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Figure 5160: DNA326518, XM_046934, gen.XM_046934
Figure 5161: DNA326519, NM_003021, gen.NM_003021
Figure 5162: PRO62302
Figure 5163: DNA326520, XM_055686, gen.XM_055686
Figure 5164: PRO37951
Figure 5165: DNA326521, XM_009222, gen.XM_009222
Figure 5166: DNA326522, XM_052635, gen.XM_052635
Figure 5167: PRO82892
Figure 5168: DNA326523, XM_052661, gen.XM_052661
Figure 5169: DNA326524, NM_016263, gen.NM_016263
Figure 5170: PRO82893
Figure 5171: DNA326525, NM_006339, gen.NM_006339
Figure 5172: PRO82894
Figure 5173: DNA326526, NM_032753, gen.NM_032753
Figure 5174: PRO82895
Figure 5175: DNA326527, XM_056421, gen.XM_056421
Figure 5176A-B: DNA326528, XM_031917, gen.XM_031917

Figure 5177: PRO82897
Figure 5178: DNA326529, NM_001961, gen.NM_001961
Figure 5179: PRO62225
Figure 5180: DNA326530, XM_016871, gen.XM_016871
Figure 5181: DNA326531, NM_016539, gen.NM_016539
Figure 5182: PRO82899
Figure 5183: DNA326532, XM_117122, gen.XM_117122
Figure 5184: DNA326533, XM_031857, gen.XM_031857
Figure 5185: PRO82901
Figure 5186: DNA326534, NM_024333, gen.NM_024333
Figure 5187: PRO82902
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Figure 5189: PRO82903
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Figure 5191: PRO82904
Figure 5192: DNA326537, XM_035638, gen.XM_035638
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Figure 5194A-B: DNA326538, XM_035636, gen.XM_035636
Figure 5195: DNA326539, XM_012862, gen.XM_012862
Figure 5196A-B: DNA326540, XM_035627, gen.XM_035627
Figure 5197A-B: DNA326541, XM_035625, gen.XM_035625
Figure 5198: PRO82909
Figure 5199: DNA274761, NM_014649, gen.NM_014649
Figure 5200: PRO62531
Figure 5201: DNA272421, NM_006012, gen.NM_006012
Figure 5202: PRO60674
Figure 5203: DNA326542, NM_003685, gen.NM_003685
Figure 5204: PRO82910
Figure 5205A-B: DNA326543, XM_009010, gen.XM_009010
Figure 5206: DNA270315, NM_004240, gen.NM_004240
Figure 5207: PRO58702
Figure 5208: DNA326544, NM_005490, gen.NM_005490
Figure 5209: PRO201
Figure 5210: DNA326546, XM_044619, gen.XM_044619
Figure 5211: PRO82912
Figure 5212: DNA326547, XM_012798, gen.XM_012798
Figure 5213: DNA326548, XM_044608, gen.XM_044608
Figure 5214: DNA326549, NM_003624, gen.NM_003624
Figure 5215: PRO82915
Figure 5216: DNA326550, NM_016579, gen.NM_016579
Figure 5217: PRO224
Figure 5218A-B: DNA326551, XM_048351, gen.XM_048351
Figure 5219: DNA326552, XM_048364, gen.XM_048364
Figure 5220: PRO82917
Figure 5221: DNA326553, XM_091938, gen.XM_091938
Figure 5222: DNA326554, XM_097300, gen.XM_097300
Figure 5223: DNA326555, XM_049282, gen.XM_049282
Figure 5224: PRO82920
Figure 5225: DNA326556, XM_058232, gen.XM_058232
Figure 5226: DNA326557, XM_045151, gen.XM_045151
Figure 5227A-B: DNA326558, XM_050435, gen.XM_050435
Figure 5228: PRO82923
Figure 5229: DNA326559, XM_113988, gen.XM_113988
Figure 5230: DNA326560, NM_058164, gen.NM_058164
Figure 5231: PRO82925
Figure 5232: DNA227280, NM_020230, gen.NM_020230
Figure 5233: PRO37743
Figure 5234: DNA270621, NM_003755, gen.NM_003755
Figure 5235: PRO58991
Figure 5236: DNA326561, XM_049502, gen.XM_049502
Figure 5237: DNA326562, NM_007065, gen.NM_007065
Figure 5238: PRO63226
Figure 5239: DNA326563, XM_049561, gen.XM_049561
Figure 5240: DNA326564, XM_017204, gen.XM_017204
Figure 5241: DNA326565, NM_005498, gen.NM_005498
Figure 5242: PRO62112
Figure 5243: DNA326566, XM_008887, gen.XM_008887
Figure 5244: DNA326567, XM_085862, gen.XM_085862
Figure 5245: PRO82930

Figure 5246: DNA326568, XM_084014, gen.XM_084014
Figure 5247A-B: DNA326569, XM_032710, gen.XM_032710
Figure 5248: DNA326570, XM_032719, gen.XM_032719
Figure 5249: PRO82933
Figure 5250: DNA326571, NM_024029, gen.NM_024029
Figure 5251: PRO23794
Figure 5252: DNA326572, XM_032724, gen.XM_032724
Figure 5253: PRO82934
Figure 5254A-B: DNA326573, NM_003072, gen.NM_003072
Figure 5255: PRO82935
Figure 5256A-B: DNA326574, XM_009082, gen.XM_009082
Figure 5257: DNA326575, XM_032774, gen.XM_032774
Figure 5258: DNA218271, NM_000121, gen.NM_000121
Figure 5259: PRO34323
Figure 5260: DNA326576, XM_057074, gen.XM_057074
Figure 5261: DNA326577, XM_032782, gen.XM_032782
Figure 5262: DNA326578, NM_032377, gen.NM_032377
Figure 5263: PRO82939
Figure 5264: DNA326579, XM_015697, gen.XM_015697
Figure 5265: PRO82940
Figure 5266: DNA326580, XM_010156, gen.XM_010156
Figure 5267: DNA326581, NM_001930, gen.NM_001930
Figure 5268: PRO58446
Figure 5269: DNA326582, NM_013406, gen.NM_013406
Figure 5270: DNA326583, NM_013407, gen.NM_013407
Figure 5271: PRO82943
Figure 5272: DNA103320, NM_002229, gen.NM_002229
Figure 5273: PRO4650
Figure 5274: DNA326584, XM_009063, gen.XM_009063
Figure 5275: PRO82944
Figure 5276: DNA326585, XM_085917, gen.XM_085917
Figure 5277: DNA274034, NM_006397, gen.NM_006397
Figure 5278: PRO61977
Figure 5279: DNA287243, NM_004461, gen.NM_004461
Figure 5280: PRO69518
Figure 5281: DNA326586, XM_032020, gen.XM_032020
Figure 5282: PRO2718
Figure 5283: DNA326587, NM_005053, gen.NM_005053
Figure 5284: PRO22613
Figure 5285: DNA326588, XM_085916, gen.XM_085916
Figure 5286: DNA326589, NM_017722, gen.NM_017722
Figure 5287: PRO82947
Figure 5288: DNA326590, NM_003765, gen.NM_003765
Figure 5289: PRO82948
Figure 5290: DNA326591, XM_051364, gen.XM_051364
Figure 5291: PRO82949
Figure 5292: DNA326592, XM_031345, gen.XM_031345
Figure 5293: PRO82950
Figure 5294: DNA326593, XM_113352, gen.XM_113352
Figure 5295: DNA326594, XM_058967, gen.XM_058967
Figure 5296: PRO82952
Figure 5297: DNA326595, XM_085909, gen.XM_085909
Figure 5298: DNA269894, NM_002730, gen.NM_002730
Figure 5299: PRO58292
Figure 5300: DNA326596, NM_018154, gen.NM_018154
Figure 5301: PRO82954
Figure 5302: DNA326597, XM_031276, gen.XM_031276
Figure 5303: DNA326598, XM_031273, gen.XM_031273
Figure 5304: PRO82956
Figure 5305: DNA326599, XM_031263, gen.XM_031263
Figure 5306: PRO82957
Figure 5307: DNA326600, XM_031251, gen.XM_031251
Figure 5308: DNA326601, NM_006844, gen.NM_006844
Figure 5309: PRO82958
Figure 5310A-C: DNA326602, XM_009303, gen.XM_009303
Figure 5311: DNA326603, XM_086074, gen.XM_086074
Figure 5312: DNA269630, NM_003290, gen.NM_003290
Figure 5313: PRO58042
Figure 5314: DNA326604, NM_005370, gen.NM_005370

Figure 5315: PRO12130
Figure 5316: DNA326605, XM_113348, gen.XM_113348
Figure 5317: DNA326606, NM_032207, gen.NM_032207
Figure 5318: PRO82962
Figure 5319A-B: DNA326607, NM_006387, gen.NM_006387
Figure 5320: PRO82963
Figure 5321: DNA326608, NM_024881, gen.NM_024881
Figure 5322: PRO82964
Figure 5323: DNA326609, NM_024104, gen.NM_024104
Figure 5324: PRO82965
Figure 5325A-C: DNA326610, XM_008854, gen.XM_008854
Figure 5326: DNA326611, NM_014173, gen.NM_014173
Figure 5327: PRO82967
Figure 5328: DNA287240, NM_004335, gen.NM_004335
Figure 5329: PRO29371
Figure 5330: DNA326612, XM_050660, gen.XM_050660
Figure 5331: DNA326613, XM_086116, gen.XM_086116
Figure 5332: DNA326614, NM_018174, gen.NM_018174
Figure 5333: PRO82970
Figure 5334: DNA326615, NM_000980, gen.NM_000980
Figure 5335: PRO82971
Figure 5336: DNA326616, XM_055230, gen.XM_055230
Figure 5337: DNA326617, XM_012179, gen.XM_012179
Figure 5338A-B: DNA326618, XM_009293, gen.XM_009293
Figure 5339: DNA326619, XM_038146, gen.XM_038146
Figure 5340: PRO82975
Figure 5341: DNA326620, XM_092046, gen.XM_092046
Figure 5342: PRO82976
Figure 5343: DNA326621, XM_038098, gen.XM_038098
Figure 5344: PRO82977
Figure 5345: DNA326622, NM_032627, gen.NM_032627
Figure 5346: PRO82978
Figure 5347: DNA326623, XM_165960, gen.XM_165960
Figure 5348: PRO82979
Figure 5349: DNA326624, XM_114004, gen.XM_114004
Figure 5350: DNA326625, NM_012181, gen.NM_012181
Figure 5351: PRO82980
Figure 5352: DNA227249, NM_007263, gen.NM_007263
Figure 5353: PRO37712
Figure 5354: DNA326626, XM_018515, gen.XM_018515
Figure 5355: DNA326627, NM_033415, gen.NM_033415
Figure 5356: PRO82982
Figure 5357: DNA326628, XM_009330, gen.XM_009330
Figure 5358: DNA326629, NM_134440, gen.NM_134440
Figure 5359: PRO82983
Figure 5360: DNA326630, NM_003721, gen.NM_003721
Figure 5361: PRO59220
Figure 5362: DNA326631, NM_015965, gen.NM_015965
Figure 5363: PRO82984
Figure 5364: DNA326632, XM_016378, gen.XM_016378
Figure 5365: PRO82985
Figure 5366: DNA326633, XM_114027, gen.XM_114027
Figure 5367: DNA326634, XM_165963, gen.XM_165963
Figure 5368: PRO82987
Figure 5369: DNA326635, XM_015769, gen.XM_015769
Figure 5370: DNA326636, XM_012812, gen.XM_012812
Figure 5371: DNA326637, XM_085971, gen.XM_085971
Figure 5372: DNA326638, XM_037662, gen.XM_037662
Figure 5373: PRO82991
Figure 5374: DNA326639, NM_001238, gen.NM_001238
Figure 5375: PRO82992
Figure 5376: DNA326640, NM_057182, gen.NM_057182
Figure 5377: PRO4756
Figure 5378: DNA326641, XM_009180, gen.XM_009180
Figure 5379: DNA326642, XM_117118, gen.XM_117118
Figure 5380: DNA326643, XM_092049, gen.XM_092049
Figure 5381: PRO82995
Figure 5382: DNA326644, XM_028672, gen.XM_028672
Figure 5383: DNA326645, XM_028666, gen.XM_028666

Figure 5384: DNA326646, XM_009338, gen.XM_009338
Figure 5385: DNA326647, XM_048258, gen.XM_048258
Figure 5386: PRO82998
Figure 5387: DNA256836, NM_018468, gen.NM_018468
Figure 5388: PRO51767
Figure 5389: DNA326648, NM_024321, gen.NM_024321
Figure 5390: PRO82999
Figure 5391A-B: DNA326649, XM_049237, gen.XM_049237
Figure 5392: PRO83000
Figure 5393: DNA326650, NM_032635, gen.NM_032635
Figure 5394: PRO23845
Figure 5395: DNA326651, XM_115615, gen.XM_115615
Figure 5396A-B: DNA326652, XM_091984, gen.XM_091984
Figure 5397: PRO83002
Figure 5398: DNA326653, XM_085986, gen.XM_085986
Figure 5399: DNA326654, XM_032285, gen.XM_032285
Figure 5400: PRO83004
Figure 5401: DNA326655, NM_002812, gen.NM_002812
Figure 5402: PRO83005
Figure 5403A-E: DNA326656, XM_029455, gen.XM_029455
Figure 5404: DNA326657, XM_029450, gen.XM_029450
Figure 5405: PRO83007
Figure 5406: DNA326658, XM_009149, gen.XM_009149
Figure 5407: PRO62500
Figure 5408: DNA326659, XM_056602, gen.XM_056602
Figure 5409: DNA326660, NM_012237, gen.NM_012237
Figure 5410: PRO83008
Figure 5411: DNA326661, NM_030593, gen.NM_030593
Figure 5412: PRO83009
Figure 5413: DNA326662, NM_017827, gen.NM_017827
Figure 5414: PRO83010
Figure 5415: DNA326663, NM_021107, gen.NM_021107
Figure 5416: PRO83011
Figure 5417: DNA326664, NM_033363, gen.NM_033363
Figure 5418: PRO83012
Figure 5419: DNA326665, XM_059045, gen.XM_059045
Figure 5420: PRO83013
Figure 5421: DNA273474, NM_005884, gen.NM_005884
Figure 5422: PRO61458
Figure 5423: DNA326666, XM_046090, gen.XM_046090
Figure 5424: PRO83014
Figure 5425: DNA326667, XM_086004, gen.XM_086004
Figure 5426: DNA272347, NM_001020, gen.NM_001020
Figure 5427: PRO60603
Figure 5428A-B: DNA326668, NM_003169, gen.NM_003169
Figure 5429: PRO12822
Figure 5430: DNA326669, XM_053074, gen.XM_053074
Figure 5431: PRO83016
Figure 5432: DNA326670, NM_016941, gen.NM_016941
Figure 5433: PRO83017
Figure 5434: DNA256840, NM_004714, gen.NM_004714
Figure 5435: PRO51771
Figure 5436: DNA326671, NM_001436, gen.NM_001436
Figure 5437: PRO83018
Figure 5438: DNA326672, XM_016410, gen.XM_016410
Figure 5439: DNA326673, XM_012860, gen.XM_012860
Figure 5440: DNA326674, XM_097365, gen.XM_097365
Figure 5441: DNA274139, NM_006503, gen.NM_006503
Figure 5442: PRO62075
Figure 5443: DNA326675, XM_009203, gen.XM_009203
Figure 5444: DNA326676, XM_047409, gen.XM_047409
Figure 5445: DNA326677, XM_047376, gen.XM_047376
Figure 5446A-B: DNA326678, XM_047374, gen.XM_047374
Figure 5447: DNA326679, XM_059052, gen.XM_059052
Figure 5448: DNA273600, NM_004596, gen.NM_004596
Figure 5449: PRO61575
Figure 5450: DNA326680, XM_030914, gen.XM_030914
Figure 5451: DNA326681, NM_052848, gen.NM_052848
Figure 5452: PRO83027
Figure 5453: DNA326682, XM_008912,

gen.XM_008912
Figure 5454: DNA326683, NM_020158, gen.NM_020158
Figure 5455: PRO83029
Figure 5456: DNA326684, XM_030901, gen.XM_030901
Figure 5457: PRO83030
Figure 5458: DNA326685, NM_018035, gen.NM_018035
Figure 5459: PRO83031
Figure 5460: DNA326686, XM_085874, gen.XM_085874
Figure 5461: DNA326687, XM_085875, gen.XM_085875
Figure 5462: DNA326688, XM_085876, gen.XM_085876
Figure 5463: DNA326689, XM_058949, gen.XM_058949
Figure 5464: PRO83035
Figure 5465: DNA326690, XM_030895, gen.XM_030895
Figure 5466: DNA326691, XM_115603, gen.XM_115603
Figure 5467: PRO83037
Figure 5468: DNA326692, NM_001022, gen.NM_001022
Figure 5469: PRO83038
Figure 5470: DNA326693, NM_004706, gen.NM_004706
Figure 5471: PRO83039
Figure 5472: DNA326694, XM_008878, gen.XM_008878
Figure 5473: PRO83040
Figure 5474: DNA326695, NM_022752, gen.NM_022752
Figure 5475: PRO83041
Figure 5476: DNA151808, NM_006494, gen.NM_006494
Figure 5477: PRO12892
Figure 5478: DNA326696, NM_001816, gen.NM_001816
Figure 5479: PRO34151
Figure 5480: DNA326697, NM_000554, gen.NM_000554
Figure 5481: PRO83042
Figure 5482: DNA326698, XM_049920, gen.XM_049920
Figure 5483: DNA326699, XM_055859, gen.XM_055859
Figure 5484A-B: DNA326700, XM_009125, gen.XM_009125
Figure 5485: DNA326701, XM_008860, gen.XM_008860
Figure 5486: DNA326702, XM_009036, gen.XM_009036
Figure 5487: DNA326703, XM_085950, gen.XM_085950
Figure 5488: DNA326704, XM_028263, gen.XM_028263
Figure 5489: DNA326705, XM_085928, gen.XM_085928
Figure 5490: PRO36963
Figure 5491: DNA326706, XM_028267, gen.XM_028267
Figure 5492: DNA326707, NM_013403, gen.NM_013403
Figure 5493: PRO83050
Figure 5494: DNA103580, NM_001743, gen.NM_001743
Figure 5495: PRO4904
Figure 5496: DNA326708, XM_009126, gen.XM_009126
Figure 5497: DNA326709, NM_006247, gen.NM_006247
Figure 5498: PRO25881
Figure 5499: DNA326710, NM_003370, gen.NM_003370
Figure 5500: PRO83052
Figure 5501: DNA326711, XM_085856, gen.XM_085856
Figure 5502: DNA150784, NM_001983, gen.NM_001983
Figure 5503: PRO12800
Figure 5504: DNA270931, NM_012099, gen.NM_012099
Figure 5505: PRO59264
Figure 5506A-B: DNA257531, NM_031417, gen.NM_031417
Figure 5507: PRO52101
Figure 5508: DNA326712, NM_001294, gen.NM_001294
Figure 5509: PRO83054
Figure 5510: DNA326713, XM_097274, gen.XM_097274
Figure 5511: DNA88084, NM_000041, gen.NM_000041
Figure 5512: PRO2644
Figure 5513: DNA256533, NM_006114, gen.NM_006114
Figure 5514: PRO51565
Figure 5515: DNA251057, NM_002856, gen.NM_002856
Figure 5516: PRO47354
Figure 5517: DNA226011, NM_005581, gen.NM_005581
Figure 5518: PRO36474
Figure 5519: DNA326714, NM_012116, gen.NM_012116
Figure 5520: PRO83056
Figure 5521: DNA326715, XM_097275, gen.XM_097275
Figure 5522: DNA326716, XM_008851,

gen.XM_008851
Figure 5523: DNA274289, NM_016440, gen.NM_016440
Figure 5524: PRO62212
Figure 5525: DNA326717, NM_012068, gen.NM_012068
Figure 5526: PRO83059
Figure 5527: DNA326718, XM_085927, gen.XM_085927
Figure 5528: DNA326719, XM_084023, gen.XM_084023
Figure 5529: DNA326720, XM_167530, gen.XM_167530
Figure 5530: DNA326721, XM_114025, gen.XM_114025
Figure 5531: DNA326722, XM_008985, gen.XM_008985
Figure 5532: DNA326723, NM_030973, gen.NM_030973
Figure 5533: PRO83065
Figure 5534: DNA326724, NM_025129, gen.NM_025129
Figure 5535: PRO83066
Figure 5536: DNA326725, NM_014203, gen.NM_014203
Figure 5537: DNA326726, XM_085934, gen.XM_085934
Figure 5538: PRO83068
Figure 5539: DNA326727, NM_001536, gen.NM_001536
Figure 5540: PRO83069
Figure 5541: DNA326728, XM_165432, gen.XM_165432
Figure 5542: DNA274823, NM_001571, gen.NM_001571
Figure 5543: PRO62582
Figure 5544A-B: DNA326729, XM_046313, gen.XM_046313
Figure 5545: PRO83071
Figure 5546: DNA326730, NM_015953, gen.NM_015953
Figure 5547: PRO83072
Figure 5548: DNA326731, XM_027904, gen.XM_027904
Figure 5549: DNA326732, XM_084026, gen.XM_084026
Figure 5550: DNA290260, NM_012423, gen.NM_012423
Figure 5551: PRO70385
Figure 5552: DNA326733, XM_058991, gen.XM_058991
Figure 5553: PRO83073
Figure 5554: DNA326734, NM_017916, gen.NM_017916
Figure 5555: PRO83074
Figure 5556: DNA326735, NM_003598, gen.NM_003598
Figure 5557: PRO83075
Figure 5558: DNA326736, NM_006666, gen.NM_006666
Figure 5559: PRO83076
Figure 5560: DNA326737, XM_114024, gen.XM_114024
Figure 5561: PRO83077
Figure 5562: DNA304658, NM_000146, gen.NM_000146
Figure 5563: PRO71085
Figure 5564: DNA326738, NM_004324, gen.NM_004324
Figure 5565: PRO38101
Figure 5566: DNA326739, NM_006184, gen.NM_006184
Figure 5567: PRO83078
Figure 5568: DNA273066, NM_001190, gen.NM_001190
Figure 5569: PRO61129
Figure 5570: DNA326740, XM_058987, gen.XM_058987
Figure 5571: DNA326741, NM_000979, gen.NM_000979
Figure 5572: PRO83080
Figure 5573: DNA326742, XM_085935, gen.XM_085935
Figure 5574: DNA326743, NM_031485, gen.NM_031485
Figure 5575: PRO61308
Figure 5576: DNA103239, NM_006801, gen.NM_006801
Figure 5577: PRO4569
Figure 5578: DNA326744, XM_046419, gen.XM_046419
Figure 5579: PRO83082
Figure 5580: DNA326745, NM_002691, gen.NM_002691
Figure 5581: PRO83083
Figure 5582: DNA326746, XM_056286, gen.XM_056286
Figure 5583: PRO83084
Figure 5584: DNA326747, XM_058990, gen.XM_058990
Figure 5585: PRO83085
Figure 5586: DNA326748, XM_091981, gen.XM_091981
Figure 5587: PRO83086
Figure 5588: DNA326749, NM_032712, gen.NM_032712
Figure 5589: PRO23238
Figure 5590: DNA83154, NM_001648, gen.NM_001648
Figure 5591: PRO2109
Figure 5592: DNA326750, XM_055658, gen.XM_055658

Figure 5593: DNA269481, NM_001985, gen.NM_001985
Figure 5594: PRO57901
Figure 5595: DNA326751, XM_091886, gen.XM_091886
Figure 5596: PRO83087
Figure 5597: DNA326752, XM_008830, gen.XM_008830
Figure 5598: DNA326753, XM_039908, gen.XM_039908
Figure 5599: PRO83089
Figure 5600: DNA326754, NM_015629, gen.NM_015629
Figure 5601: PRO83090
Figure 5602: DNA326755, XM_050236, gen.XM_050236
Figure 5603: DNA326756, XM_050589, gen.XM_050589
Figure 5604: PRO83092
Figure 5605: DNA326757, XM_117128, gen.XM_117128
Figure 5606: PRO83093
Figure 5607: DNA326758, XM_059321, gen.XM_059321
Figure 5608: DNA326759, NM_003283, gen.NM_003283
Figure 5609: PRO83095
Figure 5610A-B: DNA326760, NM_014931, gen.NM_014931
Figure 5611: PRO83096
Figure 5612: DNA326761, XM_035919, gen.XM_035919
Figure 5613: DNA326762, NM_000991, gen.NM_000991
Figure 5614: PRO83098
Figure 5615: DNA273346, NM_014501, gen.NM_014501
Figure 5616: PRO61349
Figure 5617: DNA326763, NM_013333, gen.NM_013333
Figure 5618: PRO83099
Figure 5619: DNA326764, NM_007279, gen.NM_007279
Figure 5620: PRO83100
Figure 5621: DNA326765, NM_016202, gen.NM_016202
Figure 5622: PRO83101
Figure 5623: DNA326766, XM_034377, gen.XM_034377
Figure 5624: PRO83102
Figure 5625: DNA272062, NM_014453, gen.NM_014453
Figure 5626: PRO60333
Figure 5627: DNA254548, NM_005762, gen.NM_005762
Figure 5628: PRO49653
Figure 5629: DNA326767, XM_085972, gen.XM_085972
Figure 5630: PRO83103
Figure 5631: DNA326768, NM_032792, gen.NM_032792
Figure 5632: PRO83104
Figure 5633: DNA326769, NM_001009, gen.NM_001009
Figure 5634: PRO83105
Figure 5635: DNA326770, XM_058125, gen.XM_058125
Figure 5636: DNA326771, NM_024691, gen.NM_024691
Figure 5637: PRO83107
Figure 5638: DNA297288, NM_021158, gen.NM_021158
Figure 5639: PRO70810
Figure 5640: DNA304662, NM_031229, gen.NM_031229
Figure 5641: PRO71089
Figure 5642: DNA326772, NM_031228, gen.NM_031228
Figure 5643: PRO83108
Figure 5644: DNA326773, XM_097749, gen.XM_097749
Figure 5645: PRO83109
Figure 5646: DNA326774, XM_055993, gen.XM_055993
Figure 5647: DNA326775, XM_009622, gen.XM_009622
Figure 5648: DNA326776, NM_000801, gen.NM_000801
Figure 5649: PRO59142
Figure 5650: DNA326777, NM_054014, gen.NM_054014
Figure 5651: PRO59142
Figure 5652: DNA326778, NM_016143, gen.NM_016143
Figure 5653: PRO83112
Figure 5654: DNA287270, NM_003091, gen.NM_003091
Figure 5655: PRO69541
Figure 5656: DNA326779, NM_052881, gen.NM_052881
Figure 5657: PRO83113
Figure 5658: DNA326780, XM_044914, gen.XM_044914
Figure 5659: PRO83114
Figure 5660: DNA326781, XM_044915, gen.XM_044915
Figure 5661: DNA326782, NM_006899, gen.NM_006899
Figure 5662: PRO83116
Figure 5663: DNA326783, NM_019609, gen.NM_019609
Figure 5664: PRO83117

Figure 5665: DNA326784, NM_021826, gen.NM_021826
Figure 5666: PRO83118
Figure 5667: DNA326785, XM_045418, gen.XM_045418
Figure 5668: DNA287261, NM_017874, gen.NM_017874
Figure 5669: PRO69533
Figure 5670: DNA326786, XM_086710, gen.XM_086710
Figure 5671: DNA326787, XM_045451, gen.XM_045451
Figure 5672: PRO83121
Figure 5673: DNA326788, XM_114174, gen.XM_114174
Figure 5674: DNA326789, XM_045460, gen.XM_045460
Figure 5675: DNA326790, XM_059268, gen.XM_059268
Figure 5676A-B: DNA271010, NM_014737, gen.NM_014737
Figure 5677: PRO59339
Figure 5678: DNA326791, XM_056035, gen.XM_056035
Figure 5679: DNA83170, NM_001819, gen.NM_001819
Figure 5680: PRO2615
Figure 5681: DNA227348, NM_019095, gen.NM_019095
Figure 5682: PRO37811
Figure 5683: DNA326792; NM_003092, gen.NM_003092
Figure 5684: PRO83125
Figure 5685: DNA287290, NM_014426, gen.NM_014426
Figure 5686: PRO69560
Figure 5687: DNA326793, XM_086701, gen.XM_086701
Figure 5688: DNA326794, XM_117209, gen.XM_117209
Figure 5689A-B: DNA326795, XM_046520, gen.XM_046520
Figure 5690: PRO83128
Figure 5691: DNA326796, XM_115846, gen.XM_115846
Figure 5692: PRO83129
Figure 5693: DNA326797, NM_080820, gen.NM_080820
Figure 5694: PRO83130
Figure 5695: DNA326798, XM_086715, gen.XM_086715
Figure 5696: DNA326799, XM_092760, gen.XM_092760
Figure 5697: PRO83132
Figure 5698: DNA326800, NM_012255, gen.NM_012255
Figure 5699: PRO83133
Figure 5700: DNA326801, XM_012970, gen.XM_012970
Figure 5701: DNA326802, XM_042765, gen.XM_042765
Figure 5702: PRO83135
Figure 5703: DNA150548, NM_001247, gen.NM_001247
Figure 5704: PRO12324
Figure 5705A-B: DNA326803, XM_009436, gen.XM_009436
Figure 5706: DNA326804, XM_114178, gen.XM_114178
Figure 5707: PRO83137
Figure 5708: DNA326805, XM_046160, gen.XM_046160
Figure 5709: PRO83138
Figure 5710: DNA326806, XM_046179, gen.XM_046179
Figure 5711: PRO83139
Figure 5712: DNA326807, XM_086745, gen.XM_086745
Figure 5713: DNA326808, NM_138578, gen.NM_138578
Figure 5714: PRO83141
Figure 5715: DNA326809, NM_012112, gen.NM_012112
Figure 5716: PRO83142
Figure 5717: DNA326810, XM_086736, gen.XM_086736
Figure 5718: PRO83143
Figure 5719: DNA326811, NM_030815, gen.NM_030815
Figure 5720: PRO83144
Figure 5721A-B: DNA150767, NM_014742, gen.NM_014742
Figure 5722: PRO12460
Figure 5723A-B: DNA326812, XM_047007, gen.XM_047007
Figure 5724: PRO83145
Figure 5725A-B: DNA326813, XM_047011, gen.XM_047011
Figure 5726: PRO83146
Figure 5727A-B: DNA326814, XM_047018, gen.XM_047018
Figure 5728: DNA326815, XM_009450, gen.XM_009450
Figure 5729: DNA326816, NM_033197, gen.NM_033197
Figure 5730: PRO83149
Figure 5731: DNA326817, XM_097772, gen.XM_097772
Figure 5732: PRO83150
Figure 5733: DNA326818, NM_016732, gen.NM_016732
Figure 5734: DNA97298, NM_003908,

gen.NM_003908
Figure 5735: PRO3645
Figure 5736: DNA326819, NM_000687, gen.NM_000687
Figure 5737: PRO83152
Figure 5738: DNA273517, NM_000178, gen.NM_000178
Figure 5739: PRO61498
Figure 5740: DNA326820, NM_018217, gen.NM_018217
Figure 5741: PRO83153
Figure 5742: DNA326821, NM_002212, gen.NM_002212
Figure 5743: PRO60945
Figure 5744A-C: DNA326822, NM_007186, gen.NM_007186
Figure 5745: DNA226758, NM_015966, gen.NM_015966
Figure 5746: PRO37221
Figure 5747: DNA194701, NM_003915, gen.NM_003915
Figure 5748: PRO24002
Figure 5749: DNA326823, XM_113380, gen.XM_113380
Figure 5750: DNA326824, NM_016558, gen.NM_016558
Figure 5751: PRO83155
Figure 5752: DNA326825, NM_015511, gen.NM_015511
Figure 5753: PRO83156
Figure 5754: DNA326826, XM_009501, gen.XM_009501
Figure 5755: PRO83157
Figure 5756: DNA326827, XM_057236, gen.XM_057236
Figure 5757: DNA326828, NM_024918, gen.NM_024918
Figure 5758: PRO83159
Figure 5759: DNA326829, XM_009642, gen.XM_009642
Figure 5760: DNA194807, NM_006698, gen.NM_006698
Figure 5761: PRO24077
Figure 5762: DNA326830, XM_009686, gen.XM_009686
Figure 5763: DNA326831, NM_030877, gen.NM_030877
Figure 5764: PRO83161
Figure 5765: DNA326832, XM_028806, gen.XM_028806
Figure 5766A-B: DNA326833, XM_028810, gen.XM_028810
Figure 5767: PRO83163
Figure 5768: DNA326834, XM_012931, gen.XM_012931
Figure 5769: DNA326835, NM_024855, gen.NM_024855
Figure 5770: PRO83165
Figure 5771A-B: DNA227472, NM_002660, gen.NM_002660
Figure 5772: PRO37935
Figure 5773: DNA326836, XM_097727, gen.XM_097727
Figure 5774: DNA103525, NM_002466, gen.NM_002466
Figure 5775: PRO4852
Figure 5776: DNA326837, XM_029810, gen.XM_029810
Figure 5777: PRO83167
Figure 5778: DNA326838, XM_029822, gen.XM_029822
Figure 5779: DNA326839, NM_002638, gen.NM_002638
Figure 5780: PRO2065
Figure 5781: DNA326840, NM_003064, gen.NM_003064
Figure 5782: PRO1720
Figure 5783: DNA326841, NM_015937, gen.NM_015937
Figure 5784: PRO83169
Figure 5785: DNA273320, NM_007019, gen.NM_007019
Figure 5786: PRO61327
Figure 5787: DNA326842, NM_033421, gen.NM_033421
Figure 5788: PRO83170
Figure 5789: DNA88569, NM_006227, gen.NM_006227
Figure 5790: PRO2420
Figure 5791: DNA88239, NM_004994, gen.NM_004994
Figure 5792: PRO2711
Figure 5793: DNA326843, XM_057374, gen.XM_057374
Figure 5794: DNA326844, XM_114163, gen.XM_114163
Figure 5795A-B: DNA326845, XM_097731, gen.XM_097731
Figure 5796A-B: DNA326846, XM_030044, gen.XM_030044
Figure 5797: PRO83174
Figure 5798: DNA326847, NM_017895, gen.NM_017895
Figure 5799: PRO83175
Figure 5800: DNA326848, XM_097713, gen.XM_097713
Figure 5801: PRO83176
Figure 5802: DNA326849, NM_005985, gen.NM_005985
Figure 5803: PRO83177
Figure 5804: DNA326850, NM_003349, gen.NM_003349

Figure 5805: PRO83178
Figure 5806: DNA326851, NM_022442, gen.NM_022442
Figure 5807: PRO83179
Figure 5808: DNA326852, NM_005194, gen.NM_005194
Figure 5809: DNA326853, NM_002827, gen.NM_002827
Figure 5810: PRO38066
Figure 5811: DNA326854, NM_003859, gen.NM_003859
Figure 5812: PRO83180
Figure 5813: DNA326855, XM_114165, gen.XM_114165
Figure 5814: DNA269526, NM_001324, gen.NM_001324
Figure 5815: PRO57942
Figure 5816: DNA326856, XM_009549, gen.XM_009549
Figure 5817: PRO83182
Figure 5818: DNA326857, XM_030621, gen.XM_030621
Figure 5819: DNA326858, XM_086648, gen.XM_086648
Figure 5820: PRO83183
Figure 5821: DNA326859, XM_009672, gen.XM_009672
Figure 5822: PRO83184
Figure 5823A-B: DNA326860, XM_009671, gen.XM_009671
Figure 5824: DNA326861, NM_004738, gen.NM_004738
Figure 5825: PRO983
Figure 5826: DNA326862, NM_016592, gen.NM_016592
Figure 5827: PRO83185
Figure 5828: DNA326863, NM_080425, gen.NM_080425
Figure 5829: PRO83186
Figure 5830: DNA304670, NM_000516, gen.NM_000516
Figure 5831: PRO71097
Figure 5832: DNA326864, NM_080426, gen.NM_080426
Figure 5833: PRO83187
Figure 5834: DNA326865, XM_030699, gen.XM_030699
Figure 5835: PRO83188
Figure 5836: DNA188229, NM_000114, gen.NM_000114
Figure 5837: PRO21728
Figure 5838: DNA326866, NM_002792, gen.NM_002792
Figure 5839: PRO83189
Figure 5840A-B: DNA326867, XM_037202, gen.XM_037202
Figure 5841: PRO83190
Figure 5842: DNA326868, XM_037206, gen.XM_037206
Figure 5843: PRO83191
Figure 5844: DNA103486, NM_007002, gen.NM_007002
Figure 5845: PRO4813
Figure 5846A-D: DNA326869, XM_037217, gen.XM_037217
Figure 5847: DNA326870, NM_001024, gen.NM_001024
Figure 5848: PRO83193
Figure 5849: DNA326871, NM_018270, gen.NM_018270
Figure 5850: PRO83194
Figure 5851: DNA326872, XM_028783, gen.XM_028783
Figure 5852: PRO83195
Figure 5853: DNA326873, NM_001853, gen.NM_001853
Figure 5854: PRO83196
Figure 5855: DNA326874, NM_080796, gen.NM_080796
Figure 5856: PRO83197
Figure 5857: DNA326875, NM_022105, gen.NM_022105
Figure 5858: PRO83198
Figure 5859: DNA326876, NM_080797, gen.NM_080797
Figure 5860: PRO83199
Figure 5861: DNA326877, NM_018209, gen.NM_018209
Figure 5862: PRO83200
Figure 5863A-C: DNA326878, XM_028834, gen.XM_028834
Figure 5864: PRO83201
Figure 5865: DNA326879, NM_024299, gen.NM_024299
Figure 5866: PRO83202
Figure 5867A-C: DNA326880, XM_028918, gen.XM_028918
Figure 5868: PRO83203
Figure 5869: DNA326881, NM_032527, gen.NM_032527
Figure 5870: PRO83204
Figure 5871A-B: DNA326882, XM_028966, gen.XM_028966
Figure 5872: PRO83205
Figure 5873: DNA269746, NM_012469, gen.NM_012469
Figure 5874: PRO58155
Figure 5875: DNA326883, XM_114154, gen.XM_114154
Figure 5876: DNA326884, XM_072173, gen.XM_072173
Figure 5877: DNA326885, XM_086759,

gen.XM_086759
Figure 5878: DNA326886, XM_086760, gen.XM_086760
Figure 5879: DNA326887, NM_021219, gen.NM_021219
Figure 5880: PRO28687
Figure 5881: DNA188732, NM_000484, gen.NM_000484
Figure 5882: PRO25302
Figure 5883: DNA326888, NM_016940, gen.NM_016940
Figure 5884: PRO83210
Figure 5885: DNA254572, NM_006585, gen.NM_006585
Figure 5886: PRO49675
Figure 5887: DNA326889, NM_005806, gen.NM_005806
Figure 5888: PRO83211
Figure 5889: DNA326890, XM_114185, gen.XM_114185
Figure 5890: DNA254994, NM_017613, gen.NM_017613
Figure 5891: PRO50083
Figure 5892: DNA274129, NM_001697, gen.NM_001697
Figure 5893: PRO62065
Figure 5894: DNA326891, NM_001757, gen.NM_001757
Figure 5895: PRO83212
Figure 5896A-C: DNA151898, NM_003316, gen.NM_003316
Figure 5897: PRO12135
Figure 5898: DNA326892, NM_003720, gen.NM_003720
Figure 5899: PRO83213
Figure 5900: DNA326893, NM_002606, gen.NM_002606
Figure 5901: PRO83214
Figure 5902: DNA326894, XM_033015, gen.XM_033015
Figure 5903: DNA326895, XM_033016, gen.XM_033016
Figure 5904: PRO59669
Figure 5905: DNA326896, NM_003681, gen.NM_003681
Figure 5906: PRO69486
Figure 5907: DNA326897, XM_035999, gen.XM_035999
Figure 5908: DNA326898, NM_020132, gen.NM_020132
Figure 5909: PRO83217
Figure 5910: DNA326899, XM_036011, gen.XM_036011
Figure 5911: DNA326900, NM_013369, gen.NM_013369
Figure 5912: PRO83219
Figure 5913: DNA326901, XM_036042, gen.XM_036042
Figure 5914: DNA326902, XM_086770, gen.XM_086770
Figure 5915: DNA326903, NM_004928, gen.NM_004928
Figure 5916: PRO83222
Figure 5917: DNA326904, XM_036087, gen.XM_036087
Figure 5918: PRO83223
Figure 5919: DNA326905, XM_009805, gen.XM_009805
Figure 5920: PRO83224
Figure 5921: DNA226409, NM_004339, gen.NM_004339
Figure 5922: PRO36872
Figure 5923: DNA326906, XM_036107, gen.XM_036107
Figure 5924A-B: DNA326907, XM_036175, gen.XM_036175
Figure 5925: DNA326908, XM_097817, gen.XM_097817
Figure 5926A-B: DNA326909, XM_054566, gen.XM_054566
Figure 5927: DNA326910, XM_036755, gen.XM_036755
Figure 5928: DNA326911, XM_086773, gen.XM_086773
Figure 5929: DNA326912, XM_097807, gen.XM_097807
Figure 5930: DNA326913, XM_086777, gen.XM_086777
Figure 5931: DNA326914, NM_002340, gen.NM_002340
Figure 5932: PRO83233
Figure 5933A-B: DNA326915, NM_003906, gen.NM_003906
Figure 5934: PRO83234
Figure 5935: DNA226617, NM_006272, gen.NM_006272
Figure 5936: PRO37080
Figure 5937: DNA326916, NM_033070, gen.NM_033070
Figure 5938: PRO83235
Figure 5939: DNA255046, NM_017829, gen.NM_017829
Figure 5940: PRO50134
Figure 5941: DNA326917, NM_001696, gen.NM_001696
Figure 5942: PRO83236
Figure 5943A-B: DNA326918, XM_032996, gen.XM_032996
Figure 5944: PRO83237
Figure 5945: DNA326919, XM_167538, gen.XM_167538
Figure 5946: DNA326920, XM_033090,

gen.XM_033090
Figure 5947: DNA225954, NM_000407, gen.NM_000407
Figure 5948: PRO36417
Figure 5949: DNA326921, XM_058918, gen.XM_058918
Figure 5950: DNA326922, XM_097833, gen.XM_097833
Figure 5951: DNA326923, NM_024627, gen.NM_024627
Figure 5952: PRO83242
Figure 5953: DNA326924, XM_086809, gen.XM_086809
Figure 5954: DNA326925, NM_006440, gen.NM_006440
Figure 5955: PRO83244
Figure 5956: DNA226561, NM_000754, gen.NM_000754
Figure 5957: PRO37024
Figure 5958: DNA326926, NM_007310, gen.NM_007310
Figure 5959: PRO83245
Figure 5960A-B: DNA326927, XM_033813, gen.XM_033813
Figure 5961: DNA326928, NM_022727, gen.NM_022727
Figure 5962: PRO83247
Figure 5963: DNA326929, XM_086805, gen.XM_086805
Figure 5964: DNA326930, XM_086873, gen.XM_086873
Figure 5965: DNA257549, NM_030573, gen.NM_030573
Figure 5966: PRO52119
Figure 5967: DNA326931, XM_096155, gen.XM_096155
Figure 5968: DNA326932, XM_096156, gen.XM_096156
Figure 5969A-B: DNA326933, XM_036937, gen.XM_036937
Figure 5970: PRO83252
Figure 5971: DNA326934, XM_097886, gen.XM_097886
Figure 5972: PRO83253
Figure 5973: DNA304835, NM_022044, gen.NM_022044
Figure 5974: PRO71242
Figure 5975: DNA326935, NM_006115, gen.NM_006115
Figure 5976: PRO37012
Figure 5977: DNA326936, XM_037682, gen.XM_037682
Figure 5978: PRO83254
Figure 5979: DNA326937, NM_002415, gen.NM_002415
Figure 5980: PRO83255
Figure 5981A-B: DNA326938, XM_037797, gen.XM_037797
Figure 5982: PRO83256
Figure 5983: DNA326939, NM_004175, gen.NM_004175
Figure 5984: PRO83257
Figure 5985: DNA326940, XM_086821, gen.XM_086821
Figure 5986: DNA326941, XM_092888, gen.XM_092888
Figure 5987: DNA326942, NM_005080, gen.NM_005080
Figure 5988: PRO83260
Figure 5989: DNA269830, NM_005243, gen.NM_005243
Figure 5990: PRO58232
Figure 5991: DNA326943, NM_006478, gen.NM_006478
Figure 5992: PRO83261
Figure 5993A-B: DNA326944, XM_037945, gen.XM_037945
Figure 5994: DNA103462, NM_000268, gen.NM_000268
Figure 5995: PRO4789
Figure 5996: DNA326945, NM_032204, gen.NM_032204
Figure 5997: PRO83263
Figure 5998: DNA326946, XM_066291, gen.XM_066291
Figure 5999: DNA326947, NM_005877, gen.NM_005877
Figure 6000: PRO62328
Figure 6001: DNA326948, NM_016498, gen.NM_016498
Figure 6002: PRO83265
Figure 6003: DNA254141, NM_014303, gen.NM_014303
Figure 6004: PRO49256
Figure 6005A-B: DNA151882, NM_014941, gen.NM_014941
Figure 6006: PRO12134
Figure 6007: DNA326949, NM_006932, gen.NM_006932
Figure 6008: PRO83266
Figure 6009: DNA326950, NM_134269, gen.NM_134269
Figure 6010: PRO83267
Figure 6011: DNA270697, NM_004147, gen.NM_004147
Figure 6012: PRO59061
Figure 6013: DNA326951, XM_059335, gen.XM_059335
Figure 6014: DNA326952, XM_018539, gen.XM_018539
Figure 6015: DNA326953, NM_014306, gen.NM_014306

Figure 6016: PRO83270
Figure 6017: DNA326954, NM_012179, gen.NM_012179
Figure 6018: PRO83271
Figure 6019A-B: DNA326955, XM_038584, gen.XM_038584
Figure 6020: DNA151752, NM_002133, gen.NM_002133
Figure 6021: PRO12886
Figure 6022: DNA326956, XM_009947, gen.XM_009947
Figure 6023: PRO12845
Figure 6024: DNA326957, XM_114209, gen.XM_114209
Figure 6025A-B: DNA326958, NM_002473, gen.NM_002473
Figure 6026: PRO83273
Figure 6027: DNA188740, NM_003753, gen.NM_003753
Figure 6028: PRO22481
Figure 6029: DNA326959, NM_021126, gen.NM_021126
Figure 6030: PRO70331
Figure 6031: DNA326960, XM_009967, gen.XM_009967
Figure 6032: DNA326961, NM_013365, gen.NM_013365
Figure 6033: PRO83274
Figure 6034: DNA290259, NM_018957, gen.NM_018957
Figure 6035: PRO70383
Figure 6036: DNA326962, NM_020315, gen.NM_020315
Figure 6037: PRO83275
Figure 6038: DNA304719, NM_002305, gen.NM_002305
Figure 6039: PRO71145
Figure 6040: DNA326963, NM_007032, gen.NM_007032
Figure 6041: PRO83276
Figure 6042: DNA326964, XM_009973, gen.XM_009973
Figure 6043: DNA326965, XM_086830, gen.XM_086830
Figure 6044: PRO83278
Figure 6045: DNA254240, NM_016091, gen.NM_016091
Figure 6046: PRO49352
Figure 6047A-B: DNA326966, XM_039236, gen.XM_039236
Figure 6048: PRO83279
Figure 6049: DNA326967, NM_006941, gen.NM_006941
Figure 6050: PRO83280
Figure 6051: DNA326968, XM_039248, gen.XM_039248
Figure 6052: DNA326969, NM_012323, gen.NM_012323
Figure 6053: PRO83282
Figure 6054: DNA326970, NM_012264, gen.NM_012264
Figure 6055: PRO12490
Figure 6056: DNA326971, NM_015373, gen.NM_015373
Figure 6057: PRO83283
Figure 6058: DNA326972, NM_020243, gen.NM_020243
Figure 6059: PRO23231
Figure 6060: DNA326973, XM_039339, gen.XM_039339
Figure 6061: DNA326974, NM_000967, gen.NM_000967
Figure 6062: PRO83285
Figure 6063: DNA326975, XM_010000, gen.XM_010000
Figure 6064: DNA326976, XM_010002, gen.XM_010002
Figure 6065: DNA326977, XM_039372, gen.XM_039372
Figure 6066: DNA326978, XM_013010, gen.XM_013010
Figure 6067: PRO83288
Figure 6068: DNA254165, NM_000026, gen.NM_000026
Figure 6069: PRO49278
Figure 6070: DNA326979, NM_003932, gen.NM_003932
Figure 6071: PRO4586
Figure 6072: DNA326980, NM_014248, gen.NM_014248
Figure 6073: PRO83289
Figure 6074: DNA326981, XM_086844, gen.XM_086844
Figure 6075: DNA219225, NM_002883, gen.NM_002883
Figure 6076: PRO34531
Figure 6077: DNA326982, NM_003216, gen.NM_003216
Figure 6078: PRO83291
Figure 6079: DNA270954, NM_001098, gen.NM_001098
Figure 6080: PRO59285
Figure 6081: DNA326983, NM_001469, gen.NM_001469
Figure 6082: PRO4872
Figure 6083: DNA326984, NM_005008, gen.NM_005008
Figure 6084: PRO83292
Figure 6085A-B: DNA326985, NM_004599, gen.NM_004599
Figure 6086: PRO83293
Figure 6087A-B: DNA326986, XM_010024,

gen.XM_010024
Figure 6088: DNA326987, XM_040066, gen.XM_040066
Figure 6089: DNA326988, XM_013015, gen.XM_013015
Figure 6090A-B: DNA326989, XM_084084, gen.XM_084084
Figure 6091: DNA326990, XM_040095, gen.XM_040095
Figure 6092: PRO83297
Figure 6093: DNA326991, XM_086875, gen.XM_086875
Figure 6094: DNA326992, XM_010029, gen.XM_010029
Figure 6095: DNA326993, NM_007311, gen.NM_007311
Figure 6096: PRO83300
Figure 6097: DNA326994, NM_015140, gen.NM_015140
Figure 6098: PRO83301
Figure 6099: DNA326995, XM_043614, gen.XM_043614
Figure 6100: PRO83302
Figure 6101: DNA256070, NM_022141, gen.NM_022141
Figure 6102: PRO51119
Figure 6103: DNA326996, XM_010040, gen.XM_010040
Figure 6104: DNA237931, NM_005036, gen.NM_005036
Figure 6105: PRO39030
Figure 6106A-B: DNA326997, XM_027143, gen.XM_027143
Figure 6107: PRO83304
Figure 6108A-B: DNA326998, XM_010055, gen.XM_010055
Figure 6109: DNA326999, NM_025204, gen.NM_025204
Figure 6110: PRO83306
Figure 6111: DNA327000, XM_041248, gen.XM_041248
Figure 6112: PRO83307
Figure 6113: DNA327001, XM_092966, gen.XM_092966
Figure 6114: DNA327002, XM_037468, gen.XM_037468
Figure 6115: PRO83309
Figure 6116: DNA327003, XM_037474, gen.XM_037474
Figure 6117: PRO83310
Figure 6118: DNA327004, XM_013029, gen.XM_013029
Figure 6119: DNA327005, XM_114724, gen.XM_114724
Figure 6120: PRO83312
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DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

The terms "TAT polypeptide" and "TAT" as used herein and when immediately followed by a numerical designation, refer to various polypeptides, wherein the complete designation (i.e.,TAT/number) refers to specific polypeptide sequences as described herein. The terms "TAT/number polypeptide" and "TAT/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides, polypeptide variants and fragments of native sequence polypeptides and polypeptide variants (which are further defined herein). The TAT polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "TAT polypeptide" refers to each individual TAT/number polypeptide disclosed herein. All disclosures in this specification which refer to the "TAT polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, formation of TAT binding oligopeptides to or against, formation of TAT binding organic molecules to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "TAT polypeptide" also includes variants of the TAT/number polypeptides disclosed herein.

A "native sequence TAT polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding TAT polypeptide derived from nature. Such native sequence TAT polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence TAT polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific TAT polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In certain embodiments of the invention, the native sequence TAT polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons (if indicated) are shown in bold font and underlined in the figures. Nucleic acid residues indicated as "N" in the accompanying figures are any nucleic acid residue. However, while the TAT polypeptides disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the TAT polypeptides.

The TAT polypeptide "extracellular domain" or "ECD" refers to a form of the TAT polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a TAT polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the TAT polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an

extracellular domain of a TAT polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various TAT polypeptides disclosed herein may be shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"TAT polypeptide variant" means a TAT polypeptide, preferably an active TAT polypeptide, as defined herein having at least about 80% amino acid sequence identity with a full-length native sequence TAT polypeptide sequence as disclosed herein, a TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length TAT polypeptide). Such TAT polypeptide variants include, for instance, TAT polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a TAT polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity, to a full-length native sequence TAT polypeptide sequence as disclosed herein, a TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide sequence as disclosed herein. Ordinarily, TAT variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600 amino acids in length, or more. Optionally, TAT variant polypeptides will have no more than one conservative amino acid substitution as compared to the native TAT polypeptide sequence, alternatively no more than 2, 3, 4, 5, 6, 7, 8, 9, or 10 conservative amino acid substitution as compared to the native TAT polypeptide sequence.

"Percent (%) amino acid sequence identity" with respect to the TAT polypeptide sequences identified

herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific TAT polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "TAT", wherein "TAT" represents the amino acid sequence of a hypothetical TAT polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "TAT" polypeptide of interest is being compared, and "X, "Y" and "Z" each represent different hypothetical amino acid residues. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

"TAT variant polynucleotide" or "TAT variant nucleic acid sequence" means a nucleic acid molecule

which encodes a TAT polypeptide, preferably an active TAT polypeptide, as defined herein and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence TAT polypeptide sequence as disclosed herein, a full-length native sequence TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length TAT polypeptide). Ordinarily, a TAT variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence TAT polypeptide sequence as disclosed herein, a full-length native sequence TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, TAT variant polynucleotides are at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length.

"Percent (%) nucleic acid sequence identity" with respect to TAT-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the TAT nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison

parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "TAT-DNA", wherein "TAT-DNA" represents a hypothetical TAT-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "TAT-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides. Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

In other embodiments, TAT variant polynucleotides are nucleic acid molecules that encode a TAT polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length TAT polypeptide as disclosed herein. TAT variant polypeptides may be those that are encoded by a TAT variant polynucleotide.

The term "full-length coding region" when used in reference to a nucleic acid encoding a TAT polypeptide refers to the sequence of nucleotides which encode the full-length TAT polypeptide of the invention (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures). The term "full-length coding region" when used in reference to an ATCC deposited nucleic acid refers to the TAT polypeptide-encoding portion of the cDNA that is inserted into the vector deposited with the ATCC (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures).

"Isolated," when used to describe the various TAT polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or,

preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the TAT polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" TAT polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium

chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) overnight hybridization in a solution that employs 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with a 10 minute wash at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) followed by a 10 minute high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent that those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a TAT polypeptide or anti-TAT antibody fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

"Active" or "activity" for the purposes herein refers to form(s) of a TAT polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring TAT, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring TAT other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring TAT and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring TAT.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native TAT polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native TAT polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native TAT polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a TAT polypeptide may comprise contacting a TAT polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities

normally associated with the TAT polypeptide.

"Treating" or "treatment" or "alleviation" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented. A subject or mammal is successfully "treated" for a TAT polypeptide-expressing cancer if, after receiving a therapeutic amount of an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule according to the methods of the present invention, the patient shows observable and/or measurable reduction in or absence of one or more of the following: reduction in the number of cancer cells or absence of the cancer cells; reduction in the tumor size; inhibition (i.e., slow to some extent and preferably stop) of cancer cell infiltration into peripheral organs including the spread of cancer into soft tissue and bone; inhibition (i.e., slow to some extent and preferably stop) of tumor metastasis; inhibition, to some extent, of tumor growth; and/or relief to some extent, one or more of the symptoms associated with the specific cancer; reduced morbidity and mortality, and improvement in quality of life issues. To the extent the anti-TAT antibody or TAT binding oligopeptide may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. Reduction of these signs or symptoms may also be felt by the patient.

The above parameters for assessing successful treatment and improvement in the disease are readily measurable by routine procedures familiar to a physician. For cancer therapy, efficacy can be measured, for example, by assessing the time to disease progression (TTP) and/or determining the response rate (RR). Metastasis can be determined by staging tests and by bone scan and tests for calcium level and other enzymes to determine spread to the bone. CT scans can also be done to look for spread to the pelvis and lymph nodes in the area. Chest X-rays and measurement of liver enzyme levels by known methods are used to look for metastasis to the lungs and liver, respectively. Other routine methods for monitoring the disease include transrectal ultrasonography (TRUS) and transrectal needle biopsy (TRNB).

For bladder cancer, which is a more localized cancer, methods to determine progress of disease include urinary cytologic evaluation by cystoscopy, monitoring for presence of blood in the urine, visualization of the urothelial tract by sonography or an intravenous pyelogram, computed tomography (CT) and magnetic resonance imaging (MRI). The presence of distant metastases can be assessed by CT of the abdomen, chest x-rays, or radionuclide imaging of the skeleton.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of the treatment of, alleviating the symptoms of or diagnosis of a cancer refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous

(concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN® , polyethylene glycol (PEG), and PLURONICS®.

By "solid phase" or "solid support" is meant a non-aqueous matrix to which an antibody, TAT binding oligopeptide or TAT binding organic molecule of the present invention can adhere or attach. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a TAT polypeptide, an antibody thereto or a TAT binding oligopeptide) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small" molecule or "small" organic molecule is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide, antibody, TAT binding oligopeptide, TAT binding organic molecule or an agonist or antagonist thereof as disclosed herein is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.

The term "therapeutically effective amount" refers to an amount of an antibody, polypeptide, TAT binding oligopeptide, TAT binding organic molecule or other drug effective to "treat" a disease or disorder in a subject or mammal. In the case of cancer, the therapeutically effective amount of the drug may reduce the number of cancer cells; reduce the tumor size; inhibit (i.e., slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (i.e., slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the cancer. See the definition herein of "treating". To the extent the drug may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic.

A "growth inhibitory amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide

or TAT binding organic molecule is an amount capable of inhibiting the growth of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "growth inhibitory amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule for purposes of inhibiting neoplastic cell growth may be determined empirically and in a routine manner.

A "cytotoxic amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule is an amount capable of causing the destruction of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "cytotoxic amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule for purposes of inhibiting neoplastic cell growth may be determined empirically and in a routine manner.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-TAT monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-TAT antibody compositions with polyepitopic specificity, polyclonal antibodies, single chain anti-TAT antibodies, and fragments of anti-TAT antibodies (see below) as long as they exhibit the desired biological or immunological activity. The term "immunoglobulin" (Ig) is used interchangeable with antibody herein.

An "isolated antibody" is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

The basic 4-chain antibody unit is a heterotetrameric glycoprotein composed of two identical light (L) chains and two identical heavy (H) chains (an IgM antibody consists of 5 of the basic heterotetramer unit along with an additional polypeptide called J chain, and therefore contain 10 antigen binding sites, while secreted IgA antibodies can polymerize to form polyvalent assemblages comprising 2-5 of the basic 4-chain units along with J chain). In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to a H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each H and L chain also has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable domain (V_H) followed by three constant domains (C_H) for each of the α and γ chains and four C_H domains for μ and ϵ isotypes. Each L chain has at the N-terminus, a variable domain (V_L) followed by a constant domain (C_L) at its other end. The V_L is aligned with the V_H and the C_L is aligned with the first constant domain of the heavy chain (C_H1). Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains. The pairing of a V_H and V_L together forms a single antigen-binding site. For the structure and properties of the

different classes of antibodies, see, e.g., Basic and Clinical Immunology, 8th edition, Daniel P. Stites, Abba I. Terr and Tristram G. Parslow (eds.), Appleton & Lange, Norwalk, CT, 1994, page 71 and Chapter 6.

The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (C_H), immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, having heavy chains designated α, δ, ε, γ, and μ, respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in C_H sequence and function, e.g., humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

The term "variable" refers to the fact that certain segments of the variable domains differ extensively in sequence among antibodies. The V domain mediates antigen binding and define specificity of a particular antibody for its particular antigen. However, the variability is not evenly distributed across the 110-amino acid span of the variable domains. Instead, the V regions consist of relatively invariant stretches called framework regions (FRs) of 15-30 amino acids separated by shorter regions of extreme variability called "hypervariable regions" that are each 9-12 amino acids long. The variable domains of native heavy and light chains each comprise four FRs, largely adopting a β-sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

The term "hypervariable region" when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a "complementarity determining region" or "CDR" (e.g. around about residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the V_L, and around about 1-35 (H1), 50-65 (H2) and 95-102 (H3) in the V_H; Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a "hypervariable loop" (*e.g.* residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the V_L, and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the V_H; Chothia and Lesk J. Mol. Biol. 196:901-917 (1987)).

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to polyclonal antibody preparations which include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they may be synthesized uncontaminated by other antibodies.

The modifier "monoclonal" is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies useful in the present invention may be prepared by the hybridoma methodology first described by Kohler et al., Nature, 256:495 (1975), or may be made using recombinant DNA methods in bacterial, eukaryotic animal or plant cells (see, e.g., U.S. Patent No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson et al., Nature, 352:624-628 (1991) and Marks et al., J. Mol. Biol., 222:581-597 (1991), for example.

The monoclonal antibodies herein include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (see U.S. Patent No. 4,816,567; and Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)). Chimeric antibodies of interest herein include "primatized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (*e.g.* Old World Monkey, Ape etc), and human constant region sequences.

An "intact" antibody is one which comprises an antigen-binding site as well as a C_L and at least heavy chain constant domains, C_H1, C_H2 and C_H3. The constant domains may be native sequence constant domains (*e.g.* human native sequence constant domains) or amino acid sequence variant thereof. Preferably, the intact antibody has one or more effector functions.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies (see U.S. Patent No. 5,641,870, Example 2; Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. The Fab fragment consists of an entire L chain along with the variable region domain of the H chain (V_H), and the first constant domain of one heavy chain (C_H1). Each Fab fragment is monovalent with respect to antigen binding, i.e., it has a single antigen-binding site. Pepsin treatment of an antibody yields a single large $F(ab')_2$ fragment which roughly corresponds to two disulfide linked Fab fragments having divalent antigen-binding activity and is still capable of cross-linking antigen. Fab' fragments differ from Fab fragments by having additional few residues at the carboxy terminus of the C_H1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The Fc fragment comprises the carboxy-terminal portions of both H chains held together by disulfides.

The effector functions of antibodies are determined by sequences in the Fc region, which region is also the part recognized by Fc receptors (FcR) found on certain types of cells.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This fragment consists of a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (3 loops each from the H and L chain) that contribute the amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

"Single-chain Fv" also abbreviated as "sFv" or "scFv" are antibody fragments that comprise the V_H and V_L antibody domains connected into a single polypeptide chain. Preferably, the sFv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994); Borrebaeck 1995, infra.

The term "diabodies" refers to small antibody fragments prepared by constructing sFv fragments (see preceding paragraph) with short linkers (about 5-10 residues) between the V_H and V_L domains such that inter-chain but not intra-chain pairing of the V domains is achieved, resulting in a bivalent fragment, i.e., fragment having two antigen-binding sites. Bispecific diabodies are heterodimers of two "crossover" sFv fragments in which the V_H and V_L domains of the two antibodies are present on different polypeptide chains. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

"Humanized" forms of non-human (*e.g.*, rodent) antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or non-human primate having the desired antibody specificity, affinity, and capability. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones et al., Nature 321:522-525 (1986); Riechmann et al., Nature 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol. 2:593-596 (1992).

A "species-dependent antibody," e.g., a mammalian anti-human IgE antibody, is an antibody which

has a stronger binding affinity for an antigen from a first mammalian species than it has for a homologue of that antigen from a second mammalian species. Normally, the species-dependent antibody "bind specifically" to a human antigen (i.e., has a binding affinity (Kd) value of no more than about 1 x 10^{-7} M, preferably no more than about 1 x 10^{-8} and most preferably no more than about 1 x 10^{-9} M) but has a binding affinity for a homologue of the antigen from a second non-human mammalian species which is at least about 50 fold, or at least about 500 fold, or at least about 1000 fold, weaker than its binding affinity for the human antigen. The species-dependent antibody can be of any of the various types of antibodies as defined above, but preferably is a humanized or human antibody.

A "TAT binding oligopeptide" is an oligopeptide that binds, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be chemically synthesized using known oligopeptide synthesis methodology or may be prepared and purified using recombinant technology. TAT binding oligopeptides are usually at least about 5 amino acids in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length or more, wherein such oligopeptides that are capable of binding, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening oligopeptide libraries for oligopeptides that are capable of specifically binding to a polypeptide target are well known in the art (see, e.g., U.S. Patent Nos. 5,556,762, 5,750,373, 4,708,871, 4,833,092, 5,223,409, 5,403,484, 5,571,689, 5,663,143; PCT Publication Nos. WO 84/03506 and WO84/03564; Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 81:3998-4002 (1984); Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 82:178-182 (1985); Geysen et al., in Synthetic Peptides as Antigens, 130-149 (1986); Geysen et al., J. Immunol. Meth., 102:259-274 (1987); Schoofs et al., J. Immunol., 140:611-616 (1988), Cwirla, S. E. et al. (1990) Proc. Natl. Acad. Sci. USA, 87:6378; Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363, and Smith, G. P. (1991) Current Opin. Biotechnol., 2:668).

A "TAT binding organic molecule" is an organic molecule other than an oligopeptide or antibody as defined herein that binds, preferably specifically, to a TAT polypeptide as described herein. TAT binding organic molecules may be identified and chemically synthesized using known methodology (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules are usually less than about 2000 daltons in size, alternatively less than about 1500, 750, 500, 250 or 200 daltons in size, wherein such organic molecules that are capable of binding, preferably specifically, to a TAT polypeptide as described herein may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening organic molecule libraries for molecules that are capable of binding to a polypeptide target are well known in the art (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585).

An antibody, oligopeptide or other organic molecule "which binds" an antigen of interest, e.g. a tumor-associated polypeptide antigen target, is one that binds the antigen with sufficient affinity such that the antibody, oligopeptide or other organic molecule is useful as a diagnostic and/or therapeutic agent in targeting a cell or tissue expressing the antigen, and does not significantly cross-react with other proteins. In such embodiments, the extent of binding of the antibody, oligopeptide or other organic molecule to a "non-target" protein will be less than about 10% of the binding of the antibody, oligopeptide or other organic molecule to its particular target protein as determined by fluorescence activated cell sorting (FACS) analysis or radioimmunoprecipitation (RIA). With regard to the binding of an antibody, oligopeptide or other organic molecule to a target molecule, the term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target means binding that is measurably different from a non-specific interaction. Specific binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule, which generally is a molecule of similar structure that does not have binding activity. For example, specific binding can be determined by competition with a control molecule that is similar to the target, for example, an excess of non-labeled target. In this case, specific binding is indicated if the binding of the labeled target to a probe is competitively inhibited by excess unlabeled target. The term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target as used herein can be exhibited, for example, by a molecule having a Kd for the target of at least about 10^{-4} M, alternatively at least about 10^{-5} M, alternatively at least about 10^{-6} M, alternatively at least about 10^{-7} M, alternatively at least about 10^{-8} M, alternatively at least about 10^{-9} M, alternatively at least about 10^{-10} M, alternatively at least about 10^{-11} M, alternatively at least about 10^{-12} M, or greater. In one embodiment, the term "specific binding" refers to binding where a molecule binds to a particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

An antibody, oligopeptide or other organic molecule that "inhibits the growth of tumor cells expressing a TAT polypeptide" or a "growth inhibitory" antibody, oligopeptide or other organic molecule is one which results in measurable growth inhibition of cancer cells expressing or overexpressing the appropriate TAT polypeptide. The TAT polypeptide may be a transmembrane polypeptide expressed on the surface of a cancer cell or may be a polypeptide that is produced and secreted by a cancer cell. Preferred growth inhibitory anti-TAT antibodies, oligopeptides or organic molecules inhibit growth of TAT-expressing tumor cells by greater

than 20%, preferably from about 20% to about 50%, and even more preferably, by greater than 50% (e.g., from about 50% to about 100%) as compared to the appropriate control, the control typically being tumor cells not treated with the antibody, oligopeptide or other organic molecule being tested. In one embodiment, growth inhibition can be measured at an antibody concentration of about 0.1 to 30 μg/ml or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the tumor cells to the antibody. Growth inhibition of tumor cells *in vivo* can be determined in various ways such as is described in the Experimental Examples section below. The antibody is growth inhibitory in vivo if administration of the anti-TAT antibody at about 1 μg/kg to about 100 mg/kg body weight results in reduction in tumor size or tumor cell proliferation within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

An antibody, oligopeptide or other organic molecule which "induces apoptosis" is one which induces programmed cell death as determined by binding of annexin V, fragmentation of DNA, cell shrinkage, dilation of endoplasmic reticulum, cell fragmentation, and/or formation of membrane vesicles (called apoptotic bodies). The cell is usually one which overexpresses a TAT polypeptide. Preferably the cell is a tumor cell, e.g., a prostate, breast, ovarian, stomach, endometrial, lung, kidney, colon, bladder cell. Various methods are available for evaluating the cellular events associated with apoptosis. For example, phosphatidyl serine (PS) translocation can be measured by annexin binding; DNA fragmentation can be evaluated through DNA laddering; and nuclear/chromatin condensation along with DNA fragmentation can be evaluated by any increase in hypodiploid cells. Preferably, the antibody, oligopeptide or other organic molecule which induces apoptosis is one which results in about 2 to 50 fold, preferably about 5 to 50 fold, and most preferably about 10 to 50 fold, induction of annexin binding relative to untreated cell in an annexin binding assay.

Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor); and B cell activation.

"Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refers to a form of cytotoxicity in which secreted Ig bound onto Fc receptors (FcRs) present on certain cytotoxic cells (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxins. The antibodies "arm" the cytotoxic cells and are absolutely required for such killing. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, Annu. Rev. Immunol. 9:457-92 (1991). To assess ADCC activity of a molecule of interest, an in vitro ADCC assay, such as that described in US Patent No. 5,500,362 or 5,821,337 may be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed in vivo, e.g., in a animal model such as that disclosed in Clynes et al.

(USA) 95:652-656 (1998).

"Fc receptor" or "FcR" describes a receptor that binds to the Fc region of an antibody. The preferred FcR is a native sequence human FcR. Moreover, a preferred FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. FcγRII receptors include FcγRIIA (an "activating receptor") and FcγRIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor Fc γRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain. (see review M. in Daëron, Annu. Rev. Immunol. 15:203-234 (1997)). FcRs are reviewed in Ravetch and Kinet, Annu. Rev. Immunol. 9:457-492 (1991); Capel et al., Immunomethods 4:25-34 (1994); and de Haas et al., J. Lab. Clin. Med. 126:330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term "FcR" herein. The term also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J. Immunol. 117:587 (1976) and Kim et al., J. Immunol. 24:249 (1994)).

"Human effector cells" are leukocytes which express one or more FcRs and perform effector functions. Preferably, the cells express at least Fc γRIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils; with PBMCs and NK cells being preferred. The effector cells may be isolated from a native source, e.g., from blood.

"Complement dependent cytotoxicity" or "CDC" refers to the lysis of a target cell in the presence of complement. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system (C1q) to antibodies (of the appropriate subclass) which are bound to their cognate antigen. To assess complement activation, a CDC assay, e.g., as described in Gazzano-Santoro et al., J. Immunol. Methods 202:163 (1996), may be performed.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, multiple myeloma and B-cell lymphoma, brain, as well as head and neck cancer, and associated metastases.

The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are

associated with some degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder is cancer.

"Tumor", as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

An antibody, oligopeptide or other organic molecule which "induces cell death" is one which causes a viable cell to become nonviable. The cell is one which expresses a TAT polypeptide, preferably a cell that overexpresses a TAT polypeptide as compared to a normal cell of the same tissue type. The TAT polypeptide may be a transmembrane polypeptide expressed on the surface of a cancer cell or may be a polypeptide that is produced and secreted by a cancer cell. Preferably, the cell is a cancer cell, e.g., a breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, thyroid, pancreatic or bladder cell. Cell death *in vitro* may be determined in the absence of complement and immune effector cells to distinguish cell death induced by antibody-dependent cell-mediated cytotoxicity (ADCC) or complement dependent cytotoxicity (CDC). Thus, the assay for cell death may be performed using heat inactivated serum (i.e., in the absence of complement) and in the absence of immune effector cells. To determine whether the antibody, oligopeptide or other organic molecule is able to induce cell death, loss of membrane integrity as evaluated by uptake of propidium iodide (PI), trypan blue (see Moore et al. Cytotechnology 17:1-11 (1995)) or 7AAD can be assessed relative to untreated cells. Preferred cell death-inducing antibodies, oligopeptides or other organic molecules are those which induce PI uptake in the PI uptake assay in BT474 cells.

A "TAT-expressing cell" is a cell which expresses an endogenous or transfected TAT polypeptide either on the cell surface or in a secreted form. A "TAT-expressing cancer" is a cancer comprising cells that have a TAT polypeptide present on the cell surface or that produce and secrete a TAT polypeptide. A "TAT-expressing cancer" optionally produces sufficient levels of TAT polypeptide on the surface of cells thereof, such that an anti-TAT antibody, oligopeptide ot other organic molecule can bind thereto and have a therapeutic effect with respect to the cancer. In another embodiment, a "TAT-expressing cancer" optionally produces and secretes sufficient levels of TAT polypeptide, such that an anti-TAT antibody, oligopeptide ot other organic molecule antagonist can bind thereto and have a therapeutic effect with respect to the cancer. With regard to the latter, the antagonist may be an antisense oligonucleotide which reduces, inhibits or prevents production and secretion of the secreted TAT polypeptide by tumor cells. A cancer which "overexpresses" a TAT polypeptide is one which has significantly higher levels of TAT polypeptide at the cell surface thereof, or produces and secretes, compared to a noncancerous cell of the same tissue type. Such overexpression may be caused by gene amplification or by increased transcription or translation. TAT polypeptide overexpression may be determined in a diagnostic or prognostic assay by evaluating increased levels of the TAT protein present on the surface of a cell, or secreted by the cell (e.g., via an immunohistochemistry assay using anti-TAT antibodies prepared against an isolated TAT polypeptide which may be prepared using recombinant DNA technology from an isolated nucleic acid encoding the TAT polypeptide; FACS analysis, etc.). Alternatively, or additionally, one may measure levels of TAT polypeptide-encoding nucleic acid or mRNA in the cell, e.g., via fluorescent *in situ* hybridization using a nucleic acid based probe corresponding to a TAT-encoding nucleic acid or the complement

thereof; (FISH; see WO98/45479 published October, 1998), Southern blotting, Northern blotting, or polymerase chain reaction (PCR) techniques, such as real time quantitative PCR (RT-PCR). One may also study TAT polypeptide overexpression by measuring shed antigen in a biological fluid such as serum, e.g, using antibody-based assays (see also, e.g., U.S. Patent No. 4,933,294 issued June 12, 1990; WO91/05264 published April 18, 1991; U.S. Patent 5,401,638 issued March 28, 1995; and Sias et al., J. Immunol. Methods 132:73-80 (1990)). Aside from the above assays, various *in vivo* assays are available to the skilled practitioner. For example, one may expose cells within the body of the patient to an antibody which is optionally labeled with a detectable label, e.g., a radioactive isotope, and binding of the antibody to cells in the patient can be evaluated, e.g., by external scanning for radioactivity or by analyzing a biopsy taken from a patient previously exposed to the antibody.

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody, oligopeptide or other organic molecule so as to generate a "labeled" antibody, oligopeptide or other organic molecule. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g., At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32} and radioactive isotopes of Lu), chemotherapeutic agents e.g. methotrexate, adriamicin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof such as nucleolytic enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof, and the various antitumor or anticancer agents disclosed below. Other cytotoxic agents are described below. A tumoricidal agent causes destruction of tumor cells.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially a TAT-expressing cancer cell, either *in vitro* or *in vivo*. Thus, the growth inhibitory agent may be one which significantly reduces the percentage of TAT-expressing cells in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such

as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topoisomerase II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in The Molecular Basis of Cancer, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogenes, and antineoplastic drugs" by Murakami et al. (WB Saunders: Philadelphia, 1995), especially p. 13. The taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (TAXOTERE®, Rhone-Poulenc Rorer), derived from the European yew, is a semisynthetic analogue of paclitaxel (TAXOL®, Bristol-Myers Squibb). Paclitaxel and docetaxel promote the assembly of microtubules from tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

"Doxorubicin" is an anthracycline antibiotic. The full chemical name of doxorubicin is (8S-cis)-10-[(3-amino-2,3,6-trideoxy-α-L-lyxo-hexapyranosyl)oxy]-7,8,9,10-tetrahydro-6,8,11-trihydroxy-8-(hydroxyacetyl)-1-methoxy-5,12-naphthacenedione.

The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor-α and -β; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF-β; platelet-growth factor; transforming growth factors (TGFs) such as TGF-α and TGF- β; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon -α, -β, and -γ; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL- 1a, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-11, IL-12; a tumor necrosis factor such as TNF- α or TNF-ß; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

The term "package insert" is used to refer to instructions customarily included in commercial packages of therapeutic products, that contain information about the indications, usage, dosage, administration, contraindications and/or warnings concerning the use of such therapeutic products.

Table 1

```
/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define  _M      -8        /* value of a match with a stop */

int      _day[26][26] = {
/*       A  B  C  D  E  F  G  H  I  J  K  L  M  N  O  P  Q  R  S  T  U  V  W  X  Y  Z */
/* A */  { 2, 0,-2, 0, 0,-4, 1,-1,-1, 0,-1,-2,-1, 0,_M, 1, 0,-2, 1, 1, 0, 0,-6, 0,-3, 0},
/* B */  { 0, 3,-4, 3, 2,-5, 0, 1,-2, 0, 0,-3,-2, 2,_M,-1, 1, 0, 0, 0, 0,-2,-5, 0,-3, 1},
/* C */  {-2,-4,15,-5,-5,-4,-3,-3,-2, 0,-5,-6,-5,-4,_M,-3,-5,-4, 0,-2, 0,-2,-8, 0, 0,-5},
/* D */  { 0, 3,-5, 4, 3,-6, 1, 1,-2, 0, 0,-4,-3, 2,_M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 2},
/* E */  { 0, 2,-5, 3, 4,-5, 0, 1,-2, 0, 0,-3,-2, 1,_M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 3},
/* F */  {-4,-5,-4,-6,-5, 9,-5,-2, 1, 0,-5, 2, 0,-4,_M,-5,-5,-4,-3,-3, 0,-1, 0, 0, 7,-5},
/* G */  { 1, 0,-3, 1, 0,-5, 5,-2,-3, 0,-2,-4,-3, 0,_M,-1,-1,-3, 1, 0, 0,-1,-7, 0,-5, 0},
/* H */  {-1, 1,-3, 1, 1,-2,-2, 6,-2, 0, 0,-2,-2, 2,_M, 0, 3, 2,-1,-1, 0,-2,-3, 0, 0, 2},
/* I */  {-1,-2,-2,-2,-2, 1,-3,-2, 5, 0,-2, 2, 2,-2,_M,-2,-2,-2,-1, 0, 0, 4,-5, 0,-1,-2},
/* J */  { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */  {-1, 0,-5, 0, 0,-5,-2, 0,-2, 0, 5,-3, 0, 1,_M,-1, 1, 3, 0, 0, 0,-2,-3, 0,-4, 0},
/* L */  {-2,-3,-6,-4,-3, 2,-4,-2, 2, 0,-3, 6, 4,-3,_M,-3,-2,-3,-3,-1, 0, 2,-2, 0,-1,-2},
/* M */  {-1,-2,-5,-3,-2, 0,-3,-2, 2, 0, 0, 4, 6,-2,_M,-2,-1, 0,-2,-1, 0, 2,-4, 0,-2,-1},
/* N */  { 0, 2,-4, 2, 1,-4, 0, 2,-2, 0, 1,-3,-2, 2,_M,-1, 1, 0, 1, 0, 0,-2,-4, 0,-2, 1},
/* O */  {_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M, 0,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M},
/* P */  { 1,-1,-3,-1,-1,-5,-1, 0,-2, 0,-1,-3,-2,-1,_M, 6, 0, 0, 1, 0, 0,-1,-6, 0,-5, 0},
/* Q */  { 0, 1,-5, 2, 2,-5,-1, 3,-2, 0, 1,-2,-1, 1,_M, 0, 4, 1,-1,-1, 0,-2,-5, 0,-4, 3},
/* R */  {-2, 0,-4,-1,-1,-4,-3, 2,-2, 0, 3,-3, 0, 0,_M, 0, 1, 6, 0,-1, 0,-2, 2, 0,-4, 0},
/* S */  { 1, 0, 0, 0, 0,-3, 1,-1,-1, 0, 0,-3,-2, 1,_M, 1,-1, 0, 2, 1, 0,-1,-2, 0,-3, 0},
/* T */  { 1, 0,-2, 0, 0,-3, 0,-1, 0, 0, 0,-1,-1, 0,_M, 0,-1,-1, 1, 3, 0, 0,-5, 0,-3, 0},
/* U */  { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */  { 0,-2,-2,-2,-2,-1,-1,-2, 4, 0,-2, 2, 2,-2,_M,-1,-2,-2,-1, 0, 0, 4,-6, 0,-2,-2},
/* W */  {-6,-5,-8,-7,-7, 0,-7,-3,-5, 0,-3,-2,-4,-4,_M,-6,-5, 2,-2,-5, 0,-6,17, 0, 0,-6},
/* X */  { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */  {-3,-3, 0,-4,-4, 7,-5, 0,-1, 0,-4,-1,-2,-2,_M,-5,-4,-4,-3,-3, 0,-2, 0, 0,10,-4},
/* Z */  { 0, 1,-5, 2, 3,-5, 0, 2,-2, 0, 0,-2,-1, 1,_M, 0, 3, 0, 0, 0, 0,-2,-6, 0,-4, 4}
};
```

Table 1 (cont')

```
/*
 */
#include <stdio.h>
#include <ctype.h>

#define  MAXJMP     16      /* max jumps in a diag */
#define  MAXGAP     24      /* don't continue to penalize gaps larger than this */
#define  JMPS       1024    /* max jmps in an path */
#define  MX         4       /* save if there's at least MX-1 bases since last jmp */

#define  DMAT       3       /* value of matching bases */
#define  DMIS       0       /* penalty for mismatched bases */
#define  DINS0      8       /* penalty for a gap */
#define  DINS1      1       /* penalty per base */
#define  PINS0      8       /* penalty for a gap */
#define  PINS1      4       /* penalty per residue */

struct jmp {
        short           n[MAXJMP];      /* size of jmp (neg for dely) */
        unsigned short  x[MAXJMP];      /* base no. of jmp in seq x */
};                                      /* limits seq to 2^16 -1 */

struct diag {
        int             score;          /* score at last jmp */
        long            offset;         /* offset of prev block */
        short           ijmp;           /* current jmp index */
        struct jmp      jp;             /* list of jmps */
};

struct path {
        int     spc;            /* number of leading spaces */
        short   n[JMPS]; /* size of jmp (gap) */
        int     x[JMPS]; /* loc of jmp (last elem before gap) */
};

char            *ofile;                 /* output file name */
char            *namex[2];              /* seq names: getseqs() */
char            *prog;                  /* prog name for err msgs */
char            *seqx[2];               /* seqs: getseqs() */
int             dmax;                   /* best diag: nw() */
int             dmax0;                  /* final diag */
int             dna;                    /* set if dna: main() */
int             endgaps;                /* set if penalizing end gaps */
int             gapx, gapy;             /* total gaps in seqs */
int             len0, len1;             /* seq lens */
int             ngapx, ngapy;           /* total size of gaps */
int             smax;                   /* max score: nw() */
int             *xbm;                   /* bitmap for matching */
long            offset;                 /* current offset in jmp file */
struct  diag    *dx;                    /* holds diagonals */
struct  path    pp[2];                  /* holds path for seqs */

char            *calloc(), *malloc(), *index(), *strcpy();
char            *getseq(), *g_calloc();
```

Table 1 (cont')

main

```
/* Needleman-Wunsch alignment program
 *
 * usage: progs file1 file2
 *   where file1 and file2 are two dna or two protein sequences.
 *   The sequences can be in upper- or lower-case an may contain ambiguity
 *   Any lines beginning with ';', '>' or '<' are ignored
 *   Max file length is 65535 (limited by unsigned short x in the jmp struct)
 *   A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
 *   Output is in the file "align.out"
 *
 * The program may create a tmp file in /tmp to hold info about traceback.
 * Original version developed under BSD 4.3 on a vax 8650
 */
#include "nw.h"
#include "day.h"

static   _dbval[26] = {
         1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static   _pbval[26] = {
         1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
         128, 256, 0xFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
         1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
         1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
         int      ac;
         char     *av[];
{
         prog = av[0];
         if (ac != 3) {
                  fprintf(stderr,"usage: %s file1 file2\n", prog);
                  fprintf(stderr,"where file1 and file2 are two dna or two protein sequences.\n");
                  fprintf(stderr,"The sequences can be in upper- or lower-case\n");
                  fprintf(stderr,"Any lines beginning with ';' or '<' are ignored\n");
                  fprintf(stderr,"Output is in the file \"align.out\"\n");
                  exit(1);
         }
         namex[0] = av[1];
         namex[1] = av[2];
         seqx[0] = getseq(namex[0], &len0);
         seqx[1] = getseq(namex[1], &len1);
         xbm = (dna)? _dbval : _pbval;

         endgaps = 0;              /* 1 to penalize endgaps */
         ofile = "align.out";              /* output file */

         nw();           /* fill in the matrix, get the possible jmps */
         readjmps();     /* get the actual jmps */
         print();        /* print stats, alignment */

         cleanup(0);     /* unlink any tmp files */}
```

Table 1 (cont')

nw

```
/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()
{
        char            *px, *py;           /* seqs and ptrs */
        int             *ndely, *dely;      /* keep track of dely */
        int             ndelx, delx;        /* keep track of delx */
        int             *tmp;               /* for swapping row0, row1 */
        int             mis;                /* score for each type */
        int             ins0, ins1;         /* insertion penalties */
        register        id;                 /* diagonal index */
        register        ij;                 /* jmp index */
        register        *col0, *col1;       /* score for curr, last row */
        register        xx, yy;             /* index into seqs */

        dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));
        ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
        dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
        col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
        col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
        ins0 = (dna)? DINS0 : PINS0;
        ins1 = (dna)? DINS1 : PINS1;
        smax = -10000;
        if (endgaps) {
                for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
                        col0[yy] = dely[yy] = col0[yy-1] - ins1;
                        ndely[yy] = yy;
                }
                col0[0] = 0;    /* Waterman Bull Math Biol 84 */
        }
        else
                for (yy = 1; yy <= len1; yy++)
                        dely[yy] = -ins0;
        /* fill in match matrix
         */
        for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
                /* initialize first entry in col
                 */
                if (endgaps) {
                        if (xx == 1)
                                col1[0] = delx = -(ins0+ins1);
                        else
                                col1[0] = delx = col0[0] - ins1;
                        ndelx = xx;
                }
                else {
                        col1[0] = 0;
                        delx = -ins0;
                        ndelx = 0;
                }
```

Table 1 (cont')

...nw

```
for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
        mis = col0[yy-1];
        if (dna)
                mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
        else
                mis += _day[*px-'A'][*py-'A'];

        /* update penalty for del in x seq;
         * favor new del over ongong del
         * ignore MAXGAP if weighting endgaps
         */
        if (endgaps || ndely[yy] < MAXGAP) {
                if (col0[yy] - ins0 >= dely[yy]) {
                        dely[yy] = col0[yy] - (ins0+ins1);
                        ndely[yy] = 1;
                } else {
                        dely[yy] -= ins1;
                        ndely[yy]++;
                }
        } else {
                if (col0[yy] - (ins0+ins1) >= dely[yy]) {
                        dely[yy] = col0[yy] - (ins0+ins1);
                        ndely[yy] = 1;
                } else
                        ndely[yy]++;
        }

        /* update penalty for del in y seq;
         * favor new del over ongong del
         */
        if (endgaps || ndelx < MAXGAP) {
                if (col1[yy-1] - ins0 >= delx) {
                        delx = col1[yy-1] - (ins0+ins1);
                        ndelx = 1;
                } else {
                        delx -= ins1;
                        ndelx++;
                }
        } else {
                if (col1[yy-1] - (ins0+ins1) >= delx) {
                        delx = col1[yy-1] - (ins0+ins1);
                        ndelx = 1;
                } else
                        ndelx++;
        }

        /* pick the maximum score; we're favoring
         * mis over any del and delx over dely
         */
```

...nw

```
        id = xx - yy + len1 - 1;
        if (mis >= delx && mis >= dely[yy])
                col1[yy] = mis;
```

Table 1 (cont')

```
            else if (delx >= dely[yy]) {
                    coll[yy] = delx;
                    ij = dx[id].ijmp;
                    if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
                    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                            dx[id].ijmp++;
                            if (++ij >= MAXJMP) {
                                    writejmps(id);
                                    ij = dx[id].ijmp = 0;
                                    dx[id].offset = offset;
                                    offset += sizeof(struct jmp) + sizeof(offset);
                            }
                    }
                    dx[id].jp.n[ij] = ndelx;
                    dx[id].jp.x[ij] = xx;
                    dx[id].score = delx;
            }
            else {
                    coll[yy] = dely[yy];
                    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
                    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                            dx[id].ijmp++;
                            if (++ij >= MAXJMP) {
                                    writejmps(id);
                                    ij = dx[id].ijmp = 0;
                                    dx[id].offset = offset;
                                    offset += sizeof(struct jmp) + sizeof(offset);
                            }
                    }
                    dx[id].jp.n[ij] = -ndely[yy];
                    dx[id].jp.x[ij] = xx;
                    dx[id].score = dely[yy];
            }
            if (xx == len0 && yy < len1) {
                    /* last col
                     */
                    if (endgaps)
                            coll[yy] -= ins0+ins1*(len1-yy);
                    if (coll[yy] > smax) {
                            smax = coll[yy];
                            dmax = id;
                    }
            }
        }
        if (endgaps && xx < len0)
                coll[yy-1] -= ins0+ins1*(len0-xx);
        if (coll[yy-1] > smax) {
                smax = coll[yy-1];
                dmax = id;
        }
        tmp = col0; col0 = coll; coll = tmp;        }
    (void) free((char *)ndely);
    (void) free((char *)dely);
    (void) free((char *)col0);
    (void) free((char *)coll);                 }
```

Table 1 (cont')

```
/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() - -put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC       3
#define P_LINE    256     /* maximum output line */
#define P_SPC     3       /* space between name or num and seq */

extern    _day[26][26];
int       olen;           /* set output line length */
FILE      *fx;            /* output file */

print()
{
          int     lx, ly, firstgap, lastgap;    /* overlap */

          if ((fx = fopen(ofile, "w")) == 0) {
                  fprintf(stderr,"%s: can't write %s\n", prog, ofile);
                  cleanup(1);
          }
          fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
          fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
          olen = 60;
          lx = len0;
          ly = len1;
          firstgap = lastgap = 0;
          if (dmax < len1 - 1) {        /* leading gap in x */
                  pp[0].spc = firstgap = len1 - dmax - 1;
                  ly -= pp[0].spc;
          }
          else if (dmax > len1 - 1) {  /* leading gap in y */
                  pp[1].spc = firstgap = dmax - (len1 - 1);
                  lx -= pp[1].spc;
          }
          if (dmax0 < len0 - 1) {       /* trailing gap in x */
                  lastgap = len0 - dmax0 -1;
                  lx -= lastgap;
          }
          else if (dmax0 > len0 -.1) { /* trailing gap in y */
                  lastgap = dmax0 - (len0 - 1);
                  ly -= lastgap;
          }
          getmat(lx, ly, firstgap, lastgap);
          pr_align();         }
```

print

Table 1 (cont')

getmat

```
/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)
        int     lx, ly;                 /* "core" (minus endgaps) */
        int     firstgap, lastgap;      /* leading trailing overlap */
{
        int             nm, i0, i1, siz0, siz1;
        char            outx[32];
        double          pct;
        register        n0, n1;
        register char   *p0, *p1;
        /* get total matches, score
         */
        i0 = i1 = siz0 = siz1 = 0;
        p0 = seqx[0] + pp[1].spc;
        p1 = seqx[1] + pp[0].spc;
        n0 = pp[1].spc + 1;
        n1 = pp[0].spc + 1;
        nm = 0;
        while ( *p0 && *p1 ) {
                if (siz0) {
                        p1++;
                        n1++;
                        siz0--;
                }
                else if (siz1) {
                        p0++;
                        n0++;
                        siz1--;
                }
                else {
                        if (xbm[*p0-'A']&xbm[*p1-'A'])
                                nm++;
                        if (n0++ == pp[0].x[i0])
                                siz0 = pp[0].n[i0++];
                        if (n1++ == pp[1].x[i1])
                                siz1 = pp[1].n[i1++];
                        p0++;
                        p1++;
                }
        }

        /* pct homology:
         * if penalizing endgaps, base is the shorter seq
         * else, knock off overhangs and take shorter core
         */
        if (endgaps)
                lx = (len0 < len1)? len0 : len1;
        else
                lx = (lx < ly)? lx : ly;
        pct = 100.*(double)nm/(double)lx;
        fprintf(fx, "\n");
        fprintf(fx, "<%d match%s in an overlap of %d: %.2f percent similarity\n",
                nm, (nm == 1)? "" : "es", lx, pct);
```

Table 1 (cont')

...getmat

```
        fprintf(fx, "<gaps in first sequence: %d", gapx);
        if (gapx) {
                (void) sprintf(outx, " (%d %s%s)",
                        ngapx, (dna)? "base":"residue", (ngapx == 1)? "":"s");
                fprintf(fx,"%s", outx);
        fprintf(fx, ", gaps in second sequence: %d", gapy);
        if (gapy) {
                (void) sprintf(outx, " (%d %s%s)",
                        ngapy, (dna)? "base":"residue", (ngapy == 1)? "":"s");
                fprintf(fx,"%s", outx);
        }
        if (dna)
                fprintf(fx,
                "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
                smax, DMAT, DMIS, DINS0, DINS1);
        else
                fprintf(fx,
                "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
                smax, PINS0, PINS1);
        if (endgaps)
                fprintf(fx,
                "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
                firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
                lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
        else
                fprintf(fx, "<endgaps not penalized\n");
}
static          nm;             /* matches in core -- for checking */
static          lmax;           /* lengths of stripped file names */
static          ij[2];          /* jmp index for a path */
static          nc[2];          /* number at start of current line */
static          ni[2];          /* current elem number -- for gapping */
static          siz[2];
static char     *ps[2];         /* ptr to current element */
static char     *po[2];         /* ptr to next output char slot */
static char     out[2][P_LINE]; /* output line */
static char     star[P_LINE];   /* set by stars() */
/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
        int             nn;     /* char count */
        int             more;
        register        i;

        for (i = 0, lmax = 0; i < 2; i++) {
                nn = stripname(namex[i]);
                if (nn > lmax)
                        lmax = nn;
                nc[i] = 1;
                ni[i] = 1;
                siz[i] = ij[i] = 0;
                ps[i] = seqx[i];
                po[i] = out[i];         }
```

pr_align

Table 1 (cont')

...pr_align

```
	for (nn = nm = 0, more = 1; more; ) {
		for (i = more = 0; i < 2; i++) {
			/*
			 * do we have more of this sequence?
			 */
			if (!*ps[i])
				continue;
			more++;
			if (pp[i].spc) {	/* leading space */
				*po[i]++ = ' ';
				pp[i].spc--;
			}
			else if (siz[i]) {	/* in a gap */
				*po[i]++ = '-';
				siz[i]--;
			}
			else {			/* we're putting a seq element
					 */
				*po[i] = *ps[i];
				if (islower(*ps[i]))
					*ps[i] = toupper(*ps[i]);
				po[i]++;
				ps[i]++;
				/*
				 * are we at next gap for this seq?
				 */
				if (ni[i] == pp[i].x[ij[i]]) {
					/*
					 * we need to merge all gaps
					 * at this location
					 */
					siz[i] = pp[i].n[ij[i]++];
					while (ni[i] == pp[i].x[ij[i]])
						siz[i] += pp[i].n[ij[i]++];
				}
				ni[i]++;
			}
		}
		if (++nn == olen || !more && nn) {
			dumpblock();
			for (i = 0; i < 2; i++)
				po[i] = out[i];
			nn = 0;
		}
	}
}
/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
{
	register i;
	for (i = 0; i < 2; i++)
		*po[i]-- = '\0';
```

dumpblock

Table 1 (cont')

...dumpblock

```
		(void) putc('\n', fx);
		for (i = 0; i < 2; i++) {
			if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
				if (i == 0)
					nums(i);
				if (i == 0 && *out[1])
					stars();
				putline(i);
				if (i == 0 && *out[1])
					fprintf(fx, star);
				if (i == 1)
					nums(i);
			}
		}
}
/*
 * put out a number line: dumpblock()
 */
static
nums(ix)
		int	ix;		/* index in out[] holding seq line */
{
		char		nline[P_LINE];
		register	i, j;
		register char	*pn, *px, *py;
		for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
			*pn = ' ';
		for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
			if (*py == ' ' || *py == '-')
				*pn = ' ';
			else {
				if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
					j = (i < 0)? -i : i;
					for (px = pn; j; j /= 10, px--)
						*px = j%10 + '0';
					if (i < 0)
						*px = '-';
				}
				else
					*pn = ' ';
				i++;
			}
		}
		*pn = '\0';
		nc[ix] = i;
		for (pn = nline; *pn; pn++)
			(void) putc(*pn, fx);
		(void) putc('\n', fx);
}
/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)
		int	ix;			{
```

nums

putline

Table 1 (cont')

...putline

```
	int		i;
	register char	*px;

	for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
		(void) putc(*px, fx);
	for (; i < lmax+P_SPC; i++)
		(void) putc(' ', fx);

	/* these count from 1:
	 * ni[] is current element (from 1)
	 * nc[] is number at start of current line
	 */
	for (px = out[ix]; *px; px++)
		(void) putc(*px&0x7F, fx);
	(void) putc('\n', fx);
}
```

stars

```
/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
stars()
{
	int		i;
	register char	*p0, *p1, cx, *px;

	if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
	    !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
		return;
	px = star;
	for (i = lmax+P_SPC; i; i--)
		*px++ = ' ';

	for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
		if (isalpha(*p0) && isalpha(*p1)) {

			if (xbm[*p0-'A']&xbm[*p1-'A']) {
				cx = '*';
				nm++;
			}
			else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
				cx = '.';
			else
				cx = ' ';
		}
		else
			cx = ' ';
		*px++ = cx;
	}
	*px++ = '\n';
	*px = '\0';
}
```

Table 1 (cont')

stripname

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
stripname(pn)
        char    *pn;    /* file name (may be path) */
{
        register char   *px, *py;

        py = 0;
        for (px = pn; *px; px++)
                if (*px == '/')
                        py = px + 1;
        if (py)
                (void) strcpy(pn, py);
        return(strlen(pn));

}
```

Table 1 (cont')

```
/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
 * readjmps() -- get the good jmps, from tmp file if necessary
 * writejmps() -- write a filled array of jmps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";          /* tmp file for jmps */
FILE    *fj;
int     cleanup();                           /* cleanup tmp file */
long    lseek();
/*
 * remove any tmp file if we blow
 */
cleanup(i)                                                          cleanup
        int     i;
{
        if (fj)
                (void) unlink(jname);
        exit(i);
}
/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char    *
getseq(file, len)                                                   getseq
        char    *file;  /* file name */
        int     *len;   /* seq len */
{
        char            line[1024], *pseq;
        register char   *px, *py;
        int             natgc, tlen;
        FILE            *fp;
        if ((fp = fopen(file,"r")) == 0) {
                fprintf(stderr,"%s: can't read %s\n", prog, file);
                exit(1);
        }
        tlen = natgc = 0;
        while (fgets(line, 1024, fp)) {
                if (*line == ';' || *line == '<' || *line == '>')
                        continue;
                for (px = line; *px != '\n'; px++)
                        if (isupper(*px) || islower(*px))
                                tlen++;
        }
        if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
                fprintf(stderr,"%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
                exit(1);
        }
        pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
```

Table 1 (cont')

...getseq

```
		py = pseq + 4;
		*len = tlen;
		rewind(fp);
		while (fgets(line, 1024, fp)) {
			if (*line == ';' || *line == '<' || *line == '>')
				continue;
			for (px = line; *px != '\n'; px++) {
				if (isupper(*px))
					*py++ = *px;
				else if (islower(*px))
					*py++ = toupper(*px);
				if (index("ATGCU",*(py-1)))
					natgc++;
			}
		}
		*py++ = '\0';
		*py = '\0';
		(void) fclose(fp);
		dna = natgc > (tlen/3);
		return(pseq+4);
}
char	*
g_calloc(msg, nx, sz)
		char	*msg;		/* program, calling routine */
		int	nx, sz;		/* number and size of elements */
{
		char		*px, *calloc();
		if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
			if (*msg) {
				fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
				exit(1);
			}
		}
		return(px);
}
```

g_calloc

```
/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()
{
		int		fd = -1;
		int		siz, i0, i1;
		register	i, j, xx;
		if (fj) {
			(void) fclose(fj);
			if ((fd = open(jname, O_RDONLY, 0)) < 0) {
				fprintf(stderr, "%s: can't open() %s\n", prog, jname);
				cleanup(1);
			}
		}
		for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
			while (1) {
				for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
					;
```

readjmps

Table 1 (cont')

...readjmps

```
                                if (j < 0 && dx[dmax].offset && fj) {
                                        (void) lseek(fd, dx[dmax].offset, 0);
                                        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
                                        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
                                        dx[dmax].ijmp = MAXJMP-1;                        }
                                else
                                        break;          }
                        if (i >= JMPS) {
                                fprintf(stderr, "%s: too many gaps in alignment\n", prog);
                                cleanup(1);
                        }
                        if (j >= 0) {
                                siz = dx[dmax].jp.n[j];
                                xx = dx[dmax].jp.x[j];
                                dmax += siz;
                                if (siz < 0) {                  /* gap in second seq */
                                        pp[1].n[i1] = -siz;
                                        xx += siz;
                                        /* id = xx - yy + len1 - 1                               */
                                        pp[1].x[i1] = xx - dmax + len1 - 1;
                                        gapy++;
                                        ngapy -= siz;
/* ignore MAXGAP when doing endgaps */
                                        siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
                                        i1++;
                                }
                                else if (siz > 0) { /* gap in first seq */
                                        pp[0].n[i0] = siz;
                                        pp[0].x[i0] = xx;
                                        gapx++;
                                        ngapx += siz;
/* ignore MAXGAP when doing endgaps */
                                        siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
                                        i0++;
                                }
                        }
                        else
                                break;
                }
                /* reverse the order of jmps   */
                for (j = 0, i0--; j < i0; j++, i0--) {
                        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
                        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
                }
                for (j = 0, i1--; j < i1; j++, i1--) {
                        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
                        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
                }
                if (fd >= 0)
                        (void) close(fd);
                if (fj) {
                        (void) unlink(jname);
                        fj = 0;
                        offset = 0;
                }                                       }
```

Table 1 (cont')

writejmps

```
/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejmps(ix)
        int     ix;
{
        char    *mktemp();

        if (!fj) {
                if (mktemp(jname) < 0) {
                        fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                        cleanup(1);
                }
                if ((fj = fopen(jname, "w")) == 0) {
                        fprintf(stderr, "%s: can't write %s\n", prog, jname);
                        exit(1);
                }
        }
        (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
}
```

Table 2

TAT	XXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the TAT polypeptide) =

5 divided by 15 = 33.3%

Table 3

TAT	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the TAT polypeptide) =

5 divided by 10 = 50%

Table 4

TAT-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the TAT-DNA nucleic acid sequence) =
6 divided by 14 = 42.9%

Table 5

TAT-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the TAT-DNA nucleic acid sequence) =

4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Anti-TAT Antibodies

In one embodiment, the present invention provides anti-TAT antibodies which may find use herein as therapeutic and/or diagnostic agents. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

Polyclonal antibodies are preferably raised in animals by multiple subcutaneous (sc) or intraperitoneal (ip) injections of the relevant antigen and an adjuvant. It may be useful to conjugate the relevant antigen (especially when synthetic peptides are used) to a protein that is immunogenic in the species to be immunized. For example, the antigen can be conjugated to keyhole limpet hemocyanin (KLH), serum albumin, bovine thyroglobulin, or soybean trypsin inhibitor, using a bifunctional or derivatizing agent, e.g., maleimidobenzoyl sulfosuccinimide ester (conjugation through cysteine residues), N-hydroxysuccinimide (through lysine residues), glutaraldehyde, succinic anhydride, $SOCl_2$, or $R^1N=C=NR$, where R and R^1 are different alkyl groups.

Animals are immunized against the antigen, immunogenic conjugates, or derivatives by combining, e.g., 100 μg or 5 μg of the protein or conjugate (for rabbits or mice, respectively) with 3 volumes of Freund's complete adjuvant and injecting the solution intradermally at multiple sites. One month later, the animals are boosted with 1/5 to 1/10 the original amount of peptide or conjugate in Freund's complete adjuvant by subcutaneous injection at multiple sites. Seven to 14 days later, the animals are bled and the serum is assayed for antibody titer. Animals are boosted until the titer plateaus. Conjugates also can be made in recombinant cell culture as protein fusions. Also, aggregating agents such as alum are suitably used to enhance the immune response.

2. Monoclonal Antibodies

Monoclonal antibodies may be made using the hybridoma method first described by Kohler et al., Nature, 256:495 (1975), or may be made by recombinant DNA methods (U.S. Patent No. 4,816,567).

In the hybridoma method, a mouse or other appropriate host animal, such as a hamster, is immunized

as described above to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the protein used for immunization. Alternatively, lymphocytes may be immunized *in vitro*. After immunization, lymphocytes are isolated and then fused with a myeloma cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)).

The hybridoma cells thus prepared are seeded and grown in a suitable culture medium which medium preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells (also referred to as fusion partner). For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the selective culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances prevent the growth of HGPRT-deficient cells.

Preferred fusion partner myeloma cells are those that fuse efficiently, support stable high-level production of antibody by the selected antibody-producing cells, and are sensitive to a selective medium that selects against the unfused parental cells. Preferred myeloma cell lines are murine myeloma lines, such as those derived from MOPC-21 and MPC-11 mouse tumors available from the Salk Institute Cell Distribution Center, San Diego, California USA, and SP-2 and derivatives e.g., X63-Ag8-653 cells available from the American Type Culture Collection, Manassas, Virginia, USA. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); and Brodeur et al., Monoclonal Antibody Production Techniques and Applications, pp. 51-63 (Marcel Dekker, Inc., New York, 1987)).

Culture medium in which hybridoma cells are growing is assayed for production of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunosorbent assay (ELISA).

The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis described in Munson et al., Anal. Biochem., 107:220 (1980).

Once hybridoma cells that produce antibodies of the desired specificity, affinity, and/or activity are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)). Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. In addition, the hybridoma cells may be grown *in vivo* as ascites tumors in an animal e.g,, by i.p. injection of the cells into mice.

The monoclonal antibodies secreted by the subclones are suitably separated from the culture medium, ascites fluid, or serum by conventional antibody purification procedures such as, for example, affinity chromatography (e.g., using protein A or protein G-Sepharose) or ion-exchange chromatography, hydroxylapatite chromatography, gel electrophoresis, dialysis, etc.

DNA encoding the monoclonal antibodies is readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the

heavy and light chains of murine antibodies). The hybridoma cells serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese Hamster Ovary (CHO) cells, or myeloma cells that do not otherwise produce antibody protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. Review articles on recombinant expression in bacteria of DNA encoding the antibody include Skerra et al., Curr. Opinion in Immunol., 5:256-262 (1993) and Plückthun, Immunol. Revs. 130:151-188 (1992).

In a further embodiment, monoclonal antibodies or antibody fragments can be isolated from antibody phage libraries generated using the techniques described in McCafferty et al., Nature, 348:552-554 (1990). Clackson et al., Nature, 352:624-628 (1991) and Marks et al., J. Mol. Biol., 222:581-597 (1991) describe the isolation of murine and human antibodies, respectively, using phage libraries. Subsequent publications describe the production of high affinity (nM range) human antibodies by chain shuffling (Marks et al., Bio/Technology, 10:779-783 (1992)), as well as combinatorial infection and *in vivo* recombination as a strategy for constructing very large phage libraries (Waterhouse et al., Nuc. Acids. Res. 21:2265-2266 (1993)). Thus, these techniques are viable alternatives to traditional monoclonal antibody hybridoma techniques for isolation of monoclonal antibodies.

The DNA that encodes the antibody may be modified to produce chimeric or fusion antibody polypeptides, for example, by substituting human heavy chain and light chain constant domain (C_H and C_L) sequences for the homologous murine sequences (U.S. Patent No. 4,816,567; and Morrison, et al., Proc. Natl Acad. Sci. USA, 81:6851 (1984)), or by fusing the immunoglobulin coding sequence with all or part of the coding sequence for a non-immunoglobulin polypeptide (heterologous polypeptide). The non-immunoglobulin polypeptide sequences can substitute for the constant domains of an antibody, or they are substituted for the variable domains of one antigen-combining site of an antibody to create a chimeric bivalent antibody comprising one antigen-combining site having specificity for an antigen and another antigen-combining site having specificity for a different antigen.

3. Human and Humanized Antibodies

The anti-TAT antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are

those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is very important to reduce antigenicity and HAMA response (human anti-mouse antibody) when the antibody is intended for human therapeutic use. According to the so-called "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable domain sequences. The human V domain sequence which is closest to that of the rodent is identified and the human framework region (FR) within it accepted for the humanized antibody (Sims et al., J. Immunol. 151:2296 (1993); Chothia et al., J. Mol. Biol., 196:901 (1987)). Another method uses a particular framework region derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies (Carter et al., Proc. Natl. Acad. Sci. USA, 89:4285 (1992); Presta et al., J. Immunol. 151:2623 (1993)).

It is further important that antibodies be humanized with retention of high binding affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three-dimensional models of the parental and humanized sequences. Three-dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, i.e., the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the recipient and import sequences so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the hypervariable region residues are directly and most substantially involved in influencing antigen binding.

Various forms of a humanized anti-TAT antibody are contemplated. For example, the humanized antibody may be an antibody fragment, such as a Fab, which is optionally conjugated with one or more cytotoxic agent(s) in order to generate an immunoconjugate. Alternatively, the humanized antibody may be an intact antibody, such as an intact IgG1 antibody.

As an alternative to humanization, human antibodies can be generated. For example, it is now possible to produce transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (J_H) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array into such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, e.g., Jakobovits et al., Proc. Natl. Acad. Sci. USA, 90:2551 (1993); Jakobovits et al., Nature, 362:255-258 (1993); Bruggemann et al., Year in Immuno. 7:33 (1993); U.S. Patent Nos. 5,545,806, 5,569,825, 5,591,669 (all of GenPharm); 5,545,807; and WO 97/17852.

Alternatively, phage display technology (McCafferty et al., Nature 348:552-553 [1990]) can be used to produce human antibodies and antibody fragments *in vitro*, from immunoglobulin variable (V) domain gene repertoires from unimmunized donors. According to this technique, antibody V domain genes are cloned in-frame into either a major or minor coat protein gene of a filamentous bacteriophage, such as M13 or fd, and displayed as functional antibody fragments on the surface of the phage particle. Because the filamentous particle contains a single-stranded DNA copy of the phage genome, selections based on the functional properties of the antibody also result in selection of the gene encoding the antibody exhibiting those properties. Thus, the phage mimics some of the properties of the B-cell. Phage display can be performed in a variety of formats, reviewed in, e.g., Johnson, Kevin S. and Chiswell, David J., Current Opinion in Structural Biology 3:564-571 (1993). Several sources of V-gene segments can be used for phage display. Clackson et al. Nature, 352:624-628 (1991) isolated a diverse array of anti-oxazolone antibodies from a small random combinatorial library of V genes derived from the spleens of immunized mice. A repertoire of V genes from unimmunized human donors can be constructed and antibodies to a diverse array of antigens (including self-antigens) can be isolated essentially following the techniques described by Marks et al., J. Mol. Biol. 222:581-597 (1991), or Griffith et al., EMBO J. 12:725-734 (1993). See, also, U.S. Patent Nos. 5,565,332 and 5,573,905.

As discussed above, human antibodies may also be generated by *in vitro* activated B cells (see U.S. Patents 5,567,610 and 5,229,275).

4. Antibody fragments

In certain circumstances there are advantages of using antibody fragments, rather than whole antibodies. The smaller size of the fragments allows for rapid clearance, and may lead to improved access to solid tumors.

Various techniques have been developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of intact antibodies (see, e.g., Morimoto et al., Journal of Biochemical and Biophysical Methods 24:107-117 (1992); and Brennan et al., Science, 229:81 (1985)).

However, these fragments can now be produced directly by recombinant host cells. Fab, Fv and ScFv antibody fragments can all be expressed in and secreted from *E. coli*, thus allowing the facile production of large amounts of these fragments. Antibody fragments can be isolated from the antibody phage libraries discussed above. Alternatively, Fab'-SH fragments can be directly recovered from *E. coli* and chemically coupled to form F(ab')$_2$ fragments (Carter et al., Bio/Technology 10:163-167 (1992)). According to another approach, F(ab')$_2$ fragments can be isolated directly from recombinant host cell culture. Fab and F(ab')$_2$ fragment with increased in vivo half-life comprising a salvage receptor binding epitope residues are described in U.S. Patent No. 5,869,046. Other techniques for the production of antibody fragments will be apparent to the skilled practitioner. In other embodiments, the antibody of choice is a single chain Fv fragment (scFv). See WO 93/16185; U.S. Patent No. 5,571,894; and U.S. Patent No. 5,587,458. Fv and sFv are the only species with intact combining sites that are devoid of constant regions; thus, they are suitable for reduced nonspecific binding during in vivo use. sFv fusion proteins may be constructed to yield fusion of an effector protein at either the amino or the carboxy terminus of an sFv. See Antibody Engineering, ed. Borrebaeck, supra. The antibody fragment may also be a "linear antibody", e.g., as described in U.S. Patent 5,641,870 for example. Such linear antibody fragments may be monospecific or bispecific.

5. Bispecific Antibodies

Bispecific antibodies are antibodies that have binding specificities for at least two different epitopes. Exemplary bispecific antibodies may bind to two different epitopes of a TAT protein as described herein. Other such antibodies may combine a TAT binding site with a binding site for another protein. Alternatively, an anti-TAT arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD3), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16), so as to focus and localize cellular defense mechanisms to the TAT-expressing cell. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express TAT. These antibodies possess a TAT-binding arm and an arm which binds the cytotoxic agent (e.g., saporin, anti-interferon-α, vinca alkaloid, ricin A chain, methotrexate or radioactive isotope hapten). Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g., F(ab')$_2$ bispecific antibodies).

WO 96/16673 describes a bispecific anti-ErbB2/anti-FcγRIII antibody and U.S. Patent No. 5,837,234 discloses a bispecific anti-ErbB2/anti-FcγRI antibody. A bispecific anti-ErbB2/Fc α antibody is shown in WO98/02463. U.S. Patent No. 5,821,337 teaches a bispecific anti-ErbB2/anti-CD3 antibody.

Methods for making bispecific antibodies are known in the art. Traditional production of full length bispecific antibodies is based on the co-expression of two immunoglobulin heavy chain-light chain pairs, where the two chains have different specificities (Millstein et al., Nature 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. Purification of the correct molecule, which is usually done by affinity chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in WO 93/08829, and in Traunecker et al., EMBO J. 10:3655-3659 (1991).

According to a different approach, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. Preferably, the fusion is with an Ig heavy chain constant domain, comprising at least part of the hinge, C_H2, and C_H3 regions. It is preferred to have the first heavy-chain constant region (C_H1) containing the site necessary for light chain bonding, present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host cell. This provides for greater flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yield of the desired bispecific antibody. It is, however, possible to insert the coding sequences for two or all three polypeptide chains into a single expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios have no significant affect on the yield of the desired chain combination.

In a preferred embodiment of this approach, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one arm, and a hybrid immunoglobulin heavy chain-light chain pair (providing a second binding specificity) in the other arm. It was found that this asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only one half of the bispecific molecule provides for a facile way of separation. This approach is disclosed in WO 94/04690. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology 121:210 (1986).

According to another approach described in U.S. Patent No. 5,731,168, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the C_H3 domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g., tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g., alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies include cross-linked or "heteroconjugate" antibodies. For example, one of the antibodies in the heteroconjugate can be coupled to avidin, the other to biotin. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360, WO 92/200373, and EP 03089). Heteroconjugate antibodies may be made using any convenient cross-linking methods. Suitable cross-linking agents are well known in the art, and are disclosed in U.S. Patent No. 4,676,980, along with a number of cross-linking techniques.

Techniques for generating bispecific antibodies from antibody fragments have also been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate

$F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent, sodium arsenite, to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Recent progress has facilitated the direct recovery of Fab'-SH fragments from *E. coli*, which can be chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175: 217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a V_H connected to a V_L by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See Gruber et al., J. Immunol., 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

6. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

7. Multivalent Antibodies

A multivalent antibody may be internalized (and/or catabolized) faster than a bivalent antibody by a cell expressing an antigen to which the antibodies bind. The antibodies of the present invention can be multivalent antibodies (which are other than of the IgM class) with three or more antigen binding sites (e.g. tetravalent antibodies), which can be readily produced by recombinant expression of nucleic acid encoding the polypeptide chains of the antibody. The multivalent antibody can comprise a dimerization domain and three or more antigen binding sites. The preferred dimerization domain comprises (or consists of) an Fc region or a hinge region. In this scenario, the antibody will comprise an Fc region and three or more antigen binding sites amino-terminal to the Fc region. The preferred multivalent antibody herein comprises (or consists of) three to about eight, but preferably four, antigen binding sites. The multivalent antibody comprises at least one polypeptide chain (and preferably two polypeptide chains), wherein the polypeptide chain(s) comprise two or more variable domains. For instance, the polypeptide chain(s) may comprise VD1-$(X1)_n$-VD2-$(X2)_n$-Fc, wherein VD1 is a first variable domain, VD2 is a second variable domain, Fc is one polypeptide chain of an Fc region, X1 and X2 represent an amino acid or polypeptide, and n is 0 or 1. For instance, the polypeptide chain(s) may comprise: VH-CH1-flexible linker-VH-CH1-Fc region chain; or VH-CH1-VH-CH1-Fc region chain. The multivalent antibody herein preferably further comprises at least two (and preferably four) light chain variable domain polypeptides. The multivalent antibody herein may, for instance, comprise from about two to about eight light chain variable domain polypeptides. The light chain variable domain polypeptides contemplated here comprise a light chain variable domain and, optionally, further comprise a CL domain.

8. <u>Effector Function Engineering</u>

It may be desirable to modify the antibody of the invention with respect to effector function, e.g., so as to enhance antigen-dependent cell-mediated cyotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC) of the antibody. This may be achieved by introducing one or more amino acid substitutions in an Fc region of the antibody. Alternatively or additionally, cysteine residue(s) may be introduced in the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., <u>J. Exp Med.</u> 176:1191-1195 (1992) and Shopes, B. <u>J. Immunol.</u> 148:2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff et al., <u>Cancer Research</u> 53:2560-2565 (1993). Alternatively, an antibody can be engineered which has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., <u>Anti-Cancer Drug Design</u> 3:219-230 (1989).

To increase the serum half life of the antibody, one may incorporate a salvage receptor binding epitope into the antibody (especially an antibody fragment) as described in U.S. Patent 5,739,277, for example. As used herein, the term "salvage receptor binding epitope" refers to an epitope of the Fc region of an IgG molecule (e.g., IgG_1, IgG_2, IgG_3, or IgG_4) that is responsible for increasing the *in vivo* serum half-life of the IgG molecule.

9. <u>Immunoconjugates</u>

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic

agent such as a chemotherapeutic agent, a growth inhibitory agent, a toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re. Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

Conjugates of an antibody and one or more small molecule toxins, such as a calicheamicin, maytansinoids, a trichothene, and CC1065, and the derivatives of these toxins that have toxin activity, are also contemplated herein.

Maytansine and maytansinoids

In one preferred embodiment, an anti-TAT antibody (full length or fragments) of the invention is conjugated to one or more maytansinoid molecules.

Maytansinoids are mitototic inhibitors which act by inhibiting tubulin polymerization. Maytansine was first isolated from the east African shrub *Maytenus serrata* (U.S. Patent No. 3,896,111). Subsequently, it was discovered that certain microbes also produce maytansinoids, such as maytansinol and C-3 maytansinol esters (U.S. Patent No. 4,151,042). Synthetic maytansinol and derivatives and analogues thereof are disclosed, for example, in U.S. Patent Nos. 4,137,230; 4,248,870; 4,256,746; 4,260,608; 4,265,814; 4,294,757; 4,307,016; 4,308,268; 4,308,269; 4,309,428; 4,313,946; 4,315,929; 4,317,821; 4,322,348; 4,331,598; 4,361,650; 4,364,866; 4,424,219; 4,450,254; 4,362,663; and 4,371,533, the disclosures of which are hereby expressly incorporated by reference.

Maytansinoid-antibody conjugates

In an attempt to improve their therapeutic index, maytansine and maytansinoids have been conjugated to antibodies specifically binding to tumor cell antigens. Immunoconjugates containing maytansinoids and their therapeutic use are disclosed, for example, in U.S. Patent Nos. 5,208,020, 5,416,064 and European Patent EP

0 425 235 B1, the disclosures of which are hereby expressly incorporated by reference. Liu et al., Proc. Natl. Acad. Sci. USA 93:8618-8623 (1996) described immunoconjugates comprising a maytansinoid designated DM1 linked to the monoclonal antibody C242 directed against human colorectal cancer. The conjugate was found to be highly cytotoxic towards cultured colon cancer cells, and showed antitumor activity in an *in vivo* tumor growth assay. Chari et al., Cancer Research 52:127-131 (1992) describe immunoconjugates in which a maytansinoid was conjugated via a disulfide linker to the murine antibody A7 binding to an antigen on human colon cancer cell lines, or to another murine monoclonal antibody TA.1 that binds the HER-2/*neu* oncogene. The cytotoxicity of the TA.1-maytansonoid conjugate was tested *in vitro* on the human breast cancer cell line SK-BR-3, which expresses 3 x 10^5 HER-2 surface antigens per cell. The drug conjugate achieved a degree of cytotoxicity similar to the free maytansonid drug, which could be increased by increasing the number of maytansinoid molecules per antibody molecule. The A7-maytansinoid conjugate showed low systemic cytotoxicity in mice.

Anti-TAT polypeptide antibody-maytansinoid conjugates (immunoconjugates)

Anti-TAT antibody-maytansinoid conjugates are prepared by chemically linking an anti-TAT antibody to a maytansinoid molecule without significantly diminishing the biological activity of either the antibody or the maytansinoid molecule. An average of 3-4 maytansinoid molecules conjugated per antibody molecule has shown efficacy in enhancing cytotoxicity of target cells without negatively affecting the function or solubility of the antibody, although even one molecule of toxin/antibody would be expected to enhance cytotoxicity over the use of naked antibody. Maytansinoids are well known in the art and can be synthesized by known techniques or isolated from natural sources. Suitable maytansinoids are disclosed, for example, in U.S. Patent No. 5,208,020 and in the other patents and nonpatent publications referred to hereinabove. Preferred maytansinoids are maytansinol and maytansinol analogues modified in the aromatic ring or at other positions of the maytansinol molecule, such as various maytansinol esters.

There are many linking groups known in the art for making antibody-maytansinoid conjugates, including, for example, those disclosed in U.S. Patent No. 5,208,020 or EP Patent 0 425 235 B1, and Chari et al., Cancer Research 52:127-131 (1992). The linking groups include disufide groups, thioether groups, acid labile groups, photolabile groups, peptidase labile groups, or esterase labile groups, as disclosed in the above-identified patents, disulfide and thioether groups being preferred.

Conjugates of the antibody and maytansinoid may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). Particularly preferred coupling agents include N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP) (Carlsson et al. Biochem. J. 173:723-737 [1978]) and N-succinimidyl-4-(2-pyridylthio)pentanoate (SPP) to provide for a disulfide linkage.

The linker may be attached to the maytansinoid molecule at various positions, depending on the type of the link. For example, an ester linkage may be formed by reaction with a hydroxyl group using conventional coupling techniques. The reaction may occur at the C-3 position having a hydroxyl group, the C-14 position modified with hyrdoxymethyl, the C-15 position modified with a hydroxyl group, and the C-20 position having a hydroxyl group. In a preferred embodiment, the linkage is formed at the C-3 position of maytansinol or a maytansinol analogue.

Calicheamicin

Another immunoconjugate of interest comprises an anti-TAT antibody conjugated to one or more calicheamicin molecules. The calicheamicin family of antibiotics are capable of producing double-stranded DNA breaks at sub-picomolar concentrations. For the preparation of conjugates of the calicheamicin family, see U.S. patents 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, 5,877,296 (all to American Cyanamid Company). Structural analogues of calicheamicin which may be used include, but are not limited to, γ_1^I, α_2^I, α_3^I, N-acetyl-γ_1^I, PSAG and θ^I_1 (Hinman et al., Cancer Research 53:3336-3342 (1993), Lode et al., Cancer Research 58:2925-2928 (1998) and the aforementioned U.S. patents to American Cyanamid). Another anti-tumor drug that the antibody can be conjugated is QFA which is an antifolate. Both calicheamicin and QFA have intracellular sites of action and do not readily cross the plasma membrane. Therefore, cellular uptake of these agents through antibody mediated internalization greatly enhances their cytotoxic effects.

Other cytotoxic agents

Other antitumor agents that can be conjugated to the anti-TAT antibodies of the invention include BCNU, streptozoicin, vincristine and 5-fluorouracil, the family of agents known collectively LL-E33288 complex described in U.S. patents 5,053,394, 5,770,710, as well as esperamicins (U.S. patent 5,877,296).

Enzymatically active toxins and fragments thereof which can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin and the tricothecenes. See, for example, WO 93/21232 published October 28, 1993.

The present invention further contemplates an immunoconjugate formed between an antibody and a compound with nucleolytic activity (e.g., a ribonuclease or a DNA endonuclease such as a deoxyribonuclease; DNase).

For selective destruction of the tumor, the antibody may comprise a highly radioactive atom. A variety of radioactive isotopes are available for the production of radioconjugated anti-TAT antibodies. Examples include At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32}, Pb^{212} and radioactive isotopes of Lu. When the conjugate is used for diagnosis, it may comprise a radioactive atom for scintigraphic studies, for example tc^{99m} or I^{123}, or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance

imaging, mri), such as iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

The radio- or other labels may be incorporated in the conjugate in known ways. For example, the peptide may be biosynthesized or may be synthesized by chemical amino acid synthesis using suitable amino acid precursors involving, for example, fluorine-19 in place of hydrogen. Labels such as tc^{99m} or I^{123}, $.Re^{186}$, Re^{188} and In^{111} can be attached via a cysteine residue in the peptide. Yttrium-90 can be attached via a lysine residue. The IODOGEN method (Fraker et al (1978) Biochem. Biophys. Res. Commun. 80: 49-57 can be used to incorporate iodine-123. "Monoclonal Antibodies in Immunoscintigraphy" (Chatal,CRC Press 1989) describes other methods in detail.

Conjugates of the antibody and cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science 238:1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026. The linker may be a "cleavable linker" facilitating release of the cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari et al., Cancer Research 52:127-131 (1992); U.S. Patent No. 5,208,020) may be used.

Alternatively, a fusion protein comprising the anti-TAT antibody and cytotoxic agent may be made, e.g., by recombinant techniques or peptide synthesis. The length of DNA may comprise respective regions encoding the two portions of the conjugate either adjacent one another or separated by a region encoding a linker peptide which does not destroy the desired properties of the conjugate.

In yet another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pre-targeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) which is conjugated to a cytotoxic agent (e.g., a radionucleotide).

10. Immunoliposomes

The anti-TAT antibodies disclosed herein may also be formulated as immunoliposomes. A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688 (1985); Hwang et al., Proc. Natl Acad. Sci. USA 77:4030 (1980); U.S. Pat. Nos. 4,485,045 and 4,544,545;

and WO97/38731 published October 23, 1997. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., J. Biol. Chem. 257:286-288 (1982) via a disulfide interchange reaction. A chemotherapeutic agent is optionally contained within the liposome. See Gabizon et al., J. National Cancer Inst. 81(19):1484 (1989).

B. TAT Binding Oligopeptides

TAT binding oligopeptides of the present invention are oligopeptides that bind, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be chemically synthesized using known oligopeptide synthesis methodology or may be prepared and purified using recombinant technology. TAT binding oligopeptides are usually at least about 5 amino acids in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length or more, wherein such oligopeptides that are capable of binding, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening oligopeptide libraries for oligopeptides that are capable of specifically binding to a polypeptide target are well known in the art (see, e.g., U.S. Patent Nos. 5,556,762, 5,750,373, 4,708,871, 4,833,092, 5,223,409, 5,403,484, 5,571,689, 5,663,143; PCT Publication Nos. WO 84/03506 and WO84/03564; Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 81:3998-4002 (1984); Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 82:178-182 (1985); Geysen et al., in Synthetic Peptides as Antigens, 130-149 (1986); Geysen et al., J. Immunol. Meth., 102:259-274 (1987); Schoofs et al., J. Immunol., 140:611-616 (1988), Cwirla, S. E. et al. (1990) Proc. Natl. Acad. Sci. USA, 87:6378; Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363, and Smith, G. P. (1991) Current Opin. Biotechnol., 2:668).

In this regard, bacteriophage (phage) display is one well known technique which allows one to screen large oligopeptide libraries to identify member(s) of those libraries which are capable of specifically binding to a polypeptide target. Phage display is a technique by which variant polypeptides are displayed as fusion proteins to the coat protein on the surface of bacteriophage particles (Scott, J.K. and Smith, G. P. (1990) Science 249: 386). The utility of phage display lies in the fact that large libraries of selectively randomized protein variants (or randomly cloned cDNAs) can be rapidly and efficiently sorted for those sequences that bind to a target molecule with high affinity. Display of peptide (Cwirla, S. E. et al. (1990) Proc. Natl. Acad. Sci.

USA, 87:6378) or protein (Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363) libraries on phage have been used for screening millions of polypeptides or oligopeptides for ones with specific binding properties (Smith, G. P. (1991) Current Opin. Biotechnol., 2:668). Sorting phage libraries of random mutants requires a strategy for constructing and propagating a large number of variants, a procedure for affinity purification using the target receptor, and a means of evaluating the results of binding enrichments. U.S. Patent Nos. 5,223,409, 5,403,484, 5,571,689, and 5,663,143.

Although most phage display methods have used filamentous phage, lambdoid phage display systems (WO 95/34683; U.S. 5,627,024), T4 phage display systems (Ren, Z-J. et al. (1998) Gene 215:439; Zhu, Z. (1997) CAN 33:534; Jiang, J. et al. (1997) can 128:44380; Ren, Z-J. et al. (1997) CAN 127:215644; Ren, Z-J. (1996) Protein Sci. 5:1833; Efimov, V. P. et al. (1995) Virus Genes 10:173) and T7 phage display systems (Smith, G. P. and Scott, J.K. (1993) Methods in Enzymology, 217, 228–257; U.S. 5,766,905) are also known.

Many other improvements and variations of the basic phage display concept have now been developed. These improvements enhance the ability of display systems to screen peptide libraries for binding to selected target molecules and to display functional proteins with the potential of screening these proteins for desired properties. Combinatorial reaction devices for phage display reactions have been developed (WO 98/14277) and phage display libraries have been used to analyze and control bimolecular interactions (WO 98/20169; WO 98/20159) and properties of constrained helical peptides (WO 98/20036). WO 97/35196 describes a method of isolating an affinity ligand in which a phage display library is contacted with one solution in which the ligand will bind to a target molecule and a second solution in which the affinity ligand will not bind to the target molecule, to selectively isolate binding ligands. WO 97/46251 describes a method of biopanning a random phage display library with an affinity purified antibody and then isolating binding phage, followed by a micropanning process using microplate wells to isolate high affinity binding phage. The use of*Staphlylococcus aureus* protein A as an affinity tag has also been reported (Li et al. (1998) Mol Biotech., 9:187). WO 97/47314 describes the use of substrate subtraction libraries to distinguish enzyme specificities using a combinatorial library which may be a phage display library. A method for selecting enzymes suitable for use in detergents using phage display is described in WO 97/09446. Additional methods of selecting specific binding proteins are described in U.S. Patent Nos. 5,498,538, 5,432,018, and WO 98/15833.

Methods of generating peptide libraries and screening these libraries are also disclosed in U.S. Patent Nos. 5,723,286, 5,432,018, 5,580,717, 5,427,908, 5,498,530, 5,770,434, 5,734,018, 5,698,426, 5,763,192, and 5,723,323.

C. TAT Binding Organic Molecules

TAT binding organic molecules are organic molecules other than oligopeptides or antibodies as defined herein that bind, preferably specifically, to a TAT polypeptide as described herein. TAT binding organic molecules may be identified and chemically synthesized using known methodology (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules are usually less than about 2000 daltons in size, alternatively less than about 1500, 750, 500, 250 or 200 daltons in size, wherein such organic molecules

that are capable of binding, preferably specifically, to a TAT polypeptide as described herein may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening organic molecule libraries for molecules that are capable of binding to a polypeptide target are well known in the art (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules may be, for example, aldehydes, ketones, oximes, hydrazones, semicarbazones, carbazides, primary amines, secondary amines, tertiary amines, N-substituted hydrazines, hydrazides, alcohols, ethers, thiols, thioethers, disulfides, carboxylic acids, esters, amides, ureas, carbamates, carbonates, ketals, thioketals, acetals, thioacetals, aryl halides, aryl sulfonates, alkyl halides, alkyl sulfonates, aromatic compounds, heterocyclic compounds, anilines, alkenes, alkynes, diols, amino alcohols, oxazolidines, oxazolines, thiazolidines, thiazolines, enamines, sulfonamides, epoxides, aziridines, isocyanates, sulfonyl chlorides, diazo compounds, acid chlorides, or the like.

D. Screening for Anti-TAT Antibodies, TAT Binding Oligopeptides and TAT Binding Organic Molecules With the Desired Properties

Techniques for generating antibodies, oligopeptides and organic molecules that bind to TAT polypeptides have been described above. One may further select antibodies, oligopeptides or other organic molecules with certain biological characteristics, as desired.

The growth inhibitory effects of an anti-TAT antibody, oligopeptide or other organic molecule of the invention may be assessed by methods known in the art, e.g., using cells which express a TAT polypeptide either endogenously or following transfection with the TAT gene. For example, appropriate tumor cell lines and TAT-transfected cells may treated with an anti-TAT monoclonal antibody, oligopeptide or other organic molecule of the invention at various concentrations for a few days (e.g., 2-7) days and stained with crystal violet or MTT or analyzed by some other colorimetric assay. Another method of measuring proliferation would be by comparing ^{3}H-thymidine uptake by the cells treated in the presence or absence an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule of the invention. After treatment, the cells are harvested and the amount of radioactivity incorporated into the DNA quantitated in a scintillation counter. Appropriate positive controls include treatment of a selected cell line with a growth inhibitory antibody known to inhibit growth of that cell line. Growth inhibition of tumor cells *in vivo* can be determined in various ways known in the art. Preferably, the tumor cell is one that overexpresses a TAT polypeptide. Preferably, the anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule will inhibit cell proliferation of a TAT-expressing tumor cell *in vitro* or *in vivo* by about 25-100% compared to the untreated tumor cell, more preferably, by about 30-100%, and even more preferably by about 50-100% or 70-100%, in one embodiment, at an antibody concentration of about 0.5 to 30 μg/ml. Growth inhibition can be measured at an antibody concentration of about 0.5 to 30 μg/ml or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the tumor cells to the antibody. The antibody is growth inhibitory *in vivo* if administration of the anti-TAT antibody at about 1 μg/kg to about 100 mg/kg body weight results in reduction in tumor size or reduction of tumor cell proliferation within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

To select for an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule which induces cell death, loss of membrane integrity as indicated by, e.g., propidium iodide (PI), trypan blue or 7AAD uptake may be assessed relative to control. A PI uptake assay can be performed in the absence of complement and immune effector cells. TAT polypeptide-expressing tumor cells are incubated with medium alone or medium containing the appropriate anti-TAT antibody (e.g, at about 10 μg/ml), TAT binding oligopeptide or TAT binding organic molecule. The cells are incubated for a 3 day time period. Following each treatment, cells are washed and aliquoted into 35 mm strainer-capped 12 x 75 tubes (1ml per tube, 3 tubes per treatment group) for removal of cell clumps. Tubes then receive PI (10 μg/ml). Samples may be analyzed using a FACSCAN® flow cytometer and FACSCONVERT® CellQuest software (Becton Dickinson). Those anti-TAT antibodies, TAT binding oligopeptides or TAT binding organic molecules that induce statistically significant levels of cell death as determined by PI uptake may be selected as cell death-inducing anti-TAT antibodies, TAT binding oligopeptides or TAT binding organic molecules.

To screen for antibodies, oligopeptides or other organic molecules which bind to an epitope on a TAT polypeptide bound by an antibody of interest, a routine cross-blocking assay such as that described in Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1988), can be performed. This assay can be used to determine if a test antibody, oligopeptide or other organic molecule binds the same site or epitope as a known anti-TAT antibody. Alternatively, or additionally, epitope mapping can be performed by methods known in the art . For example, the antibody sequence can be mutagenized such as by alanine scanning, to identify contact residues. The mutant antibody is initailly tested for binding with polyclonal antibody to ensure proper folding. In a different method, peptides corresponding to different regions of a TAT polypeptide can be used in competition assays with the test antibodies or with a test antibody and an antibody with a characterized or known epitope.

E. Antibody Dependent Enzyme Mediated Prodrug Therapy (ADEPT)

The antibodies of the present invention may also be used in ADEPT by conjugating the antibody to a prodrug-activating enzyme which converts a prodrug (e.g., a peptidyl chemotherapeutic agent, see WO81/01145) to an active anti-cancer drug. See, for example, WO 88/07378 and U.S. Patent No. 4,975,278.

The enzyme component of the immunoconjugate useful for ADEPT includes any enzyme capable of acting on a prodrug in such a way so as to covert it into its more active, cytotoxic form.

Enzymes that are useful in the method of this invention include, but are not limited to, alkaline phosphatase useful for converting phosphate-containing prodrugs into free drugs; arylsulfatase useful for converting sulfate-containing prodrugs into free drugs; cytosine deaminase useful for converting non-toxic 5-fluorocytosine into the anti-cancer drug, 5-fluorouracil; proteases, such as serratia protease, thermolysin, subtilisin, carboxypeptidases and cathepsins (such as cathepsins B and L), that are useful for converting peptide-containing prodrugs into free drugs; D-alanylcarboxypeptidases, useful for converting prodrugs that contain D-amino acid substituents; carbohydrate-cleaving enzymes such as β-galactosidase and neuraminidase useful for converting glycosylated prodrugs into free drugs; β-lactamase useful for converting drugs derivatized with β-lactams into free drugs; and penicillin amidases, such as penicillin V amidase or penicillin G amidase, useful

for converting drugs derivatized at their amine nitrogens with phenoxyacetyl or phenylacetyl groups, respectively, into free drugs. Alternatively, antibodies with enzymatic activity, also known in the art as "abzymes", can be used to convert the prodrugs of the invention into free active drugs (see, e.g., Massey, Nature 328:457-458 (1987)). Antibody-abzyme conjugates can be prepared as described herein for delivery of the abzyme to a tumor cell population.

The enzymes of this invention can be covalently bound to the anti-TAT antibodies by techniques well known in the art such as the use of the heterobifunctional crosslinking reagents discussed above. Alternatively, fusion proteins comprising at least the antigen binding region of an antibody of the invention linked to at least a functionally active portion of an enzyme of the invention can be constructed using recombinant DNA techniques well known in the art (see, e.g., Neuberger et al., Nature 312:604-608 (1984).

F. Full-Length TAT Polypeptides

The present invention also provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as TAT polypeptides. In particular, cDNAs (partial and full-length) encoding various TAT polypeptides have been identified and isolated, as disclosed in further detail in the Examples below.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the TAT polypeptides and encoding nucleic acids described herein, in some cases, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

G. Anti-TAT Antibody and TAT Polypeptide Variants

In addition to the anti-TAT antibodies and full-length native sequence TAT polypeptides described herein, it is contemplated that anti-TAT antibody and TAT polypeptide variants can be prepared. Anti-TAT antibody and TAT polypeptide variants can be prepared by introducing appropriate nucleotide changes into the encoding DNA, and/or by synthesis of the desired antibody or polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the anti-TAT antibody or TAT polypeptide, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the anti-TAT antibodies and TAT polypeptides described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the antibody or polypeptide that results in a change in the amino acid sequence as compared with the native sequence antibody or polypeptide. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the anti-TAT antibody or TAT polypeptide. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the anti-TAT antibody or

TAT polypeptide with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

Anti-TAT antibody and TAT polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native antibody or protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the anti-TAT antibody or TAT polypeptide.

Anti-TAT antibody and TAT polypeptide fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating antibody or polypeptide fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired antibody or polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, anti-TAT antibody and TAT polypeptide fragments share at least one biological and/or immunological activity with the native anti-TAT antibody or TAT polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the anti-TAT antibody or TAT polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

(1) hydrophobic: norleucine, met, ala, val, leu, ile;

(2) neutral hydrophilic: cys, ser, thr;

(3) acidic: asp, glu;

(4) basic: asn, gln, his, lys, arg;

(5) residues that influence chain orientation: gly, pro; and

(6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al. Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the anti-TAT antibody or TAT polypeptide variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244:1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

Any cysteine residue not involved in maintaining the proper conformation of the anti-TAT antibody or TAT polypeptide also may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) may be added to the anti-TAT antibody or TAT polypeptide to improve its stability (particularly where the antibody is an antibody fragment such as an Fv fragment).

A particularly preferred type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (e.g., a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (e.g., 6-7 sites) are mutated to generate all possible amino substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (e.g., binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the antibody and human TAT polypeptide. Such contact residues and neighboring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

Nucleic acid molecules encoding amino acid sequence variants of the anti-TAT antibody are prepared by a variety of methods known in the art. These methods include, but are not limited to, isolation from a natural source (in the case of naturally occurring amino acid sequence variants) or preparation by oligonucleotide-

mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared variant or a non-variant version of the anti-TAT antibody.

H. Modifications of Anti-TAT Antibodies and TAT Polypeptides

Covalent modifications of anti-TAT antibodies and TAT polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an anti-TAT antibody or TAT polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the anti-TAT antibody or TAT polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking anti-TAT antibody or TAT polypeptide to a water-insoluble support matrix or surface for use in the method for purifying anti-TAT antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the anti-TAT antibody or TAT polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the antibody or polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence anti-TAT antibody or TAT polypeptide (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence anti-TAT antibody or TAT polypeptide. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Glycosylation of antibodies and other polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tripeptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tripeptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-aceylgalactosamine, galactose, or xylose to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

Addition of glycosylation sites to the anti-TAT antibody or TAT polypeptide is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tripeptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the sequence of the original anti-TAT antibody or TAT polypeptide (for O-linked glycosylation sites). The anti-TAT antibody or TAT polypeptide amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the anti-TAT antibody or TAT polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the anti-TAT antibody or TAT polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the anti-TAT antibody or TAT polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of anti-TAT antibody or TAT polypeptide comprises linking the antibody or polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. The antibody or polypeptide also may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization (for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules), or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Oslo, A., Ed., (1980).

The anti-TAT antibody or TAT polypeptide of the present invention may also be modified in a way to form chimeric molecules comprising an anti-TAT antibody or TAT polypeptide fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the anti-TAT antibody or TAT polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the anti-TAT antibody or TAT polypeptide. The presence of such epitope-tagged forms of the anti-TAT antibody or TAT polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the anti-TAT

antibody or TAT polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α-tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the anti-TAT antibody or TAT polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of an anti-TAT antibody or TAT polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH_2 and CH_3, or the hinge, CH_1, CH_2 and CH_3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27, 1995.

I. Preparation of Anti-TAT Antibodies and TAT Polypeptides

The description below relates primarily to production of anti-TAT antibodies and TAT polypeptides by culturing cells transformed or transfected with a vector containing anti-TAT antibody- and TAT polypeptide-encoding nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare anti-TAT antibodies and TAT polypeptides. For instance, the appropriate amino acid sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the anti-TAT antibody or TAT polypeptide may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the desired anti-TAT antibody or TAT polypeptide.

1. Isolation of DNA Encoding Anti-TAT Antibody or TAT Polypeptide

DNA encoding anti-TAT antibody or TAT polypeptide may be obtained from a cDNA library prepared from tissue believed to possess the anti-TAT antibody or TAT polypeptide mRNA and to express it at a detectable level. Accordingly, human anti-TAT antibody or TAT polypeptide DNA can be conveniently obtained from a cDNA library prepared from human tissue. The anti-TAT antibody- or TAT polypeptide-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated

nucleic acid synthesis).

Libraries can be screened with probes (such as oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding anti-TAT antibody or TAT polypeptide is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

Techniques for screening a cDNA library are well known in the art. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for anti-TAT antibody or TAT polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, $CaCl_2$, $CaPO_4$, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology,

52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA* ; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan^r*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan^r*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

Full length antibody, antibody fragments, and antibody fusion proteins can be produced in bacteria, in particular when glycosylation and Fc effector function are not needed, such as when the therapeutic antibody is conjugated to a cytotoxic agent (e.g., a toxin) and the immunoconjugate by itself shows effectiveness in tumor cell destruction. Full length antibodies have greater half life in circulation. Production in E. coli is faster and more cost efficient. For expression of antibody fragments and polypeptides in bacteria, see, e.g., U.S. 5,648,237 (Carter et. al.), U.S. 5,789,199 (Joly et al.), and U.S. 5,840,523 (Simmons et al.) which describes translation initiation regio (TIR) and signal sequences for optimizing expression and secretion, these patents incorporated herein by reference. After expression, the antibody is isolated from the E. coli cell paste in a soluble fraction and can be purified through, e.g., a protein A or G column depending on the isotype. Final purification can be carried out similar to the process for purifying antibody expressed e.g,, in CHO cells.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for anti-TAT antibody- or TAT polypeptide-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include*Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickeramii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilarum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus; yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida; Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora, Penicillium, Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylotropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula, Candida, Kloeckera, Pichia, Saccharomyces, Torulopsis,*and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of glycosylated anti-TAT antibody or TAT polypeptide are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as Drosophila S2 and Spodoptera Sf9, as well as plant cells, such as cell cultures of cotton, corn, potato, soybean, petunia, tomato, and tobacco. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruitfly), and *Bombyx mori* have been identified. A variety of viral strains for transfection are publicly available, e.g., the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol. 36:59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub et al., Proc. Natl. Acad. Sci. USA77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23:243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2,

HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather et al., Annals N.Y. Acad. Sci. 383:44-68 (1982)); MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

Host cells are transformed with the above-described expression or cloning vectors for anti-TAT antibody or TAT polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding anti-TAT antibody or TAT polypeptide may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The TAT may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the anti-TAT antibody- or TAT polypeptide-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α-factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification

of cells competent to take up the anti-TAT antibody- or TAT polypeptide-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp*1 gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp*1 gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the anti-TAT antibody- or TAT polypeptide-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β-lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding anti-TAT antibody or TAT polypeptide.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

Anti-TAT antibody or TAT polypeptide transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the anti-TAT antibody or TAT polypeptide by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the

late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the anti-TAT antibody or TAT polypeptide coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding anti-TAT antibody or TAT polypeptide.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of anti-TAT antibody or TAT polypeptide in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Culturing the Host Cells

The host cells used to produce the anti-TAT antibody or TAT polypeptide of this invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham et alMeth. Enz. 58:44 (1979), Barnes et al., Anal. Biochem.102:255 (1980), U.S. Pat. Nos. 4,767,704; 4,657,866; 4,927,762; 4,560,655; or 5,122,469; WO 90/03430; WO 87/00195; or U.S. Patent Re. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as GENTAMYCIN™ drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

5. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA , 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence TAT polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to TAT DNA and encoding a specific antibody epitope.

6. Purification of Anti-TAT Antibody and TAT Polypeptide

Forms of anti-TAT antibody and TAT polypeptide may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of anti-TAT antibody and TAT polypeptide can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify anti-TAT antibody and TAT polypeptide from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the anti-TAT antibody and TAT polypeptide. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular anti-TAT antibody or TAT polypeptide produced.

When using recombinant techniques, the antibody can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter et al., Bio/Technology 10:163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium

acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 min. Cell debris can be removed by centrifugation. Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

The antibody composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique. The suitability of protein A as an affinity ligand depends on the species and isotype of any immunoglobulin Fc domain that is present in the antibody. Protein A can be used to purify antibodies that are based on human $\gamma 1$, $\gamma 2$ or $\gamma 4$ heavy chains (Lindmark et al., J. Immunol. Meth. 62:1-13 (1983)). Protein G is recommended for all mouse isotypes and for human $\gamma 3$ (Guss et al., EMBO J. 5:15671575 (1986)). The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the antibody comprises a C_H3 domain, the Bakerbond ABX™resin (J. T. Baker, Phillipsburg, NJ) is useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE™ chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered.

Following any preliminary purification step(s), the mixture comprising the antibody of interest and contaminants may be subjected to low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5-4.5, preferably performed at low salt concentrations (e.g., from about 0-0.25M salt).

J. Pharmaceutical Formulations

Therapeutic formulations of the anti-TAT antibodies, TAT binding oligopeptides, TAT binding organic molecules and/or TAT polypeptides used in accordance with the present invention are prepared for storage by mixing the antibody, polypeptide, oligopeptide or organic molecule having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as acetate, Tris, phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine,

histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; tonicifiers such as trehalose and sodium chloride; sugars such as sucrose, mannitol, trehalose or sorbitol; surfactant such as polysorbate; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN®, PLURONICS® or polyethylene glycol (PEG). The antibody preferably comprises the antibody at a concentration of between 5-200 mg/ml, preferably between 10-100 mg/ml.

The formulations herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. For example, in addition to an anti-TAT antibody, TAT binding oligopeptide, or TAT binding organic molecule, it may be desirable to include in the one formulation, an additional antibody, e.g., a second anti-TAT antibody which binds a different epitope on the TAT polypeptide, or an antibody to some other target such as a growth factor that affects the growth of the particular cancer. Alternatively, or additionally, the composition may further comprise a chemotherapeutic agent, cytotoxic agent, cytokine, growth inhibitory agent, anti-hormonal agent, and/or cardioprotectant. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Osol, A. Ed. (1980).

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT® (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

K. Diagnosis and Treatment with Anti-TAT Antibodies, TAT Binding Oligopeptides and TAT Binding Organic Molecules

To determine TAT expression in the cancer, various diagnostic assays are available. In one embodiment, TAT polypeptide overexpression may be analyzed by immunohistochemistry (IHC). Parrafin embedded tissue sections from a tumor biopsy may be subjected to the IHC assay and accorded a TAT protein staining intensity criteria as follows:

Score 0 - no staining is observed or membrane staining is observed in less than 10% of tumor cells.

Score 1+ - a faint/barely perceptible membrane staining is detected in more than 10% of the tumor cells. The cells are only stained in part of their membrane.

Score 2+ - a weak to moderate complete membrane staining is observed in more than 10% of the tumor cells.

Score 3+ - a moderate to strong complete membrane staining is observed in more than 10% of the tumor cells.

Those tumors with 0 or 1+ scores for TAT polypeptide expression may be characterized as not overexpressing TAT, whereas those tumors with 2+ or 3+ scores may be characterized as overexpressing TAT.

Alternatively, or additionally, FISH assays such as the INFORM® (sold by Ventana, Arizona) or PATHVISION® (Vysis, Illinois) may be carried out on formalin-fixed, paraffin-embedded tumor tissue to determine the extent (if any) of TAT overexpression in the tumor.

TAT overexpression or amplification may be evaluated using an *in vivo* diagnostic assay, e.g., by administering a molecule (such as an antibody, oligopeptide or organic molecule) which binds the molecule to be detected and is tagged with a detectable label (e.g., a radioactive isotope or a fluorescent label) and externally scanning the patient for localization of the label.

As described above, the anti-TAT antibodies, oligopeptides and organic molecules of the invention have various non-therapeutic applications. The anti-TAT antibodies, oligopeptides and organic molecules of the present invention can be useful for diagnosis and staging of TAT polypeptide-expressing cancers (e.g., in radioimaging). The antibodies, oligopeptides and organic molecules are also useful for purification or immunoprecipitation of TAT polypeptide from cells, for detection and quantitation of TAT polypeptide *in vitro*, e.g., in an ELISA or a Western blot, to kill and eliminate TAT-expressing cells from a population of mixed cells as a step in the purification of other cells.

Currently, depending on the stage of the cancer, cancer treatment involves one or a combination of the following therapies: surgery to remove the cancerous tissue, radiation therapy, and chemotherapy. Anti-TAT antibody, oligopeptide or organic molecule therapy may be especially desirable in elderly patients who do not tolerate the toxicity and side effects of chemotherapy well and in metastatic disease where radiation therapy has limited usefulness. The tumor targeting anti-TAT antibodies, oligopeptides and organic molecules of the invention are useful to alleviate TAT-expressing cancers upon initial diagnosis of the disease or during relapse. For therapeutic applications, the anti-TAT antibody, oligopeptide or organic molecule can be used alone, or in combination therapy with, e.g., hormones, antiangiogens, or radiolabelled compounds, or with surgery, cryotherapy, and/or radiotherapy. Anti-TAT antibody, oligopeptide or organic molecule treatment can be administered in conjunction with other forms of conventional therapy, either consecutively with, pre- or post-conventional therapy. Chemotherapeutic drugs such as TAXOTERE® (docetaxel), TAXOL® (palictaxel), estramustine and mitoxantrone are used in treating cancer, in particular, in good risk patients. In the present method of the invention for treating or alleviating cancer, the cancer patient can be administered anti-TAT

antibody, oligopeptide or organic molecule in conjuction with treatment with the one or more of the preceding chemotherapeutic agents. In particular, combination therapy with palictaxel and modified derivatives (see, e.g., EP0600517) is contemplated. The anti-TAT antibody, oligopeptide or organic molecule will be administered with a therapeutically effective dose of the chemotherapeutic agent. In another embodiment, the anti-TAT antibody, oligopeptide or organic molecule is administered in conjunction with chemotherapy to enhance the activity and efficacy of the chemotherapeutic agent, e.g., paclitaxel. The Physicians' Desk Reference (PDR) discloses dosages of these agents that have been used in treatment of various cancers. The dosing regimen and dosages of these aforementioned chemotherapeutic drugs that are therapeutically effective will depend on the particular cancer being treated, the extent of the disease and other factors familiar to the physician of skill in the art and can be determined by the physician.

In one particular embodiment, a conjugate comprising an anti-TAT antibody, oligopeptide or organic molecule conjugated with a cytotoxic agent is administered to the patient. Preferably, the immunoconjugate bound to the TAT protein is internalized by the cell, resulting in increased therapeutic efficacy of the immunoconjugate in killing the cancer cell to which it binds. In a preferred embodiment, the cytotoxic agent targets or interferes with the nucleic acid in the cancer cell. Examples of such cytotoxic agents are described above and include maytansinoids, calicheamicins, ribonucleases and DNA endonucleases.

The anti-TAT antibodies, oligopeptides, organic molecules or toxin conjugates thereof are administered to a human patient, in accord with known methods, such as intravenous administration, e.g.,, as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerobrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation routes. Intravenous or subcutaneous administration of the antibody, oligopeptide or organic molecule is preferred.

Other therapeutic regimens may be combined with the administration of the anti-TAT antibody, oligopeptide or organic molecule. The combined administration includes co-administration, using separate formulations or a single pharmaceutical formulation, and consecutive administration in either order, wherein preferably there is a time period while both (or all) active agents simultaneously exert their biological activities. Preferably such combined therapy results in a synergistic therapeutic effect.

It may also be desirable to combine administration of the anti-TAT antibody or antibodies, oligopeptides or organic molecules, with administration of an antibody directed against another tumor antigen associated with the particular cancer.

In another embodiment, the therapeutic treatment methods of the present invention involves the combined administration of an anti-TAT antibody (or antibodies), oligopeptides or organic molecules and one or more chemotherapeutic agents or growth inhibitory agents, including co-administration of cocktails of different chemotherapeutic agents. Chemotherapeutic agents include estramustine phosphate, prednimustine, cisplatin, 5-fluorouracil, melphalan, cyclophosphamide, hydroxyurea and hydroxyureataxanes (such as paclitaxel and doxetaxel) and/or anthracycline antibiotics. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in Chemotherapy

Service Ed., M.C. Perry, Williams & Wilkins, Baltimore, MD (1992).

The antibody, oligopeptide or organic molecule may be combined with an anti-hormonal compound; e.g., an anti-estrogen compound such as tamoxifen; an anti-progesterone such as onapristone (see, EP 616 812); or an anti-androgen such as flutamide, in dosages known for such molecules. Where the cancer to be treated is androgen independent cancer, the patient may previously have been subjected to anti-androgen therapy and, after the cancer becomes androgen independent, the anti-TAT antibody, oligopeptide or organic molecule (and optionally other agents as described herein) may be administered to the patient.

Sometimes, it may be beneficial to also co-administer a cardioprotectant (to prevent or reduce myocardial dysfunction associated with the therapy) or one or more cytokines to the patient. In addition to the above therapeutic regimes, the patient may be subjected to surgical removal of cancer cells and/or radiation therapy, before, simultaneously with, or post antibody, oligopeptide or organic molecule therapy. Suitable dosages for any of the above co-administered agents are those presently used and may be lowered due to the combined action (synergy) of the agent and anti-TAT antibody, oligopeptide or organic molecule.

For the prevention or treatment of disease, the dosage and mode of administration will be chosen by the physician according to known criteria. The appropriate dosage of antibody, oligopeptide or organic molecule will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the antibody, oligopeptide or organic molecule is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, oligopeptide or organic molecule, and the discretion of the attending physician. The antibody, oligopeptide or organic molecule is suitably administered to the patient at one time or over a series of treatments. Preferably, the antibody, oligopeptide or organic molecule is administered by intravenous infusion or by subcutaneous injections. Depending on the type and severity of the disease, about 1 μg/kg to about 50 mg/kg body weight (e.g., about 0.1-15mg/kg/dose) of antibody can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A dosing regimen can comprise administering an initial loading dose of about 4 mg/kg, followed by a weekly maintenance dose of about 2 mg/kg of the anti-TAT antibody. However, other dosage regimens may be useful. A typical daily dosage might range from about 1 μg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. The progress of this therapy can be readily monitored by conventional methods and assays and based on criteria known to the physician or other persons of skill in the art.

Aside from administration of the antibody protein to the patient, the present application contemplates administration of the antibody by gene therapy. Such administration of nucleic acid encoding the antibody is encompassed by the expression "administering a therapeutically effective amount of an antibody". See, for example, WO96/07321 published March 14, 1996 concerning the use of gene therapy to generate intracellular antibodies.

There are two major approaches to getting the nucleic acid (optionally contained in a vector) into the patient's cells; *in vivo* and *ex vivo*. For *in vivo* delivery the nucleic acid is injected directly into the patient,

usually at the site where the antibody is required. For *ex vivo* treatment, the patient's cells are removed, the nucleic acid is introduced into these isolated cells and the modified cells are administered to the patient either directly or, for example, encapsulated within porous membranes which are implanted into the patient (see, e.g., U.S. Patent Nos. 4,892,538 and 5,283,187). There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. A commonly used vector for*ex vivo* delivery of the gene is a retroviral vector.

The currently preferred *in vivo* nucleic acid transfer techniques include transfection with viral vectors (such as adenovirus, Herpes simplex I virus, or adeno-associated virus) and lipid-based systems (useful lipids for lipid-mediated transfer of the gene are DOTMA, DOPE and DC-Chol, for example). For review of the currently known gene marking and gene therapy protocols see Anderson et al., Science 256:808-813 (1992). See also WO 93/25673 and the references cited therein.

The anti-TAT antibodies of the invention can be in the different forms encompassed by the definition of "antibody" herein. Thus, the antibodies include full length or intact antibody, antibody fragments, native sequence antibody or amino acid variants, humanized, chimeric or fusion antibodies, immunoconjugates, and functional fragments thereof. In fusion antibodies an antibody sequence is fused to a heterologous polypeptide sequence. The antibodies can be modified in the Fc region to provide desired effector functions. As discussed in more detail in the sections herein, with the appropriate Fc regions, the naked antibody bound on the cell surface can induce cytotoxicity, e.g., via antibody-dependent cellular cytotoxicity (ADCC) or by recruiting complement in complement dependent cytotoxicity, or some other mechanism. Alternatively, where it is desirable to eliminate or reduce effector function, so as to minimize side effects or therapeutic complications, certain other Fc regions may be used.

In one embodiment, the antibody competes for binding or bind substantially to, the same epitope as the antibodies of the invention. Antibodies having the biological characteristics of the present anti-TAT antibodies of the invention are also contemplated, specifically including the *in vivo* tumor targeting and any cell proliferation inhibition or cytotoxic characteristics.

Methods of producing the above antibodies are described in detail herein.

The present anti-TAT antibodies, oligopeptides and organic molecules are useful for treating a TAT-expressing cancer or alleviating one or more symptoms of the cancer in a mammal. Such a cancer includes prostate cancer, cancer of the urinary tract, lung cancer, breast cancer, colon cancer and ovarian cancer, more specifically, prostate adenocarcinoma, renal cell carcinomas, colorectal adenocarcinomas, lung adenocarcinomas, lung squamous cell carcinomas, and pleural mesothelioma. The cancers encompass metastatic cancers of any of the preceding. The antibody, oligopeptide or organic molecule is able to bind to at least a portion of the cancer cells that express TAT polypeptide in the mammal. In a preferred embodiment, the antibody, oligopeptide or organic molecule is effective to destroy or kill TAT-expressing tumor cells or inhibit

the growth of such tumor cells, *in vitro* or *in vivo*, upon binding to TAT polypeptide on the cell. Such an antibody includes a naked anti-TAT antibody (not conjugated to any agent). Naked antibodies that have cytotoxic or cell growth inhibition properties can be further harnessed with a cytotoxic agent to render them even more potent in tumor cell destruction. Cytotoxic properties can be conferred to an anti-TAT antibody by, e.g., conjugating the antibody with a cytotoxic agent, to form an immunoconjugate as described herein. The cytotoxic agent or a growth inhibitory agent is preferably a small molecule. Toxins such as calicheamicin or a maytansinoid and analogs or derivatives thereof, are preferable.

The invention provides a composition comprising an anti-TAT antibody, oligopeptide or organic molecule of the invention, and a carrier. For the purposes of treating cancer, compositions can be administered to the patient in need of such treatment, wherein the composition can comprise one or more anti-TAT antibodies present as an immunoconjugate or as the naked antibody. In a further embodiment, the compositions can comprise these antibodies, oligopeptides or organic molecules in combination with other therapeutic agents such as cytotoxic or growth inhibitory agents, including chemotherapeutic agents. The invention also provides formulations comprising an anti-TAT antibody, oligopeptide or organic molecule of the invention, and a carrier. In one embodiment, the formulation is a therapeutic formulation comprising a pharmaceutically acceptable carrier.

Another aspect of the invention is isolated nucleic acids encoding the anti-TAT antibodies. Nucleic acids encoding both the H and L chains and especially the hypervariable region residues, chains which encode the native sequence antibody as well as variants, modifications and humanized versions of the antibody, are encompassed.

The invention also provides methods useful for treating a TAT polypeptide-expressing cancer or alleviating one or more symptoms of the cancer in a mammal, comprising administering a therapeutically effective amount of an anti-TAT antibody, oligopeptide or organic molecule to the mammal. The antibody, oligopeptide or organic molecule therapeutic compositions can be administered short term (acute) or chronic, or intermittent as directed by physician. Also provided are methods of inhibiting the growth of, and killing a TAT polypeptide-expressing cell.

The invention also provides kits and articles of manufacture comprising at least one anti-TAT antibody, oligopeptide or organic molecule. Kits containing anti-TAT antibodies, oligopeptides or organic molecules find use, e.g., for TAT cell killing assays, for purification or immunoprecipitation of TAT polypeptide from cells. For example, for isolation and purification of TAT, the kit can contain an anti-TAT antibody, oligopeptide or organic molecule coupled to beads (e.g., sepharose beads). Kits can be provided which contain the antibodies, oligopeptides or organic molecules for detection and quantitation of TAT *in vitro*, e.g., in an ELISA or a Western blot. Such antibody, oligopeptide or organic molecule useful for detection may be provided with a label such as a fluorescent or radiolabel.

L. Articles of Manufacture and Kits

Another embodiment of the invention is an article of manufacture containing materials useful for the treatment of anti-TAT expressing cancer. The article of manufacture comprises a container and a label or

package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is effective for treating the cancer condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). At least one active agent in the composition is an anti-TAT antibody, oligopeptide or organic molecule of the invention. The label or package insert indicates that the composition is used for treating cancer. The label or package insert will further comprise instructions for administering the antibody, oligopeptide or organic molecule composition to the cancer patient. Additionally, the article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

Kits are also provided that are useful for various purposes , e.g., for TAT-expressing cell killing assays, for purification or immunoprecipitation of TAT polypeptide from cells. For isolation and purification of TAT polypeptide, the kit can contain an anti-TAT antibody, oligopeptide or organic molecule coupled to beads (e.g., sepharose beads). Kits can be provided which contain the antibodies, oligopeptides or organic molecules for detection and quantitation of TAT polypeptide *in vitro*, e.g., in an ELISA or a Western blot. As with the article of manufacture, the kit comprises a container and a label or package insert on or associated with the container. The container holds a composition comprising at least one anti-TAT antibody, oligopeptide or organic molecule of the invention. Additional containers may be included that contain, e.g., diluents and buffers, control antibodies. The label or package insert may provide a description of the composition as well as instructions for the intended in vitro or diagnostic use.

M. Uses for TAT Polypeptides and TAT-Polypeptide Encoding Nucleic Acids

Nucleotide sequences (or their complement) encoding TAT polypeptides have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA probes. TAT-encoding nucleic acid will also be useful for the preparation of TAT polypeptides by the recombinant techniques described herein, wherein those TAT polypeptides may find use, for example, in the preparation of anti-TAT antibodies as described herein.

The full-length native sequence TAT gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length TAT cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of TAT or TAT from other species) which have a desired sequence identity to the native TAT sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence TAT. By way of example, a screening method will comprise isolating the coding region of the TAT gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety

of labels, including radionucleotides such as ^{32}P or ^{35}S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the TAT gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below. Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the TAT-encoding nucleic acids include antisense or sense oligonucleotides comprising a singe-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target TAT mRNA (sense) or TAT DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of TAT DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. Such methods are encompassed by the present invention. The antisense oligonucleotides thus may be used to block expression of TAT proteins, wherein those TAT proteins may play a role in the induction of cancer in mammals. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Preferred intragenic sites for antisense binding include the region incorporating the translation initiation/start codon (5'-AUG / 5'-ATG) or termination/stop codon (5'-UAA, 5'-UAG and 5-UGA / 5'-TAA, 5'-TAG and 5'-TGA) of the open reading frame (ORF) of the gene. These regions refer to a portion of the mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation or termination codon. Other preferred regions for antisense binding include: introns; exons; intron-exon junctions; the open reading frame (ORF) or "coding region," which is the region between the translation initiation codon and the translation termination codon; the 5' cap of an mRNA which comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage and includes 5' cap structure itself as well as the first 50 nucleotides adjacent to the cap; the 5' untranslated region (5'UTR), the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA or corresponding nucleotides on the gene; and the 3' untranslated region (3'UTR), the portion of an mRNA in the 3' direction from the translation termination codon, and thus including nucleotides between the translation termination codon and 3' end of an mRNA or corresponding nucleotides on the gene.

Specific examples of preferred antisense compounds useful for inhibiting expression of TAT proteins include oligonucleotides containing modified backbones or non-natural internucleoside linkages. Oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. Preferred modified oligonucleotide backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotri-esters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates, 5'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, selenophosphates and borano-phosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein one or more internucleotide linkages is a 3' to 3', 5' to 5' or 2' to 2' linkage. Preferred oligonucleotides having inverted polarity comprise a single 3' to 3' linkage at the 3'-most internucleotide linkage i.e. a single inverted nucleoside residue which may be abasic (the nucleobase is missing or has a hydroxyl group in place thereof). Various salts, mixed salts and free acid forms are also included. Representative United States patents that teach the preparation of phosphorus-containing linkages include, but are not limited to, U.S. Pat. Nos.: 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,194,599; 5,565,555; 5,527,899; 5,721,218; 5,672,697 and 5,625,050, each of which is herein incorporated by reference.

Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; riboacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH.sub.2 component parts. Representative United States patents that teach the preparation of such oligonucleosides include, but are not limited to,. U.S. Pat. Nos.: 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; 5,792,608; 5,646,269 and 5,677,439, each of which is herein incorporated by reference.

In other preferred antisense oligonucleotides, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic

that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Pat. Nos.: 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen et al., Science, 1991, 254, 1497-1500.

Preferred antisense oligonucleotides incorporate phosphorothioate backbones and/or heteroatom backbones, and in particular $-CH_2-NH-O-CH_2-$, $-CH_2-N(CH_3)-O-CH_2-$ [known as a methylene (methylimino) or MMI backbone], $-CH_2-O-N(CH_3)-CH_2-$, $-CH_2-N(CH_3)-N(CH_3)-CH_2-$ and $-O-N(CH_3)-CH_2-CH_2-$ [wherein the native phosphodiester backbone is represented as $-O-P-O-CH_2-$] described in the above referenced U.S. Pat. No. 5,489,677, and the amide backbones of the above referenced U.S. Pat. No. 5,602,240. Also preferred are antisense oligonucleotides having morpholino backbone structures of the above-referenced U.S. Pat. No. 5,034,506.

Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-alkyl, S-alkyl, or N-alkyl; O-alkenyl, S-alkeynyl, or N-alkenyl; O-alkynyl, S-alkynyl or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3)]_2$, where n and m are from 1 to about 10. Other preferred antisense oligonucleotides comprise one of the following at the 2' position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkenyl, alkynyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$, SO_2 CH_3, ONO_2, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy (2'-$O-CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin et al., Helv. Chim. Acta, 1995, 78, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminooxyethoxy, i.e., a $O(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, as described in examples hereinbelow, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), i.e., 2'-$O-CH_2-O-CH_2-N(CH_2)$.

A further prefered modification includes Locked Nucleic Acids (LNAs) in which the 2'-hydroxyl group is linked to the 3' or 4' carbon atom of the sugar ring thereby forming a bicyclic sugar moiety. The linkage is preferably a methelyne $(-CH_2-)_n$ group bridging the 2' oxygen atom and the 4' carbon atom wherein n is 1 or 2. LNAs and preparation thereof are described in WO 98/39352 and WO 99/14226.

Other preferred modifications include 2'-methoxy (2'-$O-CH_3$), 2'-aminopropoxy (2'-$OCH_2CH_2CH_2$

NH_2), 2'-allyl (2'-CH_2-CH=CH_2), 2'-O-allyl (2'-O-CH_2-CH=CH_2) and 2'-fluoro (2'-F). The 2'-modification may be in the arabino (up) position or ribo (down) position. A preferred 2'-arabino modification is 2'-F. Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative United States patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. Pat. Nos.: 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; 5,792,747; and 5,700,920, each of which is herein incorporated by reference in its entirety.

Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl (-C≡C-CH_3 or -CH_2-C≡CH) uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 2-F-adenine, 2-amino-adenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further modified nucleobases include tricyclic pyrimidines such as phenoxazine cytidine(1H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), phenothiazine cytidine (1H-pyrimido[5,4-b][1,4]benzothiazin-2(3H)-one), G-clamps such as a substituted phenoxazine cytidine (e.g. 9-(2-aminoethoxy)-H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), carbazole cytidine (2H-pyrimido[4,5-b]indol-2-one), pyridoindole cytidine (H-pyrido[3',2':4,5]pyrrolo[2,3-d]pyrimidin-2-one). Modified nucleobases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808, those disclosed in The Concise Encyclopedia Of Polymer Science And Engineering, pages 858-859, Kroschwitz, J. I., ed. John Wiley & Sons, 1990, and those disclosed by Englisch et al., Angewandte Chemie, International Edition, 1991, 30, 613. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2.degree. C. (Sanghvi et al, Antisense Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278) and are preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications. Representative United States patents

that teach the preparation of modified nucleobases include, but are not limited to: U.S. Pat. No. 3,687,808, as well as U.S. Pat. Nos.: 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,645,985; 5,830,653; 5,763,588; 6,005,096; 5,681,941 and 5,750,692, each of which is herein incorporated by reference.

Another modification of antisense oligonucleotides chemically linking to the oligonucleotide one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. The compounds of the invention can include conjugate groups covalently bound to functional groups such as primary or secondary hydroxyl groups. Conjugate groups of the invention include intercalators, reporter molecules, polyamines, polyamides, polyethylene glycols, polyethers, groups that enhance the pharmacodynamic properties of oligomers, and groups that enhance the pharmacokinetic properties of oligomers. Typical conjugates groups include cholesterols, lipids, cation lipids, phospholipids, cationic phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. Groups that enhance the pharmacodynamic properties, in the context of this invention, include groups that improve oligomer uptake, enhance oligomer resistance to degradation, and/or strengthen sequence-specific hybridization with RNA. Groups that enhance the pharmacokinetic properties, in the context of this invention, include groups that improve oligomer uptake, distribution, metabolism or excretion. Conjugate moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., Proc. Natl. Acad. Sci. USA, 1989, 86, 6553-6556), cholic acid (Manoharan et al., Bioorg. Med. Chem. Let., 1994, 4, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., Ann. N.Y. Acad. Sci., 1992, 660, 306-309; Manoharan et al., Bioorg. Med. Chem. Let., 1993, 3, 2765-2770), a thiocholesterol (Oberhauser et al., Nucl. Acids Res., 1992, 20, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., EMBO J., 1991, 10, 1111-1118; Kabanov et al., FEBS Lett., 1990, 259, 327-330; Svinarchuk et al., Biochimie, 1993, 75, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654; Shea et al., Nucl. Acids Res., 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., Nucleosides & Nucleotides, 1995, 14, 969-973), or adamantane acetic acid (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654), a palmityl moiety (Mishra et al., Biochim. Biophys. Acta, 1995, 1264, 229-237), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety. Oligonucleotides of the invention may also be conjugated to active drug substances, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fenbufen, ketoprofen, (S)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indomethicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic. Oligonucleotide-drug conjugates and their preparation are described in U.S. patent application Ser. No. 09/334,130 (filed Jun. 15, 1999) and United States patents Nos.: 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025;

4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941, each of which is herein incorporated by reference.

It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide. The present invention also includes antisense compounds which are chimeric compounds. "Chimeric" antisense compounds or "chimeras," in the context of this invention, are antisense compounds, particularly oligonucleotides, which contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide inhibition of gene expression. Consequently, comparable results can often be obtained with shorter oligonucleotides when chimeric oligonucleotides are used, compared to phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Chimeric antisense compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Preferred chimeric antisense oligonucleotides incorporate at least one 2' modified sugar (preferably 2'-O-$(CH_2)_2$-O-CH_3) at the 3' terminal to confer nuclease resistance and a region with at least 4 contiguous 2'-H sugars to confer RNase H activity. Such compounds have also been referred to in the art as hybrids or gapmers. Preferred gapmers have a region of 2' modified sugars (preferably 2'-O-$(CH_2)_2$-O-CH_3) at the 3'-terminal and at the 5' terminal separated by at least one region having at least 4 contiguous 2'-H sugars and preferably incorporate phosphorothioate backbone linkages. Representative United States patents that teach the preparation of such hybrid structures include, but are not limited to, U.S. Pat. Nos. 5,013,830; 5,149,797; 5,220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922, each of which is herein incorporated by reference in its entirety.

The antisense compounds used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, Calif.). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives. The compounds of the invention may also be admixed, encapsulated, conjugated or otherwise associated with other molecules, molecule structures or mixtures of compounds, as for example, liposomes, receptor targeted molecules, oral,

rectal, topical or other formulations, for assisting in uptake, distribution and/or absorption. Representative United States patents that teach the preparation of such uptake, distribution and/or absorption assisting formulations include, but are not limited to, U.S. Pat. Nos. 5,108,921; 5,354,844; 5,416,016; 5,459,127; 5,521,291; 5,543,158; 5,547,932; 5,583,020; 5,591,721; 4,426,330; 4,534,899; 5,013,556; 5,108,921; 5,213,804; 5,227,170; 5,264,221; 5,356,633; 5,395,619; 5,416,016; 5,417,978; 5,462,854; 5,469,854; 5,512,295; 5,527,528; 5,534,259; 5,543,152; 5,556,948; 5,580,575; and 5,595,756, each of which is herein incorporated by reference.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, $CaPO_4$-mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Antisense or sense RNA or DNA molecules are generally at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710,

720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related TAT coding sequences.

Nucleotide sequences encoding a TAT can also be used to construct hybridization probes for mapping the gene which encodes that TAT and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for TAT encode a protein which binds to another protein (example, where the TAT is a receptor), the TAT can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor TAT can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native TAT or a receptor for TAT. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode TAT or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding TAT can be used to clone genomic DNA encoding TAT in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding TAT. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for TAT transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding TAT introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding TAT. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential

therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of TAT can be used to construct a TAT "knock out" animal which has a defective or altered gene encoding TAT as a result of homologous recombination between the endogenous gene encoding TAT and altered genomic DNA encoding TAT introduced into an embryonic stem cell of the animal. For example, cDNA encoding TAT can be used to clone genomic DNA encoding TAT in accordance with established techniques. A portion of the genomic DNA encoding TAT can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, Cell, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., Cell, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the TAT polypeptide.

Nucleic acid encoding the TAT polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik *et al.*, Proc. Natl. Acad. Sci. USA 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau

et al., Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., J. Biol. Chem. 262, 4429-4432 (1987); and Wagner et al., Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., Science 256, 808-813 (1992).

The nucleic acid molecules encoding the TAT polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each TAT nucleic acid molecule of the present invention can be used as a chromosome marker.

The TAT polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the TAT polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. TAT nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

This invention encompasses methods of screening compounds to identify those that mimic the TAT polypeptide (agonists) or prevent the effect of the TAT polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the TAT polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins, including e.g., inhibiting the expression of TAT polypeptide from cells. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a TAT polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the TAT polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the TAT polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the TAT polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the

immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular TAT polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1- *lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β-galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a TAT polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the TAT polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence

of the TAT polypeptide indicates that the compound is an antagonist to the TAT polypeptide. Alternatively, antagonists may be detected by combining the TAT polypeptide and a potential antagonist with membrane-bound TAT polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The TAT polypeptide can be labeled, such as by radioactivity, such that the number of TAT polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the TAT polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the TAT polypeptide. Transfected cells that are grown on glass slides are exposed to labeled TAT polypeptide. The TAT polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled TAT polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro- sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled TAT polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with TAT polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the TAT polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the TAT polypeptide.

Another potential TAT polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature TAT polypeptides herein, is used to design an antisense

RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the TAT polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the TAT polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the TAT polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the TAT polypeptide, thereby blocking the normal biological activity of the TAT polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., RossCurrent Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Isolated TAT polypeptide-encoding nucleic acid can be used herein for recombinantly producing TAT polypeptide using techniques well known in the art and as described herein. In turn, the produced TAT polypeptides can be employed for generating anti-TAT antibodies using techniques well known in the art and as described herein.

Antibodies specifically binding a TAT polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders, including cancer, in the form of pharmaceutical compositions.

If the TAT polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993).

The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Analysis of Differential TAT Polypeptide Expression by GEPIS

An expressed sequence tag (EST) DNA database (LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) was searched and interesting EST sequences were identified by GEPIS. Gene expression profiling *in silico* (GEPIS) is a bioinformatics tool developed at Genentech, Inc. that characterizes genes of interest for new cancer therapeutic targets. GEPIS takes advantage of large amounts of EST sequence and library information to determine gene expression profiles. GEPIS is capable of determining the expression profile of a gene based upon its proportional correlation with the number of its occurrences in EST databases, and it works by integrating the LIFESEQ® EST relational database and Genentech proprietary information in a stringent and statistically meaningful way. In this example, GEPIS is used to identify and cross-validate novel tumor antigens, although GEPIS can be configured to perform either very specific analyses or broad screening tasks. For the initial screen, GEPIS is used to identify EST sequences from the LIFESEQ® database that correlate

to expression in a particular tissue or tissues of interest (often a tumor tissue of interest). Then, GEPIS was employed to generate a complete tissue expression profile for the various sequences of interest. Using this type of screening bioinformatics, various TAT polypeptides (and their encoding nucleic acid molecules) were identified as being significantly overexpressed in a particular type of cancer or certain cancers as compared to other cancers and/or normal non-cancerous tissues. The rating of GEPIS hits is based upon several criteria including, for example, tissue specificity, tumor specificity and expression level in normal essential and/or normal proliferating tissues. The following is a list of molecules whose tissue expression profile as determined by GEPIS evidences significant upregulation of expression in a specific tumor or tumors as compared to other tumor(s) and/or normal tissues and optionally relatively low expression in normal essential and/or normal proliferating tissues.

Under each tissue heading shown below is a list of the cDNA sequences that are detectably overexpressed in tumor tissue of the indicated tissue type as compared to normal non-tumor tissue of the same tissue type. As such, the molecules listed below (and the polypeptides they encode) are excellent nucleic acid (and polypeptide) targets for the diagnosis and therapy of cancer in mammals.

PERIPHERAL NERVOUS SYSTEM

DNA324303	DNA324573	DNA324681	DNA325296	DNA325405	DNA325407
DNA325408	DNA325409	DNA325410	DNA325449	DNA325503	DNA326083
DNA326231	DNA188229	DNA327080	DNA327081	DNA327082	

BRAIN

DNA323721	DNA323722	DNA323723	DNA323724	DNA323726	DNA323727
DNA323728	DNA323729	DNA323731	DNA323732	DNA287173	DNA151148
DNA323740	DNA323742	DNA323743	DNA323744	DNA323751	DNA323753
DNA323755	DNA323757	DNA323759	DNA323764	DNA323765	DNA323778
DNA323781	DNA323783	DNA323785	DNA323795	DNA323796	DNA323797
DNA323805	DNA323810	DNA323811	DNA323812	DNA323814	DNA83085
DNA323817	DNA323821	DNA273060	DNA323823	DNA323824	DNA256503
DNA323825	DNA323826	DNA323828	DNA323829	DNA323830	DNA323833
DNA103214	DNA323834	DNA323837	DNA323838	DNA323839	DNA323846
DNA323856	DNA323859	DNA323863	DNA323869	DNA323871	DNA323874
DNA323882	DNA323887	DNA323888	DNA323892	DNA323893	DNA323897
DNA323898	DNA323900	DNA323901	DNA323902	DNA323908	DNA210134
DNA323912	DNA323918	DNA323921	DNA323922	DNA323923	DNA323924
DNA323925	DNA323926	DNA257916	DNA323927	DNA323931	DNA323936
DNA323937	DNA323938	DNA323939	DNA323940	DNA323942	DNA226793
DNA294794	DNA323943	DNA323944	DNA323946	DNA323947	DNA323950

DNA323951	DNA103436	DNA323953	DNA323958	DNA323959	DNA323961
DNA226619	DNA323962	DNA323964	DNA323969	DNA323970	DNA323973
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TESTIS

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DNA325824	DNA325825	DNA325827	DNA325829	DNA325831	DNA325837
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DNA326002	DNA326003	DNA326009	DNA234442	DNA326020	DNA326021
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CERVIX

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NERVOUS

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EYE

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DNA324906	DNA324907	DNA324908	DNA324915	DNA324916	DNA324917
DNA324942	DNA103588	DNA324948	DNA324949	DNA324950	DNA324951
DNA324965	DNA324966	DNA324967	DNA324968	DNA324982	DNA324989
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DNA325098	DNA325110	DNA325111	DNA325116	DNA325117	DNA325118
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DNA325152	DNA325153	DNA325155	DNA325156	DNA325157	DNA325164
DNA325172	DNA325179	DNA325182	DNA325183	DNA325184	DNA325190
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DNA326099	DNA326104	DNA326105	DNA326116	DNA326121	DNA326122
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DNA326946	DNA326952	DNA326956	DNA326962	DNA254240	DNA326974
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DNA327021	DNA327023	DNA327025	DNA327026	DNA327027	DNA327029
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DNA327070	DNA327072	DNA327077	DNA327078	DNA327079	DNA227181
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<u>OVARY</u>

DNA287173	DNA323865	DNA323867	DNA324048	DNA324148	DNA324295

DNA324340	DNA324341	DNA324642	DNA324694	DNA324697	DNA324737
DNA324874	DNA325601	DNA225632	DNA325720	DNA325786	DNA287331
DNA326099	DNA326657	DNA327025			

ADIPOSE

DNA325952	DNA325957	DNA325958

WHOLE BLOOD

DNA323718	DNA323719	DNA323752	DNA323754	DNA323788	DNA83085
DNA323886	DNA323889	DNA323890	DNA323911	DNA323957	DNA323980
DNA324002	DNA324020	DNA324021	DNA324033	DNA324040	DNA324041
DNA324052	DNA324240	DNA324296	DNA225910	DNA324317	DNA324320
DNA324515	DNA324560	DNA324562	DNA324722	DNA324742	DNA324784
DNA324861	DNA324875	DNA324884	DNA324885	DNA324887	DNA324888
DNA324923	DNA325016	DNA325017	DNA325038	DNA325055	DNA325056
DNA325057	DNA325059	DNA325060	DNA325061	DNA325063	DNA325177
DNA325255	DNA88562	DNA325335	DNA325360	DNA325401	DNA325516
DNA325609	DNA325623	DNA325631	DNA325641	DNA290294	DNA325678
DNA226014	DNA325750	DNA325758	DNA325764	DNA325803	DNA281436
DNA325829	DNA226105	DNA325912	DNA326089	DNA326090	DNA326113
DNA326115	DNA326160	DNA326240	DNA326254	DNA88378	DNA88554
DNA326371	DNA326479	DNA326655	DNA326802	DNA326834	DNA88239
DNA326906	DNA326958	DNA326977	DNA327052	DNA327116	

THYROID

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DNA324697	DNA324873	DNA324874	DNA324905	DNA325191	DNA325192
DNA325232	DNA325234	DNA325335	DNA325503	DNA325720	DNA325845
DNA326259	DNA326275	DNA326862	DNA326863	DNA304670	DNA326864

PITUITARY GLAND

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DNA325523	DNA325533	DNA325589	DNA325617	DNA325967	DNA325970

SKIN

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DNA227529	DNA227577	DNA323925	DNA323927	DNA323947	DNA226619
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DNA324645	DNA324678	DNA324682	DNA324687	DNA324690	DNA324692
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DNA324965	DNA324966	DNA324967	DNA324968	DNA324982	DNA272090
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KIDNEY

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DNA326603	DNA326615	DNA326625	DNA326626	DNA326633	DNA326634
DNA326642	DNA326651	DNA326657	DNA326660	DNA326661	DNA274139
DNA326676	DNA326683	DNA326684	DNA326685	DNA326687	DNA326688
DNA326690	DNA326691	DNA326692	DNA326698	DNA326702	DNA103580
DNA326726	DNA326727	DNA326731	DNA290260	DNA326736	DNA326739
DNA326741	DNA326742	DNA326756	DNA326758	DNA326761	DNA273346
DNA254548	DNA326769	DNA326773	DNA287270	DNA326781	DNA326782
DNA326787	DNA326789	DNA326798	DNA326801	DNA326808	DNA326818
DNA326819	DNA273517	DNA194701	DNA103525	DNA326844	DNA326884
DNA326885	DNA326886	DNA254572	DNA326901	DNA326902	DNA326921
DNA326937	DNA269830	DNA326952	DNA326953	DNA326972	DNA326974
DNA326981	DNA326983	DNA327005	DNA327023	DNA327025	DNA327029
DNA327033	DNA327054	DNA327060	DNA327067	DNA327068	DNA327077
DNA327078	DNA327079	DNA327085	DNA327111	DNA227013	

BREAST

DNA323717	DNA273712	DNA226262	DNA323778	DNA323784	DNA323804
DNA323805	DNA323817	DNA323820	DNA323829	DNA323836	DNA323845
DNA323858	DNA323859	DNA323862	DNA323863	DNA323867	DNA323868
DNA323869	DNA323870	DNA323871	DNA323872	DNA323919	DNA323922
DNA323936	DNA323943	DNA323944	DNA323947	DNA323953	DNA323964
DNA323980	DNA323990	DNA323998	DNA324004	DNA324009	DNA324013
DNA324042	DNA324047	DNA324054	DNA324063	DNA324075	DNA324090
DNA324091	DNA324092	DNA324101	DNA324103	DNA324110	DNA324111
DNA324112	DNA227795	DNA324134	DNA227190	DNA324149	DNA324154
DNA324159	DNA324170	DNA324178	DNA324189	DNA324192	DNA324193
DNA324207	DNA324210	DNA324218	DNA324224	DNA324230	DNA324236
DNA324243	DNA324276	DNA324285	DNA226547	DNA324295	DNA150976
DNA324320	DNA324338	DNA324340	DNA324341	DNA324346	DNA324347
DNA324373	DNA324390	DNA324391	DNA324394	DNA324412	DNA324417
DNA324418	DNA324423	DNA324434	DNA324437	DNA324438	DNA139747

DNA253804	DNA324471	DNA324472	DNA324478	DNA324479	DNA324483
DNA324489	DNA324495	DNA324502	DNA324503	DNA324506	DNA324509
DNA324511	DNA324512	DNA225584	DNA324517	DNA324521	DNA324525
DNA324549	DNA324550	DNA324551	DNA324554	DNA324561	DNA324564
DNA324565	DNA324568	DNA324574	DNA324576	DNA324577	DNA324579
DNA324591	DNA324592	DNA324595	DNA324596	DNA324597	DNA324599
DNA324600	DNA324601	DNA324605	DNA324613	DNA324624	DNA103380
DNA324632	DNA324633	DNA324641	DNA324643	DNA324645	DNA324679
DNA324682	DNA324684	DNA324685	DNA324690	DNA324712	DNA324714
DNA324717	DNA324720	DNA324727	DNA304680	DNA324736	DNA324737
DNA324746	DNA324749	DNA324751	DNA324755	DNA304661	DNA287227
DNA324773	DNA324785	DNA324790	DNA324796	DNA324797	DNA324807
DNA324810	DNA324811	DNA324824	DNA324827	DNA324841	DNA324844
DNA324858	DNA324866	DNA324874	DNA324878	DNA324879	DNA225631
DNA324902	DNA324905	DNA324910	DNA324928	DNA324945	DNA304710
DNA324963	DNA324966	DNA324967	DNA324968	DNA304801	DNA272090
DNA324987	DNA324989	DNA325000	DNA325006	DNA325010	DNA325015
DNA325024	DNA325026	DNA325027	DNA325034	DNA325078	DNA325079
DNA325080	DNA325081	DNA325099	DNA325101	DNA325103	DNA325104
DNA325106	DNA325111	DNA325113	DNA325116	DNA325117	DNA325118
DNA325119	DNA325120	DNA325121	DNA325123	DNA325127	DNA325141
DNA325152	DNA325153	DNA325155	DNA325156	DNA325157	DNA325162
DNA325164	DNA325179	DNA325180	DNA325182	DNA325183	DNA325184
DNA325190	DNA325200	DNA325202	DNA325206	DNA325209	DNA325222
DNA325229	DNA325231	DNA325232	DNA325234	DNA325250	DNA325278
DNA325291	DNA325292	DNA325295	DNA325301	DNA325326	DNA325339
DNA325340	DNA325343	DNA325344	DNA325346	DNA325347	DNA325356
DNA325358	DNA325374	DNA325381	DNA325386	DNA325389	DNA325391
DNA325395	DNA325428	DNA325430	DNA325431	DNA325436	DNA325437
DNA97285	DNA325442	DNA325451	DNA325452	DNA75863	DNA325475
DNA325483	DNA325523	DNA325525	DNA325528	DNA325535	DNA325549
DNA325576	DNA325584	DNA325596	DNA325601	DNA225632	DNA325618
DNA325625	DNA325633	DNA325642	DNA325644	DNA325645	DNA325662
DNA270458	DNA227092	DNA325674	DNA325680	DNA325696	DNA325697
DNA325711	DNA325712	DNA325731	DNA325736	DNA325757	DNA325762
DNA325765	DNA325783	DNA325786	DNA302016	DNA325789	DNA325804
DNA325806	DNA325809	DNA325810	DNA325811	DNA325812	DNA325814

DNA325837	DNA325838	DNA325839	DNA325843	DNA325844	DNA325848
DNA325900	DNA325906	DNA325907	DNA325908	DNA325913	DNA325922
DNA325930	DNA325933	DNA325935	DNA325966	DNA227559	DNA325985
DNA325986	DNA227206	DNA325990	DNA325991	DNA219233	DNA325994
DNA325998	DNA326000	DNA326002	DNA326022	DNA326041	DNA326046
DNA326047	DNA326075	DNA326079	DNA326099	DNA326113	DNA326115
DNA97293	DNA326122	DNA326124	DNA326128	DNA326129	DNA326136
DNA326156	DNA287355	DNA326187	DNA326233	DNA326234	DNA326251
DNA326254	DNA326260	DNA97300	DNA326273	DNA326278	DNA326280
DNA326281	DNA304715	DNA326282	DNA326286	DNA290292	DNA326289
DNA326291	DNA326292	DNA66475	DNA326324	DNA326326	DNA326327
DNA326364	DNA326378	DNA326381	DNA326396	DNA326415	DNA326449
DNA326450	DNA326451	DNA326452	DNA326453	DNA326454	DNA326457
DNA326463	DNA326469	DNA326499	DNA287636	DNA326529	DNA326541
DNA270315	DNA326546	DNA326557	DNA326559	DNA326562	DNA326579
DNA326615	DNA326620	DNA227249	DNA326633	DNA326634	DNA326635
DNA326651	DNA326657	DNA272347	DNA326669	DNA326686	DNA326687
DNA326688	DNA326698	DNA326732	DNA290260	DNA326741	DNA326742
DNA83154	DNA326756	DNA326758	DNA326759	DNA326769	DNA326777
DNA287270	DNA326792	DNA326796	DNA326798	DNA326799	DNA326816
DNA194701	DNA103525	DNA326841	DNA326862	DNA326863	DNA304670
DNA326864	DNA326866	DNA326870	DNA326885	DNA326886	DNA326903
DNA326921	DNA326952	DNA326969	DNA326971	DNA326974	DNA326981
DNA327016	DNA327023	DNA327025	DNA327029	DNA273992	DNA327060
DNA327062	DNA273254	DNA327067	DNA327068	DNA327073	DNA327085
DNA327087	DNA327090	DNA327092	DNA276159	DNA327127	

STOMACH

DNA287173	DNA323805	DNA323849	DNA323864	DNA323865	DNA323866
DNA323873	DNA323884	DNA323920	DNA323925	DNA323934	DNA323990
DNA324028	DNA324029	DNA324039	DNA324048	DNA324065	DNA227545
DNA227795	DNA324155	DNA324179	DNA324180	DNA324216	DNA324243
DNA324244	DNA324294	DNA324362	DNA324364	DNA324398	DNA324417
DNA324418	DNA324471	DNA324504	DNA324541	DNA324552	DNA324555
DNA324556	DNA324558	DNA324624	DNA324630	DNA304680	DNA324756
DNA324769	DNA324790	DNA324808	DNA324850	DNA225631	DNA324906
DNA324907	DNA324908	DNA324922	DNA304710	DNA324962	DNA324963

DNA324972	DNA324973	DNA324982	DNA324997	DNA325033	DNA325074
DNA325078	DNA325079	DNA325104	DNA325105	DNA325106	DNA325148
DNA325149	DNA325156	DNA325157	DNA89242	DNA325186	DNA325191
DNA325192	DNA325202	DNA325224	DNA325233	DNA325235	DNA325236
DNA325251	DNA325262	DNA325268	DNA325306	DNA325316	DNA325318
DNA325320	DNA325368	DNA325418	DNA97285	DNA325441	DNA325442
DNA325444	DNA325446	DNA325474	DNA325480	DNA325506	DNA325534
DNA325535	DNA325570	DNA325601	DNA225632	DNA325642	DNA325644
DNA325645	DNA270458	DNA227092	DNA325773	DNA325775	DNA325776
DNA325803	DNA325804	DNA274058	DNA325843	DNA325873	DNA325941
DNA325986	DNA325993	DNA326019	DNA287331	DNA326043	DNA326133
DNA326196	DNA326284	DNA326311	DNA326333	DNA326347	DNA326397
DNA326427	DNA326517	DNA326603	DNA326641	DNA326642	DNA326698
DNA326750	DNA326791	DNA326846	DNA326859	DNA326862	DNA326863
DNA304670	DNA326864	DNA326865	DNA326918	DNA326961	DNA326977
DNA326983	DNA327040	DNA327042	DNA327055	DNA273254	DNA327099
DNA327116	DNA327127				

BONE

DNA323765	DNA323817	DNA323820	DNA323829	DNA323864	DNA323867
DNA323869	DNA323871	DNA323914	DNA323947	DNA323964	DNA324004
DNA324009	DNA324090	DNA324091	DNA324092	DNA324111	DNA324112
DNA324154	DNA324155	DNA324200	DNA324201	DNA324210	DNA324230
DNA324293	DNA226547	DNA324295	DNA324326	DNA324347	DNA324390
DNA324417	DNA324418	DNA324423	DNA324437	DNA324472	DNA324483
DNA324488	DNA324501	DNA324502	DNA324503	DNA324504	DNA324505
DNA324512	DNA324521	DNA324525	DNA324541	DNA324549	DNA324550
DNA324551	DNA324554	DNA324555	DNA324556	DNA324557	DNA324558
DNA324575	DNA324576	DNA324579	DNA324595	DNA324596	DNA324604
DNA324613	DNA324624	DNA324632	DNA324641	DNA324645	DNA324682
DNA324687	DNA324697	DNA324717	DNA324720	DNA324737	DNA324756
DNA304661	DNA324785	DNA324796	DNA324797	DNA150772	DNA324828
DNA324829	DNA324844	DNA324866	DNA324902	DNA324904	DNA324905
DNA324906	DNA324926	DNA324989	DNA325015	DNA325024	DNA325026
DNA325027	DNA325034	DNA325111	DNA325116	DNA131588	DNA325156
DNA325157	DNA325164	DNA325179	DNA325182	DNA325183	DNA325184
DNA325202	DNA325206	DNA325222	DNA325229	DNA325231	DNA325232

DNA325234	DNA325236	DNA325250	DNA325301	DNA325303	DNA325326
DNA325339	DNA325340	DNA325347	DNA325358	DNA325395	DNA325430
DNA325437	DNA325451	DNA325452	DNA325523	DNA325558	DNA325570
DNA325576	DNA325601	DNA225632	DNA325633	DNA325731	DNA325733
DNA325736	DNA325762	DNA325786	DNA302016	DNA325789	DNA325806
DNA325810	DNA325811	DNA325812	DNA325843	DNA325844	DNA325906
DNA325908	DNA325913	DNA325922	DNA325935	DNA325985	DNA326002
DNA326041	DNA326046	DNA326099	DNA326233	DNA326234	DNA326251
DNA97300	DNA304715	DNA326286	DNA326289	DNA326381	DNA326457
DNA326580	DNA326633	DNA326634	DNA326635	DNA326651	DNA290260
DNA326796	DNA326884	DNA326886	DNA326974	DNA326977	DNA327005
DNA327025	DNA327060	DNA327062	DNA327067	DNA327114	

EXAMPLE 2: Use of TAT as a hybridization probe

The following method describes use of a nucleotide sequence encoding TAT as a hybridization probe for, i.e., diagnosis of the presence of a tumor in a mammal.

DNA comprising the coding sequence of full-length or mature TAT as disclosed herein can also be employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of TAT) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled TAT-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence TAT can then be identified using standard techniques known in the art.

EXAMPLE 3: Expression of TAT in *E. coli*

This example illustrates preparation of an unglycosylated form of TAT by recombinant expression in *E. coli*.

The DNA sequence encoding TAT is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the TAT coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized TAT protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

TAT may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding TAT is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110

fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g $(NH_4)_2SO_4$, 0.71 g sodium citrate•2H2O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM $MgSO_4$) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded TAT polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using

this technique(s).

EXAMPLE 4: Expression of TAT in mammalian cells

This example illustrates preparation of a potentially glycosylated form of TAT by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the TAT DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the TAT DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-TAT.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μg pRK5-TAT DNA is mixed with about 1 μg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 μl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M $CaCl_2$. To this mixture is added, dropwise, 500μl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM $NaPO_4$, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μCi/ml ^{35}S-cysteine and 200 μCi/ml ^{35}S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of TAT polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, TAT may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μg pRK5-TAT DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μg/ml bovine insulin and 0.1 μg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed TAT can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, TAT can be expressed in CHO cells. The pRK5-TAT can be transfected into CHO cells using known reagents such as $CaPO_4$ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S-methionine. After determining the presence of TAT polypeptide, the culture medium may be replaced

with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed TAT can then be concentrated and purified by any selected method.

Epitope-tagged TAT may also be expressed in host CHO cells. The TAT may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged TAT insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged TAT can then be concentrated and purified by any selected method, such as by Ni^{2+}-chelate affinity chromatography.

TAT may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Quiagen), Dosper® or Fugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3 x 10^7 cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3 x 10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2 x 10^6 cells/mL. On day 0, the cell number pH ie determined. On day

1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μL of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using this technique(s).

EXAMPLE 5: Expression of TAT in Yeast

The following method describes recombinant expression of TAT in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of TAT from the ADH2/GAPDH promoter. DNA encoding TAT and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of TAT. For secretion, DNA encoding TAT can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native TAT signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of TAT.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant TAT can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The

concentrate containing TAT may further be purified using selected column chromatography resins.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using this technique(s).

EXAMPLE 6: Expression of TAT in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of TAT in Baculovirus-infected insect cells.

The sequence coding for TAT is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding TAT or the desired portion of the coding sequence of TAT such as the sequence encoding an extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged TAT can then be purified, for example, by Ni^{2+}-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM $MgCl_2$; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni^{2+}-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A_{280} with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A_{280} baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni^{2+}-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His_{10}-tagged TAT are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) TAT can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using

this technique(s).

EXAMPLE 7: Preparation of Antibodies that Bind TAT

This example illustrates preparation of monoclonal antibodies which can specifically bind TAT.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified TAT, fusion proteins containing TAT, and cells expressing recombinant TAT on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the TAT immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-TAT antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of TAT. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against TAT. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against TAT is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-TAT monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 8: Purification of TAT Polypeptides Using Specific Antibodies

Native or recombinant TAT polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-TAT polypeptide, mature TAT polypeptide, or pre-TAT polypeptide is purified by immunoaffinity chromatography using antibodies specific for the TAT polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-TAT polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium

sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of TAT polypeptide by preparing a fraction from cells containing TAT polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble TAT polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble TAT polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of TAT polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/TAT polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and TAT polypeptide is collected.

EXAMPLE 9: *In Vitro* Tumor Cell Killing Assay

Mammalian cells expressing the TAT polypeptide of interest may be obtained using standard expression vector and cloning techniques. Alternatively, many tumor cell lines expressing TAT polypeptides of interest are publicly available, for example, through the ATCC and can be routinely identified using standard ELISA or FACS analysis. Anti-TAT polypeptide monoclonal antibodies (and toxin conjugated derivatives thereof) may then be employed in assays to determine the ability of the antibody to kill TAT polypeptide expressing cells *in vitro*.

For example, cells expressing the TAT polypeptide of interest are obtained as described above and plated into 96 well dishes. In one analysis, the antibody/toxin conjugate (or naked antibody) is included throughout the cell incubation for a period of 4 days. In a second independent analysis, the cells are incubated for 1 hour with the antibody/toxin conjugate (or naked antibody) and then washed and incubated in the absence of antibody/toxin conjugate for a period of 4 days. Cell viability is then measured using the CellTiter-Glo Luminescent Cell Viability Assay from Promega (Cat# G7571). Untreated cells serve as a negative control.

EXAMPLE 10: *In Vivo* Tumor Cell Killing Assay

To test the efficacy of conjugated or unconjugated anti-TAT polypeptide monoclonal antibodies, anti-TAT antibody is injected intraperitoneally into nude mice 24 hours prior to receiving tumor promoting cells subcutaneously in the flank. Antibody injections continue twice per week for the remainder of the study. Tumor volume is then measured twice per week.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to

practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having a nucleotide sequence that has at least 80% nucleic acid sequence identity to:

(a) a DNA molecule encoding the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a DNA molecule encoding the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a DNA molecule encoding an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) a DNA molecule encoding an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(g) the complement of (a), (b), (c), (d), (e) or (f).

2. Isolated nucleic acid having:

(a) a nucleotide sequence that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a nucleotide sequence that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a nucleotide sequence that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) a nucleotide sequence that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(g) the complement of (a), (b), (c), (d), (e) or (f).

3. Isolated nucleic acid that hybridizes to:

(a) a nucleic acid that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a nucleic acid that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a nucleic acid that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) a nucleic acid that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(g) the complement of (a), (b), (c), (d), (e) or (f).

4. The nucleic acid of Claim 3, wherein the hybridization occurs under stringent conditions.

5. The nucleic acid of Claim 3 which is at least about 5 nucleotides in length.

6. An expression vector comprising the nucleic acid of Claim 1, 2 or 3.

7. The expression vector of Claim 6, wherein said nucleic acid is operably linked to control sequences recognized by a host cell transformed with the vector.

8. A host cell comprising the expression vector of Claim 7.

9. The host cell of Claim 8 which is a CHO cell, an *E. coli* cell or a yeast cell.

10. A process for producing a polypeptide comprising culturing the host cell of Claim 8 under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture.

11. An isolated polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

12. An isolated polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

13. A chimeric polypeptide comprising the polypeptide of Claim 11 or 12 fused to a heterologous polypeptide.

14. The chimeric polypeptide of Claim 13, wherein said heterologous polypeptide is an epitope tag sequence or an Fc region of an immunoglobulin.

15. An isolated antibody that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

16. An isolated antibody that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

17. The antibody of Claim 15 or 16 which is a monoclonal antibody.

18. The antibody of Claim 15 or 16 which is an antibody fragment.

19. The antibody of Claim 15 or 16 which is a chimeric or a humanized antibody.

20. The antibody of Claim 15 or 16 which is conjugated to a growth inhibitory agent.

21. The antibody of Claim 15 or 16 which is conjugated to a cytotoxic agent.

22. The antibody of Claim 21, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

23. The antibody of Claim 21, wherein the cytotoxic agent is a toxin.

24. The antibody of Claim 23, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

25. The antibody of Claim 23, wherein the toxin is a maytansinoid.

26. The antibody of Claim 15 or 16 which is produced in bacteria.

27. The antibody of Claim 15 or 16 which is produced in CHO cells.

28. The antibody of Claim 15 or 16 which induces death of a cell to which it binds.

29. The antibody of Claim 15 or 16 which is detectably labeled.

30. An isolated nucleic acid having a nucleotide sequence that encodes the antibody of Claim 15 or 16.

31. An expression vector comprising the nucleic acid of Claim 30 operably linked to control sequences recognized by a host cell transformed with the vector.

32. A host cell comprising the expression vector of Claim 31.

33. The host cell of Claim 32 which is a CHO cell, an *E. coli* cell or a yeast cell.

34. A process for producing an antibody comprising culturing the host cell of Claim 32 under conditions suitable for expression of said antibody and recovering said antibody from the cell culture.

35. An isolated oligopeptide that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

36. An isolated oligopeptide that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355

(SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

37. The oligopeptide of Claim 35 or 36 which is conjugated to a growth inhibitory agent.

38. The oligopeptide of Claim 35 or 36 which is conjugated to a cytotoxic agent.

39. The oligopeptide of Claim 38, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

40. The oligopeptide of Claim 38, wherein the cytotoxic agent is a toxin.

41. The oligopeptide of Claim 40, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

42. The oligopeptide of Claim 40, wherein the toxin is a maytansinoid.

43. The oligopeptide of Claim 35 or 36 which induces death of a cell to which it binds.

44. The oligopeptide of Claim 35 or 36 which is detectably labeled.

45. A TAT binding organic molecule that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

46. The organic molecule of Claim 45 that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown

in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

47. The organic molecule of Claim 45 or 46 which is conjugated to a growth inhibitory agent.

48. The organic molecule of Claim 45 or 46 which is conjugated to a cytotoxic agent.

49. The organic molecule of Claim 48, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

50. The organic molecule of Claim 48, wherein the cytotoxic agent is a toxin.

51. The organic molecule of Claim 50, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

52. The organic molecule of Claim 50, wherein the toxin is a maytansinoid.

53. The organic molecule of Claim 45 or 46 which induces death of a cell to which it binds.

54. The organic molecule of Claim 45 or 46 which is detectably labeled.

55. A composition of matter comprising:

(a) the polypeptide of Claim 11;

(b) the polypeptide of Claim 12;

(c) the chimeric polypeptide of Claim 13;

(d) the antibody of Claim 15;

(e) the antibody of Claim 16;

(f) the oligopeptide of Claim 35;

(g) the oligopeptide of Claim 36;

(h) the TAT binding organic molecule of Claim 45; or

(i) the TAT binding organic molecule of Claim 46; in combination with a carrier.

56. The composition of matter of Claim 55, wherein said carrier is a pharmaceutically acceptable carrier.

57. An article of manufacture comprising:

(a) a container; and

(b) the composition of matter of Claim 55 contained within said container.

58. The article of manufacture of Claim 57 further comprising a label affixed to said container, or a package insert included with said container, referring to the use of said composition of matter for the therapeutic treatment of or the diagnostic detection of a cancer.

59. A method of inhibiting the growth of a cell that expresses a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-

6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said cell with an antibody, oligopeptide or organic molecule that binds to said protein, the binding of said antibody, oligopeptide or organic molecule to said protein thereby causing an inhibition of growth of said cell.

60. The method of Claim 59, wherein said antibody is a monoclonal antibody.

61. The method of Claim 59, wherein said antibody is an antibody fragment.

62. The method of Claim 59, wherein said antibody is a chimeric or a humanized antibody.

63. The method of Claim 59, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

64. The method of Claim 59, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

65. The method of Claim 64, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

66. The method of Claim 64, wherein the cytotoxic agent is a toxin.

67. The method of Claim 66, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

68. The method of Claim 66, wherein the toxin is a maytansinoid.

69. The method of Claim 59, wherein said antibody is produced in bacteria.

70. The method of Claim 59, wherein said antibody is produced in CHO cells.

71. The method of Claim 59, wherein said cell is a cancer cell.

72. The method of Claim 71, wherein said cancer cell is further exposed to radiation treatment or a chemotherapeutic agent.

73. The method of Claim 71, wherein said cancer cell is selected from the group consisting of a breast cancer cell, a colorectal cancer cell, a lung cancer cell, an ovarian cancer cell, a central nervous system cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer cell, a melanoma cell and a leukemia cell.

74. The method of Claim 71, wherein said protein is more abundantly expressed by said cancer cell as compared to a normal cell of the same tissue origin.

75. The method of Claim 59 which causes the death of said cell.

76. The method of Claim 59, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures

1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

77. A method of therapeutically treating a mammal having a cancerous tumor comprising cells that express a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising administering to said mammal a therapeutically effective amount of an antibody, oligopeptide or organic molecule that binds to said protein, thereby effectively treating said mammal.

78. The method of Claim 77, wherein said antibody is a monoclonal antibody.

79. The method of Claim 77, wherein said antibody is an antibody fragment.

80. The method of Claim 77, wherein said antibody is a chimeric or a humanized antibody.

81. The method of Claim 77, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

82. The method of Claim 77, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

83. The method of Claim 82, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

84. The method of Claim 82, wherein the cytotoxic agent is a toxin.

85. The method of Claim 84, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

86. The method of Claim 84, wherein the toxin is a maytansinoid.

87. The method of Claim 77, wherein said antibody is produced in bacteria.

88. The method of Claim 77, wherein said antibody is produced in CHO cells.

89. The method of Claim 77, wherein said tumor is further exposed to radiation treatment or a chemotherapeutic agent.

90. The method of Claim 77, wherein said tumor is a breast tumor, a colorectal tumor, a lung tumor, an ovarian tumor, a central nervous system tumor, a liver tumor, a bladder tumor, a pancreatic tumor, or a cervical tumor.

91. The method of Claim 77, wherein said protein is more abundantly expressed by the cancerous cells of said tumor as compared to a normal cell of the same tissue origin.

92. The method of Claim 77, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

93. A method of determining the presence of a protein in a sample suspected of containing said protein, wherein said protein has at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising exposing said sample to an antibody, oligopeptide or organic molecule that binds to said protein and determining binding of said antibody, oligopeptide or organic molecule to said protein in said sample, wherein binding of the antibody, oligopeptide or organic molecule to said protein is indicative of the presence of said protein in said sample.

94. The method of Claim 93, wherein said sample comprises a cell suspected of expressing said protein.

95. The method of Claim 94, wherein said cell is a cancer cell.

96. The method of Claim 93, wherein said antibody, oligopeptide or organic molecule is detectably labeled.

97. The method of Claim 93, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

98. A method of diagnosing the presence of a tumor in a mammal, said method comprising determining the level of expression of a gene encoding a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), in a test sample of tissue cells obtained from said mammal and in a control sample of known normal cells of the same tissue origin, wherein a higher level of expression of said protein in the test sample, as compared to the control sample, is indicative of the presence of tumor in the mammal from which the test sample was obtained.

99. The method of Claim 98, wherein the step of determining the level of expression of a gene encoding said protein comprises employing an oligonucleotide in an *in situ* hybridization or RT-PCR analysis.

100. The method of Claim 98, wherein the step determining the level of expression of a gene encoding said protein comprises employing an antibody in an immunohistochemistry or Western blot analysis.

101. The method of Claim 98, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal pêptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

102. A method of diagnosing the presence of a tumor in a mammal, said method comprising contacting a test sample of tissue cells obtained from said mammal with an antibody, oligopeptide or organic molecule that binds to a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), and detecting the formation of a complex between said antibody, oligopeptide or organic molecule and said protein in the test sample, wherein the formation of a complex is indicative of the presence of a tumor in said mammal.

103. The method of Claim 102, wherein said antibody, oligopeptide or organic molecule is detectably labeled.

104. The method of Claim 102, wherein said test sample of tissue cells is obtained from an individual suspected of having a cancerous tumor.

105. The method of Claim 102, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

106. A method for treating or preventing a cell proliferative disorder associated with increased expression or activity of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising administering to a subject in need of such treatment an effective amount of an antagonist of said protein, thereby effectively treating or preventing said cell proliferative disorder.

107. The method of Claim 106, wherein said cell proliferative disorder is cancer.

108. The method of Claim 106, wherein said antagonist is an anti-TAT polypeptide antibody, TAT binding oligopeptide, TAT binding organic molecule or antisense oligonucleotide.

109. A method of binding an antibody, oligopeptide or organic molecule to a cell that expresses a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said cell with an antibody,

oligopeptide or organic molecule that binds to said protein and allowing the binding of the antibody, oligopeptide or organic molecule to said protein to occur, thereby binding said antibody, oligopeptide or organic molecule to said cell.

110. The method of Claim 109, wherein said antibody is a monoclonal antibody.

111. The method of Claim 109, wherein said antibody is an antibody fragment.

112. The method of Claim 109, wherein said antibody is a chimeric or a humanized antibody.

113. The method of Claim 109, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

114. The method of Claim 109, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

115. The method of Claim 114, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

116. The method of Claim 114, wherein the cytotoxic agent is a toxin.

117. The method of Claim 116, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

118. The method of Claim 116, wherein the toxin is a maytansinoid.

119. The method of Claim 109, wherein said antibody is produced in bacteria.

120. The method of Claim 109, wherein said antibody is produced in CHO cells.

121. The method of Claim 109, wherein said cell is a cancer cell.

122. The method of Claim 121, wherein said cancer cell is further exposed to radiation treatment or a chemotherapeutic agent.

123. The method of Claim 121, wherein said cancer cell is selected from the group consisting of a breast cancer cell, a colorectal cancer cell, a lung cancer cell, an ovarian cancer cell, a central nervous system cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer cell, a melanoma cell and a leukemia cell.

124. The method of Claim 123, wherein said protein is more abundantly expressed by said cancer cell as compared to a normal cell of the same tissue origin.

125. The method of Claim 109 which causes the death of said cell.

126. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

127. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for treating a tumor.

128. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

129. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

130. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of

medicament for treating a tumor.

131. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

132. Use of a host cell as claimed in any of Claims 8, 9, 32, or 33 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

133. Use of a host cell as claimed in any of Claims 8, 9, 32 or 33 in the preparation of a medicament for treating a tumor.

134. Use of a host cell as claimed in any of Claims 8, 9, 32 or 33 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

135. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

136. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for treating a tumor.

137. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

138. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

139. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for treating a tumor.

140. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

141. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

142. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for treating a tumor.

143. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

144. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

145. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for treating a tumor.

146. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

147. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

148. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for treating a tumor.

149. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

150. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

151. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for treating a tumor.

152. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

153. A method for inhibiting the growth of a cell, wherein the growth of said cell is at least in part dependent upon a growth potentiating effect of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said protein with an antibody, oligopeptide or organic molecule that binds to said protein, there by inhibiting the growth of said cell.

154. The method of Claim 153, wherein said cell is a cancer cell.

155. The method of Claim 153, wherein said protein is expressed by said cell.

156. The method of Claim 153, wherein the binding of said antibody, oligopeptide or organic molecule to said protein antagonizes a cell growth-potentiating activity of said protein.

157. The method of Claim 153, wherein the binding of said antibody, oligopeptide or organic molecule to said protein induces the death of said cell.

158. The method of Claim 153, wherein said antibody is a monoclonal antibody.

159. The method of Claim 153, wherein said antibody is an antibody fragment.

160. The method of Claim 153, wherein said antibody is a chimeric or a humanized antibody.

161. The method of Claim 153, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

162. The method of Claim 153, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

163. The method of Claim 162, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

164. The method of Claim 162, wherein the cytotoxic agent is a toxin.

165. The method of Claim 164, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

166. The method of Claim 164, wherein the toxin is a maytansinoid.

167. The method of Claim 153, wherein said antibody is produced in bacteria.

168. The method of Claim 153, wherein said antibody is produced in CHO cells.

169. The method of Claim 153, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

170. A method of therapeutically treating a tumor in a mammal, wherein the growth of said tumor is at least in part dependent upon a growth potentiating effect of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said protein with an antibody, oligopeptide or organic molecule that binds to said protein, thereby effectively treating said tumor.

171. The method of Claim 170, wherein said protein is expressed by cells of said tumor.

172. The method of Claim 170, wherein the binding of said antibody, oligopeptide or organic molecule to said protein antagonizes a cell growth-potentiating activity of said protein.

173. The method of Claim 170, wherein said antibody is a monoclonal antibody.

174. The method of Claim 170, wherein said antibody is an antibody fragment.

175. The method of Claim 170, wherein said antibody is a chimeric or a humanized antibody.

176. The method of Claim 170, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

177. The method of Claim 170, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

178. The method of Claim 177, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

179. The method of Claim 177, wherein the cytotoxic agent is a toxin.

180. The method of Claim 179, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

181. The method of Claim 179, wherein the toxin is a maytansinoid.

182. The method of Claim 170, wherein said antibody is produced in bacteria.

183. The method of Claim 170, wherein said antibody is produced in CHO cells.

184. The method of Claim 170, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

FIGURE 1

ATCACATGCCTATCATATAGTAAAACCCAGCCCATGGCCCCTAACAGGGGCCCTCTCAGCCCTCCTAATGACCTC
CGGCCTAGCCATGTGATTTCACTTCCACTCCACAACCCTCCTCATACTAGGCCTACTAACCAACACACTAACCAT
ATACCAATGATGGCGCGATGTAACACGAGAAAGCACATACCAAGGCCACCACACACCACCTGTCCAGAAAGGCGT
TCGATACGGGATAATCCTATTTATTACCTCAGAAGTTTTTTTCTTCGCAGGATTTTTCTGAGCCTTTTACCACTC
CAGCCTAGCTCCCACCCCCCAACTAGGGGGACACTGGCCCCCAACAGGCATCACCCCGCTAAATCCCCTAGAAGT
CCCACTCCTAAACACATCCGTATTACTCGCATCAGGGGTATCAATCACCTGAGCTCACCATAGTCTAATAGTCTA
TTTTACCCTCCTACAAGCCTCAGAGTACTTCGAG

FIGURE 2

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATTCAGTTGCAGGAAAACAAGCTTA
ACACGCCCACTAATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTATGTCAC
GGCAGCCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CAGCCTCTACAGTCCCAAAGTCTGCCTCACAGCAGATTCTTCACGCCCAGCATCTACCTCACTTGGACCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCAGCCTCTGC
CTCACAGCGGACTCTC

FIGURE 3

CAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTACGTCACGGCAGCCTCCGCAGATGAGCCTACTGC
CTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTT
CTCTCCAGGCTCTGAACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGAGTGTAGTAGTGCTATCGCAGCTGA
CTGCAGCCTCAACCTTCCAGGCTGAAGCGATCCTCCCACCTCAACCTCCCACGTGGCTGAGACTACAGGTGCTTG
CCACTATGCCCAACTAACATTTGGAATTTTCGTATACGTGGATTCCAGAGGGGTGACAGCGAAACGTGGGACCAT
TCAGTTGCAGGAAAACAAGCTTAACACGCCCACTAATTCTACATTATGCTCCTACCTCCCGGCAGCCTCTCCAGG
CCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATG

FIGURE 4

CGTCGGCCCCCGGCCCCCCAGCAGCCTCCAAAGCCCTGTGACTCACAGCCCTGCTTCCACGGGGGGACCTGCCAG
GACTGGGCATTGGGCGGGGGCTTCACCTGCAGCTGCCCGGCAGGCAGGGGAGGCGCCGTCTGTGAGAAGGTGCTT
GGCGCCCCTGTGCCGGCCTTCGAGGGCCGCTCCTTCCTGGCCTTCCCCACTCTCCGCGCCTACCACACGCTGCGC
CTGGCACTGGAATTCCGGGCGCTGGAGCCTCAGGGGCTGCTGCTGTACAATGGCAACGCCCGGGGCAAGGACTTC
CTGGCATTGGCGCTGCTAGATGGCCGCGTGCAGCTCAGGTTTGACACAGGTTCGGGGCCGGCGGTGCTGACCAGT
GCCGTGCCGGTAGAGCCGGGCCAGTGGCACCGCCTGGAGCTGTCCCGGCACTGGCGCCGGGGCACCCTCTCGGTG
GATGGTGAGACCCCTGTTCTGGGCGAGAGTCCCAGTGGCACCGACGGCCTCAACCTGGACACAGACCTCTTTGTG
GGCGGCGTACCCGAGGACCAGGCTGCCGTGGCGCTGGAGCGGACCTTCGTGGGCGCCGGCCTGAGGGGGTGCATC
CGTTTGCTGGACGTCAACAACCAGCGCCTGGAGCTTGGCATTGGGCCGGGGGCTGCCACCCGAGGCTCTGGCGTG
GGCAAGTGCGGGGACCACCCCTGCCTGCCCAACCCCTGCCATGGCGGGGCCCCATGCCAGAACCTGGAGGCTGGA
AGGTTCCATTGCCAGTGCCCGCCCGGCCGCGTCGGACCAACCTGTGCCGATGAGAAGAGCCCCTGCCAGCCCAAC
CCCTGCCATGGGGCGGCGCCCTGCCGTGTGCTGCCCGAGGGTGGTGCTCAGTGCGAGTGCCCCCTGGGGCGTGAG
GGCACCTTCTGCCAGACAGCCTCGGGGCAGGACGGCTCTGGGCCCTTCCTGGCTGACTTCAACGGCTTCTCCCAC
CTGGAGCTGAGAGGCCTGCACACCTTTGCACGGGACCTGGGGGAGAAGATGGCGCTGGAGGTCGTGTTCCTGGCA
CGAGGCCCCAGCGGCCTCCTGCTCTACAACGGGCAGAAGACGGACGGCAAGGGGGACTTCGTGTCGCTGGCACTG
CGGGACCGCCGCCTGGAGTTCCGCTACGACCTGGGCAAGGGGGCAGCGGTCATCAGGAGCAGGGAGCCAGTCACC
CTGGGAGCCTGGACCAGGGTCTCACTGGAGCGAAACGGCCGCAAGGGTGCCCTGCGTGTGGGCGACGGCCCCCGT
GTGTTGGGGGAGTCCCCGGTTCCGCACACCGTCCTCAACCTGAAGGAGCCGCTCTACGTAGGGGGCGCTCCCGAC
TTCAGCAAGCTGGCCCGTGCTGCTGCCGTGTCCTCTGGCTTCGACGGTGCCATCCAGCTGGTCTCCCTCGGAGGC
CGCCAGCTGCTGACCCCGGAGCACGTGCTGCGGCAGGTGGACGTCACGTCCTTTGCAGGTCACCCCTGCACCCGG
GCCTCAGGCCACCCCTGCCTCAATGGGGCCTCCTGCGTCCCGAGGGAGGCTGCCTATGTGTGCCTGTGTCCCGGG
GGATTCTCAGGACCGCACTGCGAGAAGGGGCTGGTGGAGAAGTCAGCGGGGGACGTGGATACCTTGGCCTTTGAC
GGGCGGACCTTTGTCGAGTACCTCAACGCTGTGACCGAGAGCGAGAAGGCACTGCAGAGCAACCACTTTGAACTG
AGCCTGCGCACTGAGGCCACGCAGGGGCTGGTGCTCTGGAGTGGCAAGGCCACGGAGCGGGCAGACTATGTGGCA
CTGGCCATTGTGGACGGGCACCTGCAACTGAGCTACAACCTGGGCTCCCAGCCCGTGGTGCTGCGTTCCACCGTG
CCCGTCAACACCAACCGCTGGTTGCGGGTCGTGGCACATAGGGAGCAGAGGGAAGGTTCCCTGCAGGTGGGCAAT
GAGGCCCCTGTGACCGGCTCCTCCCCGCTGGGCGCCACGCAGCTGGACACTGATGGAGCCCTGTGGCTTGGGGGC
CTGCCGGAGCTGCCCGTGGGCCCAGCACTGCCCAAGGCCTACGGCACAGGCTTTGTGGGCTGCTTGCGGGACGTG
GTGGTGGGCCGGCACCCGCTGCACCTGCTGGAGGACGCCGTCACCAAGCCAGAGCTGCGGCCCTGCCCCACCCCA
TGAGCTGGCACCAGAGCCCCGCGCCCGCTGTAATTATTTCTATTTTTGTAAACTTGTTGCTTTTTGATATGATT
TTCTTGCCTGAGTGTTGGCCGGAGGGACTGCTGGCCCGGCCTCCCTTCCGTCCAGGCAGCCGTGCTGCAGACAGA
CCTAGTGCCGAGGGATGGACAGGCGAGGTGGCAGCGTGGAGGGCTCGGCGTGGATGGCAGCCTCAGGACACACAC
CCCTGCCTCAAGGTGCTGAGCCCCCGCCTTGCACTGCGCCTGCCCCACGGTGTCCCCGCCGGGAAGCAGCCCCGG
CTCCTGAATCACCCTCGCTCCGTCAGGCGGGACTCGTGTCCCAGAGAGGAAGGGGCTGCTGAGGTCTGATGGGGC
CCTTCCTCCGGGTGACCCCACAGGGCCTTTCCAAGCCCCCATTTGAGCTGCTCCTTCCTGTGTGTGCTCTGGGCC
CTGCCTCGGCCTCCTGCGCCAATACTGTGACTTCCAAACAATGTTACTGCTGGGCACAGCTCTGCGTTGCTCCCG
TGCTGCCTGCGCCAGCCCCAGGCTGCTGAGGAGCAGAGGCCAGACCAGGGCCGATCTGGGTGTCCTGACCCTCAG
CTGGCCCTGCCCAGCCACCCTGGACATGACCGTATCCCTCTGCCACACCCCAGGCCCTGCGAGGGGCTATCGAGA
GGAGCTCACTGTGGGATGGGGTTGACCTCTGCCGCCTGCCTGGGTATCTGGGCCTGGCCATGGCTGTGTTCTTCA
TGTGTTGATTTTATTTGACCCCTGGAGTGGTGGGTCTCATCTTTCCCATCTCGCCTGAGAGCGGCTGAGGGCTGC
CTCACTGCAAATCCTCCCCACAGCGTCAGTGAAAGTCGTCCTTGTCTCAGAATGACCAGGGGCCAGCCAGTGTCT
GACCAAGGTCAAGGGGCAGGTGCAGAGGTGGCAGGGATGGCTCCGAAGCCAGAAATGCCTTAAACTGCAACGTCC
CGTCCCTTCCCCACCCCCATCCCATCCCCACCCCCAGCCCCAGCCCAGTCCTCCTAGGAGCAGGACCCGATGAAG
CGGGCGGCGGTGGGGCTGGGTGCCGTGTTACTAACTCTAGTATGTTTCTGTGTCAATCGCTGTGAAATAAAGTCT
GAAAACTTT

FIGURE 5

MLNSSLMRITLRNLEEVEFCVEDKPGTHFTPVPPTPPDACRGMLCGFGAVCEPNAEGPGRASCVCKKSPCPSVVA
PVCGSDASTYSNECELQRAQCSQQRRIRLLSRGPCGSRDPCSNVTCSFGSTCARSADGLTASCLCPATCRGAPEG
TVCGSDGADYPGECQLLRRACARQENVFKKFDGPCDPCQGALPDPSRSCRVNPRTRRPEMLLRPESCPARQAPVC
GDDGVTYENDCVMGRSGAARGLLLQKVRSGQCQGRDQCPEPCRFNAVCLSRRGRPRCSCDRVTCDGAYRPVCAQD
GRTYDSDCWRQQAECRQQRAIPSKHQGPCDQAPSPCLGVQCAFGATCAVKNGQAACECLQACSSLYDPVCGSDGV
TYGSACELEATACTLGREIQVARKGPCDRCGQCRFGALCEAETGRCVCPSECVALAQPVCGSDGHTYPSECMLHV
HACTHQISLHVASAGPCETCGDAVCAFGAVCSAGQCVCPRCEHPPPGPVCGSDGVTYGSACELREAACLQQTQIE
EARAGPCEQAECGSGGSGSGEDGDCEQELCRQRGGIWDEDSEDGPCVCDFSCQSVPGSPVCGSDGVTYSTECELK
KARCESQRGLYVAAQGACRGPTFAPLPPVAPLHCAQTPYGCCQDNITAARGVGLAGCPSACQCNPHGSYGGTCDP
ATGQCSCRPGVGGLRCDRCEPGFWNFRGIVTDGRSGCTPCSCDPQGAVRDDCEQMTGLCSCKPGVAGPKCGQCPD
GRALGPAGCEADASAPATCAEMRCEFGARCVEESGSAHCVCPMLTCPEANATKVCGSDGVTYGNECQLKTIACRQ
GLQISIQSLGPCQEAVAPSTHPTSASVTVTTPGLLLSQALPAPPGALPLAPSSTAHSQTTPPPSSRPRTTASVPR
TTVWPVLTVPPTAPSPAPSLVASAFGESGSTDGSSDEELSGDQEASGGGSGGLEPLEGSSVATPGPPVERASCYN
SALGCCSDGKTPSLDAEGSNCPATKVFQGVLELEGVEGQELFYTPEMADPKSELFGETARSIESTLDDLFRNSDV
KKDFRSVRLRDLGPGKSVRAIVDVHFDPTTAFRAPDVARALLRQIQVSRRRSLGVRRPLQEHVRFMDFDWFPAFI
TGATSGAIAAGATARATTASRLPSSAVTPRAPHPSHTSQPVAKTTAAPTTRRPPTTAPSRVPGRRPPAPQQPPKP
CDSQPCFHGGTCQDWALGGGFTCSCPAGRGGAVCEKVLGAPVPAFEGRSFLAFPTLRAYHTLRLALEFRALEPQG
LLLYNGNARGKDFLALALLDGRVQLRFDTGSGPAVLTSAVPVEPGQWHRLELSRHWRRGTLSVDGETPVLGESPS
GTDGLNLDTDLFVGGVPEDQAAVALERTFVGAGLRGCIRLLDVNNQRLELGIGPGAATRGSGVGKCGDHPCLPNP
CHGGAPCQNLEAGRFHCQCPPGRVGPTCADEKSPCQPNPCHGAAPCRVLPEGGAQCECPLGREGTFCQTASGQDG
SGPFLADFNGFSHLELRGLHTFARDLGEKMALEVVFLARGPSGLLLYNGQKTDGKGDFVSLALRDRRLEFRYDLG
KGAAVIRSREPVTLGAWTRVSLERNGRKGALRVGDGPRVLGESPVPHTVLNLKEPLYVGGAPDFSKLARAAAVSS
GFDGAIQLVSLGGRQLLTPEHVLRQVDVTSFAGHPCTRASGHPCLNGASCVPREAAYVCLCPGGFSGPHCEKGLV
EKSAGDVDTLAFDGRTFVEYLNAVTESEKALQSNHFELSLRTEATQGLVLWSGKATERADYVALAIVDGHLQLSY
NLGSQPVVLRSTVPVNTNRWLRVVAHREQREGSLQVGNEAPVTGSSPLGATQLDTDGALWLGGLPELPVGPALPK
AYGTGFVGCLRDVVVGRHPLHLLEDAVTKPELRPCPTP

FIGURE 6

ACAGAGACCCCGAGTTCTACAAGTTCCTGCAGGAGAATGACCAGAGCCTGCTAAACTTCAGCGACTCGGACAGCT
CTGAGGAGGAAGAGGGGCCGTTCCACTCCCTGCCAGATGTGCTGGAGGAAGCCAGTGAGGAGGAGGATGGAGCGG
AGGAAGGAGAAGATGGGGACAGAGTCCCCAGAGGGCTGAAGGGGAAGAAGAATTCTGTTCCTGTGACCGTCGCCA
TGGTTGAGAGATGGAAGCAGGCAGCAAAGCAACGCCTCACTCCAAAGCTGTTCCATGAAGTGGTACAGGCGTTCC
GAGCAGCTGTGGCCACCACCCGAGGGGACCAGGAAAGTGCTGAGGCCAACAAATTCCAGGTCACGGACAGTGCTG
CATTCAATGCTCTGGTTACCTTCTGCATCAGAGACCTCATTGGCTGTCTCCAGAAGCTGCTGTTTGGAAAGGTGG
CAAAGGATAGCAGCAGGATGCTGCAGCCGTCCAGCAGCCCGCTCTGGGGGAAGCTTCGTGTGGACATCAAGGCTT
ACCTGGGCTCGGCCATACAGCTGGTGTCCTGTCTGTCGGAGACGACGGTGTTGGCGGCCGTGCTGCGGCACATCA
GCGTGCTGGTGCCCTGCTTCCTGACCTTCCCCAAGCAGTGCCGCATGCTGCTCAAGAGAATGGTGATCGTATGGA
GCACTGGGGAAGAGTCTCTGCGGGTGCTGGCTTTCCTGGTCCTCAGCAGAGTCTGCCGGCACAAGAAGGACACTT
TCCTTGGCCCCGTCCTCAAGCAAATGTACATCACGTATGTGAGGAACTGCAAGTTCACCTCGCCTGGTGCCCTCC
CCTTCATCAGTTTCATGCAGTGGACCTTGACGGAGCTGCTGGCCCTGGAGCCGGGTGTGGCCTACCAGCACGCCT
TCCTCTACATCCGCCAGCTCGCCATACACCTGCGCAACGCCATGACCACTCGCAAGAAGGAAACATACCAGTCTG
TGTACAACTGGCAGTATGTGCACTGCCTCTTCCTGTGGTGCCGGGTCCTGAGCACTGCGGGCCCCAGCGAAGCCC
TCCAGCCCTTGGTCTACCCCCTTGCCCAAGTCATCATTGGCTGTATCAAGCTCATCCCCACTGCCCGCTTCTACC
CGCTGCGAATGCACTGCATCCGTGCCCTGACGCTGCTCTCGGGGAGCTCGGGGGCCTTCATCCCGGTGCTGCCTT
TCATCCTGGAGATGTTCCAGCAGGTCGACTTCAACAGGAAGCCAGGGCGCATGAGCTCCAAGCCCATCAACTTCT
CCGTGATCCTGAAGCTGTCCAATGTCAACCTGCAGGAGAAGGCGTACCGGGACGGCCTGGTGGAGCAGCTGTACG
ACCTCACCCTGGAGTACCTGCACAGCCAGGCACACTGCATCGGCTTCCCGGAGCTGGTGCTGCCTGTGGTCCTGC
AGCTGAAGTCGTTCCTCCGGGAGTGCAAGGTGGCCAACTACTGCCGGCAGGTGCAGCAGCTGCTTGGGAAGGTTC
AGGAGAACTCGGCATACATCTGCAGCCGCCGCCAGAGGGTTTCCTTCGGCGTCTCTGAGCAGCAGGCAGTGGAAG
CCTGGGAGAAGCTGACCCGGGAAGAGGGGACACCCCTGACCTTGTACTACAGCCACTGGCGCAAGCTGCGTGACC
GGGAGATCCAGCTGGAGATCAGTGGCAAAGAGCGGCTGGAAGACCTGAACTTCCCTGAGATCAAACGAAGGAAGA
TGGCTGACAGGAAGGATGAGGACAGGAAGCAATTTAAAGACCTCTTTGACCTGAACAGCTCTGAAGAGGACGACA
CCGAGGGATTCTCGGAGAGAGGGATACTGAGGCCCCTGAGCACTCGGCATGGGGTGGAAGACGATGAAGAGGACG
AGGAGGAGGGCGAGGAGGACAGCAGCAACTCGGAGGATGGAGACCCAGACGCAGAGGCGGGGCTGGCCCCTGGGG
AGCTGCAGCAGCTGGCCCAGGGGCCGGAGGACGAGCTGGAGGATCTGCAGCTCTCAGAGGACGACTGAGGCAGCC
CATCTGGGGGGCCTGTAGGGGCTGCCGGGCTGGTGGCCAGTGTTTCCACCTCCCTGGCAGTCAGGCCTAGAGGCT
GGCGTCTGTGCAGTTGGGGGAGGCAGTAGACACGGGACAGGCTTTATTATTTATTTTTCAGCATGAAAGACCAAA
CGTATCGAGAGCTGGGCTGGGCTGGGCTGGTGTGGCTGCTGAAGCCCCACAGCTGTGGGCTGCTGAAGTCAGCTC
CGCGGGGGAGCTGACCCTGACGTCAGCAGACCGAGACCAGTCCCAGTTCCAGGGGGAGGCCTGCAGGCCCCTGGC
CCCTTCCACCACCTCTGCCCTCCGTCTGCAGACCTCGTCCATCTGCACCAGGCTCTGCCTTCACTCCCCCAAGTC
TTTGAAAATTTGTTCCTTTCCTTTGAAGTCACATTTTCTTTTAAAATTTTTTGTTTTGCATCCGAAACCGAAAGA
AATAAAGCGGTGGGAGGCAGGGCCATTGTGTTG

FIGURE 7

MAAAGSRKRRLAELTVDEFLASGFDSESESESESENSPQAETREAREAARSPDKPGGSPSASRRKGRASEHKDQLSR
LKDRDPEFYKFLQENDQSLLNFSDSDSSEEEEGPFHSLPDVLEEASEEEDGAEEGEDGDRVPRGLKGKKNSVPVT
VAMVERWKQAAKQRLTPKLFHEVVQAFRAAVATTRGDQESAEANKFQVTDSAAFNALVTFCIRDLIGCLQKLLFG
KVAKDSSRMLQPSSSPLWGKLRVDIKAYLGSAIQLVSCLSETTVLAAVLRHISVLVPCFLTFPKQCRMLLKRMVI
VWSTGEESLRVLAFLVLSRVCRHKKDTFLGPVLKQMYITYVRNCKFTSPGALPFISFMQWTLTELLALEPGVAYQ
HAFLYIRQLAIHLRNAMTTRKKETYQSVYNWQYVHCLFLWCRVLSTAGPSEALQPLVYPLAQVIIGCIKLIPTAR
FYPLRMHCIRALTLLSGSSGAFIPVLPFILEMFQQVDFNRKPGRMSSKPINFSVILKLSNVNLQEKAYRDGLVEQ
LYDLTLEYLHSQAHCIGFPELVLPVVLQLKSFLRECKVANYCRQVQQLLGKVQENSAYICSRRQRVSFGVSEQQA
VEAWEKLTREEGTPLTLYYSHWRKLRDREIQLEISGKERLEDLNFPEIKRRKMADRKDEDRKQFKDLFDLNSSEE
DDTEGFSERGILRPLSTRHGVEDDEEDEEEGEEDSSNSEDGDPDAEAGLAPGELQQLAQGPEDELEDLQLSEDD

FIGURE 8

GTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAGCTGAGCCCATGAGCTC
CCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGGTAGTCCCCATCCTGGAGGGGCAGGCTCT
GCGCATCTGCTCCTGGC**ATG**GCGCTGCGGCACCTCGCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGT
CCATGGAGAACACGGCCCAGCTGCCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCCAGGCGCAA
GTCTGTGTGGTCCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGAA
CCCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCGGGTGCGCCATTCCCCATGAACAGAAGCT
CAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCCTCCCTCTTCCTGGGCACGTTCTTCATTA
GCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCTTCTACCTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACA
GAAGAAACAAAGCTCCGGCCCTGCAGCCTGGCGAAGCCGCTGCAATGATCCCCCCGCCACAGTCCTCAGTACGGA
AGCCGCGCTACGTCAGGCGGGAGCGGCCCCTGGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCGTA
TCAGCAATGTC**TGA**CCTGGAGGCCGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGC
GGGAACCAGCACAAAGTGTTGGCATCGCCCGGCGCCCGGGACAGTCCTGGGCACAGCCTCGGCTCTGGGTCCCTC
CGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCCTGAGGCTCCTCCCCACCACAGCCATCTCGTTTATCG
GACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGCCTTGGGGGGTCCGGGCCCCCCCAGGAAAC
ACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGGCACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCA
GGGGCTCTGCTGCCGTGCCCTCCAGAGCCCACAGCGGGCAGGACTCCTCCAGCACCACCACACCCAGTGGCCCGA
GACCCCTCTGAGAACAGTGAGGCTGGTCCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGCCT
AGGAACCAGCTGCCTGAGACCAGGGTGCCTCTGGGCTGTCCTCCCGCGTGGCGGAGACCCCAAGCACGCAGCCAC
CCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAGCAGAAATTCATTGTGCTGAAAAGTC
CTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACCCCCATGCCTGGCTGATCCCTGCCCACGTGGGGCAGGC
CCACATCTAACCCCCACAAGTCACTGCCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCCTGGGGTCCCT
CCCGGAGTTCCTGGGAGAAAGGCGCCGTCGTGGCCGCCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCA
GACGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCCTTCGGGGTCC
CCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTGGGCCAGCGGGAACGTGGGGGCA
CTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 9

MALRHLALLAGLLVGVASKSMENTAQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGSASCVRCGNGTLPAYN
GSECRSFAGPGAPFPMNRSSGTPGRPHPGAPRVAASLFLGTFFISSGLILSVAGFFYLKRSSKLPRACYRRNKAP
ALQPGEAAAMIPPPQSSVRKPRYVRRERPLDRATDPAAFPGEARISNV

FIGURE 10

AAAAAAAAAAAAAAAACCGGCTCGCGGCGCGTGGAGGCTGCTCCCAGCCGCGCGCGAGTCAGACTCGGGTGGGGG
TCCCGGCGGCGGTAGCGGCGGCGGCGGTGCGAGC**ATG**TCGTGGCTCTTCGGCATTAACAAGGGCCCCAAGGGTGA
AGGCGCGGGGCCGCCGCCGCCTTTGCCGCCCGCGCAGCCCGGGGCCGAGGGCGGCGGGGACCGCGGCTTGGGAGA
CCGGCCGGCGCCCAAGGACAAATGGAGCAACTTCGACCCCACCGGCCTGGAGCGCGCCGCCAAGGCGGCGCGCGA
GCTGGAGCACTCGCGTTATGCCAAGGACGCCCTGAATCTGGCACAGATGCAGGAGCAGACGCTGCAGTTGGAGCA
ACAGTCCAAGCTCAAAGAGTATGAGGCCGCCGTGGAGCAGCTCAAGAGCGAGCAGATCCGGGCGCAGGCTGAGGA
GAGGAGGAAGACCCTGAGCGAGGAGACCCGGCAGCACCAGGCCAGGGCCCAGTATCAAGACAAGCTGGCCCGGCA
GCGCTACGAGGACCAACTGAAGCAGCAGCAACTTCTCAATGAGGAGAATTTACGGAAGCAGGAGGAGTCCGTGCA
GAAGCAGGAAGCCATGCGGCGAGCCACCGTGGAGCGGGAGATGGAGCTGCGGCACAAGAATGAGATGCTGCGAGT
GGAGGCCGAGGCCCGGGCGCGCGCCAAGGCCGAGCGGGAGAATGCAGACATCATCCGCGAGCAGATCCGCCTGAA
GGCGGCCGAGCACCGTCAGACCGTCTTGGAGTCCATCAGGACGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGC
CTTTGTGACAGACTGGGACAAAGTGACAGCCACGGTGGCTGGGCTGACGCTGCTGGCTGTTGGGGTCTACTCAGC
CAAGAATGCCACGCTTGTCGCCGGCCGCTTCATCGAGGCTCGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTC
CCGCATCACGGTGCTTGAGGCGCTGCGGCACCCCATCCAGGTCAGCCGGCGGCTCCTCAGTCGACCCCAGGACGC
GCTGGAGGGTGTTGTGCTCAGTCCCAGCCTGGAAGCACGGGTGCGCGACATCGCCATAGCAACAAGGAACACCAA
GAAGAACCGCAGCCTGTACAGGAACATCCTGATGTACGGGCCACCAGGCACCGGGAAGACGCTGTTTGCCAAGAA
ACTCGCCCTGCACTCAGGCATGGACTACGCCATCATGACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGT
GACCGCCATGCACAAGCTCTTTGACTGGGCCAATACCAGCCGGCGCGGCCTCCTGCTCTTTGTGGATGAAGCGGA
CGCCTTCCTTCGGAAGCGAGCCACCGAGAAGATAAGCGAGGACCTCAGGGCCACACTGAACGCCTTCCTGTACCG
CACGGGCCAGCACAGCAACAAGTTCATGCTGGTCCTGGCCAGCAACCAACCAGAGCAGTTCGACTGGGCCATCAA
TGACCGCATCAATGAGATGGTCCACTTCGACCTGCCAGGGCAGGAGGAACGGGAGCGCCTGGTGAGAATGTATTT
TGACAAGTATGTTCTTAAGCCGGCCACAGAAGGAAAGCAGCGCCTGAAGCTGGCCCAGTTTGACTACGGGAGGAA
GTGCTCGGAGGTCGCTCGGCTGACGGAGGGCATGTCGGGCCGGGAGATCGCTCAGCTGGCCGTGTCCTGGCAGGC
CACGGCGTATGCCTCCGAGGACGGGGTCCTGACCGAGGCCATGATGGACACCCGCGTGCAAGATGCTGTCCAGCA
GCACCAGCAGAAGATGTGCTGGCTGAAGGCGGAAGGGCCTGGGCGTGGGGACGAGCCTTCCCCATCC**TGA**GTCCA
CAGGGAGATCCACAGCTCACGGAGCCTGGCCGCGGACCCCTCCCACCCCTGCCTTGCCGGCCCCTGCACATTTAG
GATATGCTCCTGGGTGGGGACTGGGCTGTGCCCAGGGCCTCTGTCCCCCAGGATGTCTTGTGGTGCGGGTCGGCC
GTTCTGCCCCCCCAGGGCACCCCCTGTTGTAGGCACTGGCTAGGGAGGGGCAGGCCTCCTTCCTGCCCCTCGAGAC
ACTCTTGGGAGATGCATTTTCCGTCTGGCTCACAGGGGGAGGGTGAGGCTTTGCACCCCAGCCCCTGCCCAGGCC
ACTGTGAGGGTGGGTGCTGGCTGACCCCCCGGGGCAGCAGGAGCCAGGCAGGTGATGTCTTTGTTCTCGGCTCCC
ACAGCAGAGCCAGGTGAGGGGGCGCCTGCCAGGGCCAGACCCAGGTGGGGCAGCCTGAACCCTGCTTCCCCCTGT
GGCCGGCATGCCCCGATCTTTCACACACTGGTGACCCTGAGAGAGGAGGGAGGAGGGAACCTGGCGGGGGTGTCT
GAGGCCGCACTGTCAGCTGGCCGGTCCAAGCCTGTGGCTGGAGCTGGGGTCTGTTTACCTAATAAAGTCCCACAG
GTGCCTCATT

FIGURE 11

MSWLFGINKGPKGEGAGPPPPLPPAQPGAEGGGDRGLGDRPAPKDKWSNFDPTGLERAAKAARELEHSRYAKDAL
NLAQMQEQTLQLEQQSKLKEYEAAVEQLKSEQIRAQAEERRKTLSEETRQHQARAQYQDKLARQRYEDQLKQQQL
LNEENLRKQEESVQKQEAMRRATVEREMELRHKNEMLRVEAEARARAKAERENADIIREQIRLKAAEHRQTVLES
IRTAGTLFGEGFRAFVTDWDKVTATVAGLTLLAVGVYSAKNATLVAGRFIEARLGKPSLVRETSRITVLEALRHP
IQVSRRLLSRPQDALEGVVLSPSLEARVRDIAIATRNTKKNRSLYRNILMYGPPGTGKTLFAKKLALHSGMDYAI
MTGGDVAPMGREGVTAMHKLFDWANTSRRGLLLFVDEADAFLRKRATEKISEDLRATLNAFLYRTGQHSNKFMLV
LASNQPEQFDWAINDRINEMVHFDLPGQEERERLVRMYFDKYVLKPATEGKQRLKLAQFDYGRKCSEVARLTEGM
SGREIAQLAVSWQATAYASEDGVLTEAMMDTRVQDAVQQHQQKMCWLKAEGPGRGDEPSPS

FIGURE 12

ATCAGTTCTCGCCCGTCTGGGCGTGGGCGTGGCCGGCGTGGCTGCTCGGGACCACCCGAACCCGCGGCC**ATG**GCC
CCGGCCGCCGCCAGCCCCCCGGAGGTGATCCGCGCGGCGCAGAAGGACGAGTACTACCGCGGTGGGCTGCGGAGC
GCGGCGGGCGGCGCCCTGCACAGCCTGGCGGGTGCGAGGAAGTGGCTGGAGTGGAGGAAGGAGGTTGAGCTGCTC
TCAGATGTGGCCTACTTTGGCCTCACCACACTTGCAGGCTACCAGACCCTGGGGGAGGAGTACGTCAGCATCATC
CAGGTGGACCCATCGCGGATACATGTGCCCTCCTCGCTGCGCCGTGGCGTGCTGGTGACGCTGCATGCCGTCCTG
CCCTACCTGCTGGACAAGGCCCTGCTCCCCCTGGAGCAGGAGCTGCAGGCTGACCCCGACAGTGGGCGACCCTTG
CAGGGGAGCCTGGGGCCAGGTGGGCGTGGCTGCTCAGGGGCGCGGCGCTGGATGCGTCACCACACGGCCACCCTG
ACTGAGCAGCAGAGGAGGGCGCTGCTGCGGGCGGTCTTCGTCCTCAGACAGGGCCTCGCCTGCCTCCAGCGGCTA
CATGTTGCCTGGTTTTACATCCACGGTGTCTTCTACCACCTGGCCAAGAGGCTCACGGGGATCACGTACCTCCGT
GTCCGCAGCCTGCCCGGAGAGGACCTGAGGGCCCGTGTTAGCTACAGGCTGCTGGGGGTCATCTCACTGCTGCAC
CTGGTGCTGTCCATGGGGCTGCAGCTGTACGGTTTCAGGCAGCGGCAGCGAGCCAGGAAGGAGTGGAGGCTGCAC
CGCGGCCTGTCTCACCGCAGGGCCTCCTTGGAGGAGAGAGCCGTTTCCAGAAACCCCCTGTGCACCCTGTGCCTG
GAGGAGCGCAGGCACCCAACAGCCACGCCCTGCGGCCACCTGTTCTGCTGGGAGTGCATCACCGCGTGGTGCAGC
AGCAAGGCGGAGTGTCCCCTCTGCCGGGAGAAGTTCCCTCCCCAGAAGCTCATCTACCTTCGGCACTACCGC**TGA**

GCCGGCGCCCGGGTGGGCCTGGACACAGATGACCTCTACGGGAGTCTGAACGCCAAGATTTAGTCTCAGGATTAA
CCTTGCTTGCACAGAAGTTAGAACACTCTCAGTTTTTTGTCATGTAAGATACTAACCTAGCCACCCTGGGAGAGA
ACAGAAAGCTGTCCCTGGCTGCGCTTTCTCAGCCCTGGGAGGGGCGCCTGAACCCAGAACATTTCCCTAACCCCA
ACCTGGTAGGACTCAGCCACTTCTTCAGGAATTTCACTTATTTGGACGGGATTTTAGGTTTCCCTCCCTTCCCCA
AACCATACAGTTGAGAAGTAATTCAGAAGTAGGCCAGAAGACACTTTATTCGTTTATATTGTGAGAAAACAGCCC
CATCAGGCTTGTGTTAAGGCAATGGACTGAATGAGTGCGTGCTGGGTGGGGTGGGGCACGGAGGCTGGCGGGTTG
CTTCAGCCAGTGCAGTGAGAACAGCAGCCCCACGGCCCCATGGGAGGCGGCGCTGCTCTCCCCGAGGGCGGCTGG
GCAGAGCACATCCCCCAGGACTTGATGACCACACGGGGCAGAGAGAAACCAACCAAGGCCAGCACCTCCGTCGGA
AGCATTTGGCACACACACCTTCAATACACGTCAAGGTCGCTTCCAGTTTTAGAAAACAGAAATCTGCATCTCAGC
CTGAGACGCACAGAGAGGTCTCTTCCTGACCCAGACGCACTCACGAGCCAGGTCCTGGGGGTATGGGGGCTGCCA
GGGGCGCCCGAGCCCTCTCCTGGGGGGCCTGCTGGGCAGGCGACCTGCTGACCCACGGTCACTGCTGTGTTCAGC
CCCTCAGCTCGGCCCCAGCCTATTTCCCGCCTCCATTTGATGTTTCCAGGTTTTCAAAACTGCATTTAACCTGCG
CCAGAGAGTTCACCGTAGGCATCTTTAATAAACTAACTCCAGCAAAAAAAAAAAAAAA

FIGURE 13

MAPAAASPPEVIRAAQKDEYYRGGLRSAAGGALHSLAGARKWLEWRKEVELLSDVAYFGLTTLAGYQTLGEEYVS
IIQVDPSRIHVPSSLRRGVLVTLHAVLPYLLDKALLPLEQELQADPDSGRPLQGSLGPGGRGCSGARRWMRHHTA
TLTEQQRRALLRAVFVLRQGLACLQRLHVAWFYIHGVFYHLAKRLTGITYLRVRSLPGEDLRARVSYRLLGVISL
LHLVLSMGLQLYGFRQRQRARKEWRLHRGLSHRRASLEERAVSRNPLCTLCLEERRHPTATPCGHLFCWECITAW
CSSKAECPLCREKFPPQKLIYLRHYR

FIGURE 14

GGGCGGCGAGTGGGGAGCGGGGCCGGGAGTGGAGCAGCCGCCGCGGCGGGACTGGACCGAGCCTCGCCGGCGCGC
ACCTGCCCGCAGCGCCCGCGGAGCGCGCAGCGCGGCCCGAGCGCGACGACCTGCCGAGCGGCGGCCGAGGCGGCG
GTGTGGGCGCGTCAGGCCGCGACGAGGGCGCTGAGACAAATTTACATGTATTGGAGACCAGACCAGAAGCCCTTC
TGAATTAAGATCTCACATTCTTGAAGGTGGCATTGAAGAGCACTAAGATCGGAAGATGAGTGAGCTTGACCAGTT
ACGGCAGGAGGCCGAGCAACTTAAGAACCAGATTCGAGACGCCAGGAAAGCATGTGCAGATGCAACTCTCTCTCA
GATCACAAACAACATCGACCCAGTGGGAAGAATCCAAATGCGCACGAGGAGGACACTGCGGGGGCACCTGGCCAA
GATCTACGCCATGCACTGGGGCACAGACTCCAGGCTTCTCGTCAGTGCCTCGCAGGATGGTAAACTTATCATCTG
GGACAGCTACACCACCAACAAGGTCCACGCCATCCCTCTGCGCTCCTCCTGGGTCATGACCTGTGCATATGCCCC
TTCTGGGAACTATGTGGCCTGCGGTGGCCTGGATAACATTTGCTCCATTTACAATCTGAAAACTCGTGAGGGGAA
CGTGCGCGTGAGTCGTGAGCTGGCAGGACACACAGGTTACCTGTCCTGCTGCCGATTCCTGGATGACAATCAGAT
CGTCACCAGCTCTGGAGACACCACGTGTGCCCTGTGGGACATCGAGACCGGCCAGCAGACGACCACGTTTACCGG
ACACACTGGAGATGTCATGAGCCTTTCTCTTGCTCCTGACACCAGACTGTTCGTCTCTGGTGCTTGTGATGCTTC
AGCCAAACTCTGGGATGTGCGAGAAGGCATGTGCCGGCAGACCTTCACTGGCCACGAGTCTGACATCAATGCCAT
TTGCTTCTTTCCAAATGGCAATGCATTTGCCACTGGCTCAGACGACGCCACCTGCAGGCTGTTTGACCTTCGTGC
TGACCAGGAGCTCATGACTTACTCCCATGACAACATCATCTGCGGGATCACCTCTGTCTCCTTCTCCAAGAGCGG
GCGCCTCCTCCTTGCTGGGTACGACGACTTCAACTGCAACGTCTGGGATGCACTCAAAGCCGACCGGGCAGGTGT
CTTGGCTGGGCATGACAACCGCGTCAGCTGCCTGGGCGTGACTGACGATGGCATGGCTGTGGCGACAGGGTCCTG
GGATAGCTTCCTCAAGATCTGGAACTAACGCCAGTAGCATGTGGATGCCATGGAGACTGGAAGACCATTCCAACT
TGGACGCGTTACCATGAGAGCATATCCTATCCAACCGTACTAACGTGGACACCCTACACCTCCCCTCAGAACTTC
AAAAGGGCAAGATCTTTTTTCCTTCACTTATTGCTGAAACCAAGAGCACAATTCCCATTGAGAGAAAGATCTCTG
TGCTGTAAACTAAAACAAATTGTGCATTCCTTCCGGGGCCATCGTCTTTGTTTTCTTTTTTGTCTTGAATGAATT
TTAAAAGGAAATATATAATAAAAATGTTAACCAGAAGGTAAACTTGAGTGTAATTGTCAGACAGACACACTTTTC
CACCAGTGTATTTGAATTTTAGACCAGTGACCCTGTTTTGTGGCATTCATGCAAAACATGCTGAGGGCTTTGTTC
ATCTGGTCATCGTGTCCAAATTTCAGTCATGTTTGTAGCAAGATTTTGGAAGCATTCATATTTCCTTTTTAAAAT
GTATTCCTTTGTGTTCAACAGTTAATCAAAACCAGAGAGTCTAGGGCAGCCTCTCTGATGTTGTCAATGATGTAA
ATTCAGTCCCTGGTTTTTAATTTTCTGTCTGATGTCACAGATCATTGTTGCACACAAACGTGGCATAGAAAAGAA
CATGTTCAGAAGCCATGGGGCCAAGCACATGCGGGGACGGTCTCAAATGCGTGATCAGAGAATCCTTCACCTTTG
CTGAAAAGTGAGCTCAGATCCAGCACCATGTTCCTCCTGACCCATCCTGTCTATCTTCTCAGTTGAGTTTTTAAT
CTCACTTTGGGTTTCCTTGTGAAGTTGGAGGGAAGTTTATAATAGCCTAACACTACCCCACCCCCAACTAGGAGG
AACCTCTGTTTTCAAGAGAGATGCCTGTCCTGTGCTTGGATAGTCAGTCAATTATTTGTGTATGAAACAATGTAC
AAATCAATGTTTTGAAAATAATGATCTCAGACTTTCTAAGTTAAATTTTAAAAATTTTGATTGTTTGCCATATTG
GGTGGGTTTACTCTTAGAATCGCATGCTGTAGAAATGCTCAAAAGTGCATATGGGACTCAGTCCTTAGGTGTTCT
TTTTCTTTTAAGAAATAACCTCTTACAGTTGTAACCATTGCGGCTCTGTCCACTTCTCGTTGCTGCTCTGTGGCA
CATATCGGAAGCAGTACAGCGCGCGGCTCTACACGCTTGGGTAGCGGGATAAGTCACTGTTTTCTTTATTTCTTT
AAAAAAAAAAAAGTTCTGTTGCAAACGACTGCTGTTGGATTCTGAGGGTGGGGAGGGAGAGAGAGGGAGGGAGAG
GGAGTGAAGAGCCTGCCCTCCTATATGGATTCTTCAGGGCCCTCCACATCTGAGGTGGCTCATTCCCATCACACA
CAGATTGTCCTGGTGTTCATTTCAAGGCCAGTGTTCAGCAGCAGCGTTTGGAAAGCAGGTTCTGTGGGACCCCCC
GCCCCGCCCCCCGCACTCCTTCATAGCAGCAGTAGTGGCTTCTCCATCCTGTTTTCTGCAACATTCTATACAAAA
CTGTGCTGTGACCTTGCGGTAGGCCTGGATCTGGCAAAGAGAATACAAATGAAACCCCTTCTTTCTCTTTCCGTC
CAACAACTCTGTAGAGCTCTCTGCACCCTTACCCCTTTCCACCTTTTGTATTTAATTTTAAAGTCAGTGTACTGC
AAGGAAGCTGGATGCAAGATAGATACTATATTAAACTGTACTGTTATTTAAGATGTAATAAAGCAGTTTGACATG

FIGURE 15

ATCAAACCACCCCAGCAAATGTCTCGGAAAGAAAAAGTTCATCACAGAAAAGATGAAAAGAGAAAAGAAAAAATGT
AGGCATCATAGCCATTCAGCAGAAGGGGGAAGCATGCTAGAGTGAAAGAAAGAGAGCACGAACGTCGGAAACGA
CATCGAGAAGAACAGGATAAAGCTCGCCGGGA**ATG**GGAAAGACAGAAGAGAAGGGAAATGGCAAGGGAGCATTCC
AGGAGAGAAAGGGACCGCTTGGAGCAGTTAGAAAGGAAGCGGGAGCGGGAGCGCAAGATGCGGGAGCAGCAGAAG
GAGCAGCAGTCAAGAAGATGACCTTCAGCGAGCACCCCTACAACAACCTCCGCAAGCGCTTCGGGGCTCTGCTCT
CAGACCAGGGCTTCGACCTCATGAACAAGTTCCTGACCTACTTCCCCGGGAGGAGGATCAGCGCTGAGGACGGCC
TCAAGCATGAGTATTTCCGCGAGACCCCCCTCCCCATCGACCCCTCCATGTTCCCCACGTGGCCCGCCAAGAGCG
AGCAGCAGCGTGTGAAGCGGGGCACCAGCCCGAGGCCCCCTGAGGGAGGCCTGGGCTACAGCCAGCTGGGTGACG
ACGACCTGAAGGAGACGGGCTTCCACCTTACCACCACGAACCAGGGGGCCTCTGCCGCGGGCCCCGGCTTCAGCC
TCAAGTTC**TGA**AGGTCAGAGTGGACCCCGTCATGGGG

FIGURE 16

MGKTEEKGNGKGAFQERKGPLGAVRKEAGAGAQDAGAAEGAAVKKMTFSEHPYNNLRKRFGALLSDQGFDLMNKF
LTYFPGRRISAEDGLKHEYFRETPLPIDPSMFPTWPAKSEQQRVKRGTSPRPPEGGLGYSQLGDDDLKETGFHLT
TTNQGASAAGPGFSLKF

FIGURE 17

TCGCGCGGAAGCCGCGGTAGGGTGGGAACCCAAGCGGGAGAGCCGCGGGATTTGCGGCCGCCGCC**ATG**CCGTCGT
CCCCGCTGCGGGTGGCGGTGGTGTGCTCGAGCAACCAGAACCGGAGCATGGAGGCGCACAACATCCTCAGCAAAC
GGGGATTCAGCGTCCGATCCTTTGGAACAGGGACTCACGTGAAGCTTCCAGGACCAGCTCCCGACAAGCCCAATG
TTTATGATTTCAAAACCACATATGACCAGATGTACAATGATCTTCTTAGGAAAGACAAAGAACTCTATACACAGA
ATGGGATTTTACATATGCTGGACAGAAATAAGAGAATCAAGCCCCGGCCAGAAAGATTCCAGAACTGCAAAGACC
TGTTTGATCTGATCCTCACTTGCGAAGAGAGAGTGTATGACCAGGTGGTGGAAGATCTGAATTCCAGAGAACAGG
AGACCTGCCAGCCCGTGCACGTGGTCAATGTGGACATCCAGGACAACCACGAGGAGGCCACCCTGGGGGCGTTTC
TCATCTGTGAGCTCTGCCAGTGTATCCAGCACACGGAAGACATGGAGAACGAGATCGACGAGCTGCTGCAGGAGT
TCGAGGAGAAGAGTGGCCGCACCTTTCTGCACACCGTCTGCTTCTAC**TGA**GCCCAGCGCCCGCATGGAGCCGCCT
CTGGAGCTTCCTGTTGTTCATACTTTTTCCTTCCTGACATTTGTTTTTACTTACAGGTGTTCTGCTGGTGACGGT
AGCATTACCCAAATAAACTGTGCATATGAAATGGGAGAGGAGATGCCAAAACGCCAGATGAAAGCAATCAAGTTT
CTTCTTTTCCACTTTTACTTATGAGCGGGATATTGATTACAAAGTTTTTCTTCTTTAACCAAAAAGGAAAGACAA
CGGTTTGTGTGCACTTCCCGACATACCTGTGTCTTCGTGTGCCTGCCTTCCCTCCCTCCTCCCCACCGGGCCGGA
CTGTACAGAGCCCTGCTGCGGCGTGTTAGGAATGACCTGGAATTGTCAATAAACAGATGCTGCTGTCAAAAAAAA
AAAAAAAAA

FIGURE 18

MPSSPLRVAVVCSSNQNRSMEAHNILSKRGFSVRSFGTGTHVKLPGPAPDKPNVYDFKTTYDQMYNDLLRKDKEL
YTQNGILHMLDRNKRIKPRPERFQNCKDLFDLILTCEERVYDQVVEDLNSREQETCQPVHVVNVDIQDNHEEATL
GAFLICELCQCIQHTEDMENEIDELLQEFEEKSGRTFLHTVCFY

FIGURE 19

CCTGGCCACCGGCTCGCGGCGCGTGGAGGCTGCTCCCAGCCGCGCCCGAGTCAGACTCGGGTGGGGGTCCCGGCG
GCGGTAGCGGCGGCGGCGGTGCGAGCATGTCGTGGCTCTTCGGCGTTAACAAGGGCCCCAAGGGTGAAGGCGCGG
GGCCGCCGCCGCCTTTGCCGCCCGCGCAGCCCGGGGCCGAGGGCGGCGGGGACCGCGGTTTGGGAGACCGGCCGG
CGCCCAAGGACAAATGGAGCAACTTCGACCCCACCGGCCTGGAGCGCGCCGCCAAGGCGGCGCGCGAGCTGGAGC
ACTCGCGTTACGCCAAGGAGGCCCTGAATCTGGCGCAGATGCAGGAGCAGACGCTGCAGTTGGAGCAACAGTCCA
AGCTCAAAGAGTATGAGGCCGCCGTGGAGCAGCTCAAGAGCGAGCAGATCCGGGCGCAGGCTGAGGAGAGGAGGA
AGACCCTGAGCGAGGAGACCCGGCAGCACCAGGCCAGGGCCCAGTATCAAGACAAGCTGGCCCGGCAGCGCTACG
AGGACCAACTGAAGCAGCAGCAACTTCTCAATGAGGAGAATTTACGGAAGCAGGAGGAGTCCGTGCAGAAGCAGG
AAGCCATGCGGCGAGCCACCGTGGAGCGGGAGATGGAGCTGCGGCACAAGAATGAGATGCTGCGAGTGGAGACCG
AGGCCCGGGCGCGCGCCAAGGCCGAGCGGGAGAATGCAGACATCATCCGCGAGCAGATCCGCCTGAAGGCGTCCG
AGCACCGTCAGACCGTCTTGGAGTCCATCAGGACGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGCCTTTGTGA
CAGACCGGGACAAAGTGACAGCCACGGTGGCTGGGCTGACGCTGCTGGCTGTCGGGGTCTACTCAGCCAAGAATG
CGACAGCCGTCACTGGCCGCTTCATCGAGGCTCGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTCCCGCATCA
CGGTGCTGGAGGCGCTGCGGCACCCCATCCAGGTCAGCCGGCGGCTCCTCAGTCGACCCCAGGACGTGCTGGAGG
GTGTTGTGCTTAGTCCCAGCCTGGAAGCACGGGTGCGCGACATCGCCATAGCAACCAGGAACACCAAGAAGAACC
GGGGCCTGTACAGGCACATCCTGCTGTATGGGCCACCAGGCACCGGGAAGACGCTGTTTGCCAAGAAACTCGCCC
TGCACTCAGGCATGGACTACGCCATCATGACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGTGACCGCCA
TGCACAAGCTCTTTGACTGGGCCAATACCAGCCGGCGCGGCCTCCTGCTCTTCATGGATGAAGCAGACGCCTTCC
TTCGGAAGCGAGCCACTGAGGAGATAAGCAAGGACCTCAGAGCCACACTGAACGCCTTCCTGTACCACATGGGCC
AACACAGCAACAAATTCATGCTGGTCCTGGCCAGCAATCTGCCTGAGCAGTTCGACTGTGCCATCAACAGCCGCA
TTGACGTGATGGTCCACTTCGACCTGCCGCAGCAGGAGGAGCGGGAGCGCCTGGTGAGACTGCATTTTGACAACT
GTGTTCTTAAGCCGGCCACAGAAGGAAAACGGCGCCTGAAGCTGGCCCAGTTTGACTACGGGAGGAAGTGCTCGG
AGGTCGCTCGGCTGACGGAGGGCATGTCGGGCCGGGAGATCGCTCAGCTGGCCGTGTCCTGGCAGGCCACGGCAT
ATGCCTCCAAGGACGGGGTCCTCACTGAGGCCATGATGGACGCCTGTGTGCAAGATGCTGTCCAGCAGTACCGAC
AGAAGATGCGCTGGCTGAAGGCGGAGGGGCCTGGGCGCGGGGTCGAGCACCCCCTATCCGGAGTCCAAGGCGAGA
CCCTCACCTCATGGAGCCTGGCCACGGACCCCTCCTACCCCTGCCTTGCCGGCCCCTGCACATTTAGGATATGCT
CCTGGATGGGGACTGGGCTGTGCCCAGGGCCTCTGTCCCCCAGGATGTCTTGTGGTGGCGGTCGGCCGTTCTGCC
CCCCAGGGCACCCCCTGTTGTAGGCACTGGCTAGGGAGGGGCAGGCCTCCTTCCTGCCCCTCGAGACACTCTTGG
GAGATGCATTTTCCGTCTGGCTCACAGGGGGAGGGTGAGGCTTTGTACCCCAGCCCCTGCCCAGGCCACTGTGAG
GGTGGGTGCTGGCTGAGCCCCTGGGGCAGAAGGAGTGGGGCAGGCGGGGTCTTTGTTCTCGGCTCCCACAGCAGA
GCCAGGTGAGGGGGGGCCTGCCAGGACTAGACAGAAGTGGGGCGGC

FIGURE 20

ATGAGGCTGCAGAGTGATGTGGGGGCCAGCGGTGACTTCATGACCACACTGCGCCCAGGTGTAAGAGGGCACGCT
TCTGCCCAGGCATCGTCCATGGAAGACACGCAGTCGGCCACTGCAGCCTCGGTCCTGGGTGCCCTGGGGCTGGGT
CACTGGGGGCCACAGGCCACACTGAGAGACCACAGTCCTGGCATGCCATGCAGCTCCCTGTCCCCAGAGGCCATG
TCAAAGGACGCCCTGAATCTGGCGCAGATGCAGGAGCAGACGCTGCAGTTGGAGCAACAGTCCAAGCTCAAACAA
CTTGTCAATGAGGATTTACGGAAGCAGGAGGAGTCCGTGCAGAAGCACCATCAGACCTTCTTGGAGTCCATCAGG
GCGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGCCTTTGTGACAGACCGGGACAAAGTGACAGCCACGGTGGCT
GGGCTGACGCTGCTGGCTGTCGGGGTCTACTCAGCCAAGAATGCGACAGCCGTCACTGGCCGCTACATCGAGGCT
CGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTCCCGCATCACGGTGCTTGAGGCGCTGCGGCACCCCATCCAG
CAGGTCAGCCGGCGGCTCCTCAGTCGACCCCAGGACGTGCTGGAGGGTGTTGTGCTTAGTCCCAGCCTGGAAGCA
CGGGTGCGCGACATCGCCATAATGACAAGGAACATCAAGAAGAACCGGGGCCTGTACAGGCACATCCTGCTGTAC
GGGCCACCAGGCACCGGGAAGACGCTGTTTGCCAAGAAACTCGCCCTGCACTCAGGCATGGACTACGCCATCATG
ACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGTGACCGCCATGCACAAGCTCTTTGACTGGGCCAATACC
AGCCGGCGCGGCCTCCTGCTCTTTGTGGATGAAGCGGACGCCTTCCTTCGGAAGCGAGCCACTGAGAAGATAAGC
GAGGACCTCAGGGCCACACTGAACGCCTTCCTGTACCGCACGGGCCAGCACAGCAACAAATTCATGCTGATCCTG
GCCAGCTGCCACCCCGAGCAGTTCGACTGGGCCATCAATGCCTGCATCGACGTGATGGTCCACTTCGACCTGCCA
GGGCAGGAGGAGCGGGCGCGCCTGGGATTGGAGGGAGAGGCTCCTCATGAGACCCCCATGTCGGGACTAGAGGGA
GAGGCTCCTCATGGTCCACTGCTGGCTTCTGGCCTGGCCTCCCTGCAGCTGCCACACCCGGCCCTGGAGCCTCGT
GGTGTGGGGCGCGGCTCTTGCTTCCTGCTGCACATGTGCCTTGAGGCTGTCAGGCTCCCTGTTGCTGGCGGGCCC
CGGTTTCTGAGTCCTTCTGTGCACCTGACCCAAATCCCTGCTGTCGCCAGTGACGACAAAAGCTGCTCTGTTCCA
AAGAGAGCCTGGTTCTCCCCTGCCGACCCCTCCACTGCCGCCTGCTCCATGCTAGACCAGCTTTCCGGGCGTCTG
AAGCTGGCCCAGTTTGACTACGGGAGGAAGTGCTTAGAGATCGCTCGGCTGACAGAGGGCATGTCATGCCGGAAG
ATCGCACAGCTGGCCGTGTCCTGGCAGGCCACGGCGTATGCCTCCAAGGACGGGGTCCTGACCGAGGCCATGATG
GACGCCTGCGTGCAAGACTTTGTCCAGCAGCACCAGCAGATGATGCGCTGGCTGAAGGGGGAGAGGCCTGGGCCC
GAGGACGAGCAACCCTCATCC**TGA**

FIGURE 21

MRLQSDVGASGDFMTTLRPGVRGHASAQASSMEDTQSATAASVLGALGLGHWGPQATLRDHSPGMPCSSLSPEAM
SKDALNLAQMQEQTLQLEQQSKLKQLVNEDLRKQEESVQKHHQTFLESIRAAGTLFGEGFRAFVTDRDKVTATVA
GLTLLAVGVYSAKNATAVTGRYIEARLGKPSLVRETSRITVLEALRHPIQQVSRRLLSRPQDVLEGVVLSPSLEA
RVRDIAIMTRNIKKNRGLYRHILLYGPPGTGKTLFAKKLALHSGMDYAIMTGGDVAPMGREGVTAMHKLFDWANT
SRRGLLLFVDEADAFLRKRATEKISEDLRATLNAFLYRTGQHSNKFMLILASCHPEQFDWAINACIDVMVHFDLP
GQEERARLGLEGEAPHETPMSGLEGEAPHGPLLASGLASLQLPHPALEPRGVGRGSCFLLHMCLEAVRLPVAGGP
RFLSPSVHLTQIPAVASDDKSCSVPKRAWFSPADPSTAACSMLDQLSGRLKLAQFDYGRKCLEIARLTEGMSCRK
IAQLAVSWQATAYASKDGVLTEAMMDACVQDFVQQHQQMMRWLKGERPGPEDEQPSS

FIGURE 22

AAGTGCCCGAGGGCGGCCGCAGAACGGTCAATTTGAGCCGCGTCGAGCTCCCCTGGACCTGTGGCCGCCGCCCA
CAGACC**ATG**CTCCTGGGGCGCCTGACTTCCCAGCTGTTGAGGGCCGTTCCTTGGGCAGGCGGCCGCCCGCCTTGG
CCCGTCTCTGGAGTGCTGGGCAGCCGGGTCTGCGGGCCCCTTTACAGCACATCGCCGGCCGGCCCAGGTAGGGCG
GCCTCTCTCCCTCGCAAGGGGGCCCAGCTGGAGCTGGAGGAGATGCTGGTCCCCAGGAAGATGTCCGTCAGCCCC
CTGGAGAGCTGGCTCACGGCCCGCTGCTTCCTGCCCAGACTGGATACCGGGACCGCAGGGACTGTGGCTCCACCG
CAATCCTACCAGTGTCCGCCCAGCCAGATAGGGGAAGGGGCCGAGCAGGGGGATGAAGGCGTCGCGGATGCGCCT
CAAATTCAGTGCAAAAACGTGCTGAAGATCCGCCGGCGGAAGATGAACCACCACAAGTACCGGAAGCTGGTGAAG
AAGACGCGGTTCCTGCGGAGGAAGGTCCAGGAGGGACGCCTGAGACGCAAGCAGATCAAGTTCGAGAAAGACCTG
AGGCGCATCTGGCTGAAGGCGGGGCTAAAGGAAGCCCCCGAAGGCTGGCAGACCCCCAAGATCTACCTGCGGGGC
AAA**TGA**GTCTGGCGCCGCCCTTCCCGCCCGTTGCTGCTGTGATCCGTAGTAATAAATTCTCAGAGGACTCAGCCT
TTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 23

MLLGRLTSQLLRAVPWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPGRAASLPRKGAQLELEEMLVPRKMSVSPLE
SWLTARCFLPRLDTGTAGTVAPPQSYQCPPSQIGEGAEQGDEGVADAPQIQCKNVLKIRRRKMNHHKYRKLVKKT
RFLRRKVQEGRLRRKQIKFEKDLRRIWLKAGLKEAPEGWQTPKIYLRGK

FIGURE 24

GCGGTGCGGGCCGGGCGGGGCGCAGGCGGGCGGGCGGGTAGCGCCCCGCGTCCGAGCCCCGGGCCGGGCCCTGAG
CGCGCGGGCTCCGCGCCGCCGCCGCGCC<u>ATG</u>GCGGAGACCAAGATTATCTACCACATGGACGAGGAGGAGACGCC
GTACCTGGTCAAGCTGCCCGTGGCCCCCGAGCGCGTCACGCTGGCCGACTTCAAGAACGTGCTCAGCAACCGGCC
CGTGCACGCCTACAAATTCTTCTTTAAGTCCATGGACCAGGACTTCGGGGTGGTGAAGGAGGAGATCTTTGATGA
CAATGCCAAGCTTCCCTGCTTCAACGGCCGCGTGGTCTCCTGGCTGGTCCTGGCTGAGGGTGCTCACTCGGATGC
GGGGTCCCAGGGCACGGACAGCCACACAGACCTGCCCCCGCCTCTTGAGCGGACAGGCGGCATCGGGGACTCCCG
GCCCCCCTCCTTCCACCCAAATGTGGCCAGCAGCCGTGACGGGATGGACAACGAGACAGGCACGGAGTCCATGGT
CAGTCACCGGCGGGAGCGTGCCCGACGCCGGAACCGCGAGGAGGCCGCCCGGACCAATGGGCACCCAAGGGGAGA
CCGACGGCGGGATGTGGGGCTGCCCCCAGACAGCGCGTCCACCGCCCTCAGCAGCGAGCTTGAGTCCAGCAGCTT
TGTGGACTCGGACGAGGATGGCAGCACGAGCAGGCTCAGCAGCTCCACGGAGCAGAGCACCTCATCCAGACTCAT
CCGGAAGCACAAACGCCGGCGGAGGAAGCAGCGCCTTCGGCAGGCGGACCGGGCCTCCTCCTTCAGCAGCATAAC
CGACTCCACCATGTCCCTCAACATCGTCACTGTCACGCTCAACATGGAAAGACATCACTTTCTGGGCATCAGCAT
CGTGGGGCAGAGCAACGACCGTGGAGACGGCGGCATCTACATTGGCTCCATCATGAAGGGCGGGGCTGTGGCCGC
TGACGGCCGCATCGAGCCCGGCGACATGTTGCTGCAGGTGAATGACGTGAACTTTGAGAACATGAGCAATGACGA
TGCCGTGCGGGTGCTGCGGGAGATCGTTTCCCAGACGGGGCCCATCAGCCTCACTGTGGCCAAGTGCTGGGACCC
AACGCCCCGAAGCTACTTCACCGTCCCACGGGCTGACCCGGTGCGGCCCATCGACCCCGCCGCCTGGCTGTCCCA
CACGGCGGCACTGACAGGAGCCCTGCCCCGCTACGAGCTGGAAGAGGCGCCGCTGACGGTGAAGAGTGACATGAG
CGCCGTCGTCCGGGTCATGCAGCTGCCAGACTCGGGACTGGAGATCCGCGACCGCATGTGGCTCAAGATCACCAT
CGCCAATGCCGTCATCGGGGCGGACGTGGTGGACTGGCTGTACACACACGTGGAGGGCTTCAAGGAGCGGCGGGA
GGCCCGGAAGTACGCCAGCAGCTTGCTGAAGCACGGCTTCCTGCGGCACACGGTCAACAAGATCACCTTCTCCGA
GCAGTGCTACTACGTCTTCGGGGATCTCTGCAGCAATCTCGCCACCCTGAACCTCAACAGTGGCTCCAGTGGGAC
TTCGGATCAGGACACGCTGGCCCCGCTGCCCCACCCGGCTGCCCCCTGGCCTCTGGGTCAGGGCTACCCCTACCA
GTACCCGGGACCCCCACCCTGCTTCCCGCCTGCCTACCAGGACCCGGGCTTTAGCTATGGCAGCGGCAGCACCGG
GAGTCAGCAGAGTGAAGGGAGCAAAAGCAGTGGGTCCACCCGGAGCAGCCGCCGGGCCCCGGGCCGTGAGAAGGA
GCGTCGGGCGGCGGGAGCTGGGGGCAGTGGCAGTGAATCGGATCACACGGCACCGAGTGGGGTGGGGAGCAGCTG
GCGAGAGCGTCCGGCCGGCCAGCTCAGCCGTGGCAGCAGCCCACGCAGTCAGGCCTCGGCTACCGCCCCGGGGCT
CCCCCCGCCCCACCCCACGACCAAGGCCTATACAGTGGTGGGGGGGCCACCCGGGGGACCCCCTGTCCGGGAGCT
GGCTGCCGTCCCCCCGGAATTGACAGGCAGCCGCCAGTCCTTCCAGAAGGCTATGGGGAACCCCTGCGAGTTCTT
CGTGGACATCATG<u>TGA</u>CTCGTGGCGCATGCCCCAGCCCTGCCTGAGGTGGGGAGCTGGCGGTCCTGCCGCATGCA
GAGCTCGCGTGGGCTTGCCTTCGTGGGGGCCAGGACGGGAGGCAGGGTGGGGGGCAGGCTGGACCACCACCATCT
GCCCTGGCAGCCTGGCTGCTCCAGCTCCTGACAGCACCTGTGTCTGAGCAGCCGTGTTGGGGGCGCTCCCTCTCT
GCCCCTCAGCGAGAGCCTCGGACCTCCCAACCCCTTGTGTCTGGTGGGGATCCCTCCTGGGATGAGGAAGACCCC
CTCGGGCTCTCGGCTGACCCCCACCTCCTGCACAGCTGTGCCCAGGCCCCCAGGGTGGTCCATGCGGGGCAACCC
CCTGCGGTGCACAGGCCCCCTGTCTGGAGTAGGGATCTAATTTATTTATTTATTGCCTGGCCGGTGACTCGGGGG
AGGAGGCGACCCTGTCATCTGTCCCACCTGCTGCTGCCCCTTGGAGCAGCCTGCACCTTCTCTCCTCCCATCCGG
CAACAGTCTGAAAGTACGTGGAGGACGGGACCGGAAGACGAGAGAGGGCTGGACATCCTGCCCACCGTGTCCCAG
CCAGGGCAGGGAGGGACCATGGCCCGCAGGGTCAAGGGGCCCCGATGTGCACAGCTGCCACAGGGAGGGAGGTCT
TGGGGAGATGGGCAGTCAGGTGGCCCGTCCTTGGTGAGTGCACACACTGCGCGCACACATCGCGGCCTTCCTGGC
TTCTCTGGCCCCCACGTGTCTGTGCTGTAGATACTGTATCAAAGTCCCAGCGTTTAGATGGTTAACATAGAGCTG
CTTCTGTGTAAATGCTGCTTATTTTAAACACTAAAAAGCGTTTAATTTTATGGG

FIGURE 25

MAETKIIYHMDEEETPYLVKLPVAPERVTLADFKNVLSNRPVHAYKFFFKSMDQDFGVVKEEIFDDNAKLPCFNG
RVVSWLVLAEGAHSDAGSQGTDSHTDLPPPLERTGGIGDSRPPSFHPNVASSRDGMDNETGTESMVSHRRERARR
RNREEAARTNGHPRGDRRRDVGLPPDSASTALSSELESSSFVDSDEDGSTSRLSSSTEQSTSSRLIRKHKRRRRK
QRLRQADRASSFSSITDSTMSLNIVTVTLNMERHHFLGISIVGQSNDRGDGGIYIGSIMKGGAVAADGRIEPGDM
LLQVNDVNFENMSNDDAVRVLREIVSQTGPISLTVAKCWDPTPRSYFTVPRADPVRPIDPAAWLSHTAALTGALP
RYELEEAPLTVKSDMSAVVRVMQLPDSGLEIRDRMWLKITIANAVIGADVVDWLYTHVEGFKERREARKYASSLL
KHGFLRHTVNKITFSEQCYYVFGDLCSNLATLNLNSGSSGTSDQDTLAPLPHPAAPWPLGQGYPYQYPGPPPCFP
PAYQDPGFSYGSGSTGSQQSEGSKSSGSTRSSRRAPGREKERRAAGAGGSGSESDHTAPSGVGSSWRERPAGQLS
RGSSPRSQASATAPGLPPPHPTTKAYTVVGGPPGGPPVRELAAVPPELTGSRQSFQKAMGNPCEFFVDIM

FIGURE 26

GCACCGCCCCCGCCCGCAAGAAAGATGGCAGTGGCCTGATCCGGGCCCGTTGGCGGCGTCACTGACGCTTCGCTC
CGGTCCTCGGATCCCGAGCGCGGGGAGGCAGACCGACTGTGAGCTGCTTGTCCCCATCCTGCGGCCGTCCTGGGG
ACACAGAGCCCTCCGTGGTGCCCGGGGATTGGATTGGAGCCAGGACCTCACTTCCTCCTCTGCCCCTGCCCCTGC
CCCTCCCAGCACCTGGCCCACACCCTGCAGCCCGCCCC**ATG**GTCTGGCCCTGGGTGGCGATGGCGTCCAGGTGGG
GTCCCCTCATTGGCCTGGCTCCGTGCTGCCTCTGGCTCCTGGGGGCAGTCCTTCTGATGGACGCGTCTGCACGGC
CTGCCAACCACTCGTCCACTCGAGAGAGAGTAGCCAACAGGGAGGAGAATGAGATCCTGCCCCCAGACCACCTGA
ACGGGGTGAAGCTGGAGATGGACGGGCACCTCAATCGCGGCTTCCACCAGGAGGTCTTCCTAGGCAAGGACCTGG
GTGGCTTTGATGAGGACGCGGAGCCGCGGCGGAGCCGGAGGAAGCTGATGGTCATCTTTTCCAAGGTGGATGTGA
ACACTGACCGGAAGATCAGTGCCAAGGAGATGCAGCGCTGGATCATGGAGAAGACGGCCGAGCACTTCCAGGAGG
CCATGGAGGAGAGCAAGACACACTTCCGCGCCGTGGACCCTGACGGGGACGGTCACGTGTCTTGGGACGAGTATA
AGGTGAAGTTTTTGGCGAGTAAAGGCCATAGCGAGAAGGAGGTTGCCGACGCCATCAGGCTCAACGAGGAACTCA
AAGTGGACGAGGAAACACAGGAAGTCCTGGAGAACCTGAAGGACCGCTGGTACCAGGCGGACAGCCCCCCTGCAG
ACCTGCTGCTGACGGAGGAGGAGTTCCTGTCGTTCCTCCACCCCGAGCACAGCCGGGGAATGCTCAGGTTCATGG
TGAAGGAGATCGTCCGGGACCTGGACCAGGACGGTGACAAGCAGCTCTCTGTGCCCGAGTTCATCTCCCTGCCCG
TGGGCACCGTGGAGAACCAGCAGGGCCAGGACATTGACGACAACTGGGTGAAAGACAGAAAAAAGGAGTTTGAGG
AGCTCATTGACTCCAACCACGACGGCATCGTGACCGCCGAGGAGCTGGAGAGCTACATGGACCCCATGAACGAGT
ACAACGCGCTGAACGAGGCCAAGCAGATGATCGCCGTCGCCGACGAGAACCAGAACCACCACCTGGAGCCCGAGG
AGGTGCTCAAGTACAGCGAGTTCTTCACGGGCAGCAAGCTGGTGGACTACGCGCGCAGCGTGCACGAGGAGTTT**T**
GAGCGCCCGGCCGCGCCCCGCGCCGCCCCCCACGCACCACCGGGGCGGCCTCGCGGGTGACTCCGGGCTCCGTGG
CTGTCCCGGACCCCACCTCTTCCCTGCCGCCCGCCACCGGCCGACCGACCGCGGCTGCCCCAGTTGATGAGCGGC
GTGTCCCCTCTGCAGCGCGCACCCCGGCGGGGCTTTGGCTGTGACGCGGTCGGGGCGCGGGGCTGGGCTGTGGCC
CCGCGGCGCCGCCTCCTCCCTGGTCCCTCGAAATCGTGGCATCTCACTTCTGAGAACGAAATCTCGCTTCAGTCA
CTCTGCCGAAGGCGCTGACGGCATCGCGGCCGGAACCTCTGGGCCCGGCCCCTCCCAGGGCCGCCGCTCCGTGGG
AAAAAACAGCTCCTCCATTTCCTTGAAAACTGAACGATTATTAAAAATAGATTAAACTTCGCTGGAAATGAGTAG
CCAGGAAGTTCAGGGGAGGGTGCCGGGTCCTTCCCGGGCCTGGCGTGTCGGAGCCACCCAGGTCCCGCAGCTGCC
GCTGAGAAAATGCAAATATTTGTTGTGACAAGAATCACATACATTTACTTTAAATATAGTTGCCTTTTTTGGTCA
GCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 27

MVWPWVAMASRWGPLIGLAPCCLWLLGAVLLMDASARPANHSSTRERVANREENEILPPDHLNGVKLEMDGHLNR
GFHQEVFLGKDLGGFDEDAEPRRSRRKLMVIFSKVDVNTDRKISAKEMQRWIMEKTAEHFQEAMEESKTHFRAVD
PDGDGHVSWDEYKVKFLASKGHSEKEVADAIRLNEELKVDEETQEVLENLKDRWYQADSPPADLLLTEEEFLSFL
HPEHSRGMLRFMVKEIVRDLDQDGDKQLSVPEFISLPVGTVENQQGQDIDDNWVKDRKKEFEELIDSNHDGIVTA
EELESYMDPMNEYNALNEAKQMIAVADENQNHHLEPEEVLKYSEFFTGSKLVDYARSVHEEF

FIGURE 28

AAGGGGCCAAAAGGTCCACCTGATGAACCTGTTGCACGCGAAAAGTTCAGAACCACTGCTGCCAAGATGCTGACA
GAAGCCTTGAGAAGCACCTGCTGCGGGAAAAGACGTGCAGGCCTCACAGGTGCAGTGCGGTCTTCAGCGCGCTTG
AAAGCACGAAGTTGTTCGGCAGCCAGGTTGGCCTCTGCCCAGGAAGTTGCTGGTTCCACGTCTGCCAAGACAGCA
TGTCTGACCCGGGCCCTGATCCTAGCACCCGCCCACCCGTGTACTTCCTCATCCCACAAAGCCACAGACACGCGA
ACGTCCAAGAAGTTCAAATGTGACAAAGGACATCTTGTGAAGTCAGAATTACAGAAGCTTGTCCCTAAGAATGAC
AGCGCTTCTTTGCCAAAAGTGACACCTGAGACCCCTTGTGAAAATGAGTTTGCTGAAGGCAGTGCCTTGCTTCCA
GGCAGCGAGGCTGGCGTTTCTGTGCAGCAGGGGGCTGCAAGTCTTCCTCTCGGTGGCTGCAGAGTTGTGAGTGAC
TCTCGCTTAGCAAAGACTAGAGATGGCCTGTCCGTGCCAAAACACAGTGCCGGGTCCGGAGCAGAAGAATCCAAC
AGCAGCTCCACTGTGCAGAAGCAGAATGAGCCAGGGCTACAGACAGAGGATGTGCAGAAGCCACCACTTCAGATG
GACAACAGCGTCTTTCTAGATGACGACAGCAATCAGCCAATGCCCGTGAGCCGGTTCTTTGGAAACGTTGAGCTC
ATGCAGGCCATAGAGAGGTCCGTGTGCAGCTGCCTGACGAGAACTGCATTCCCCAGCCCCAGCGGCGTCAGGGAG
CACCTCACCGTGTGTTCTCGCCCAGGGCAGTGGAGACAAGCCATTGGGAGTGCTCTCTCCATGGCCTCTTCCTGC
CGCCACCTGCACATAGAAGCTGAGTGGACCAACCAGGAGCAAGCTGGGGTCCCCGGGTGA

FIGURE 29

AGAGGCGAGAACGACCCCGGGACCGACCAAAGCCCGCGCGCCGCCGCATCCCGCGTACAGCACCTACATCCCGCC
ACCGTCACCGCCACCACCATGCCCAAGAGAAAGGCTGAAGGGGATGCTAAAGGAGGTAAAGCCAAGGTGAAGGAC
GAACCACAGAGAAGGTCTGCAAGGTTGTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCAAGCCTAAAAAGACC
CCTGCAAAGAAGGCAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGATGCCCAGGAGGAGGGATTCCCTGAC
TTTGACACACATGGCCACCTTGGCACAAAAGCCTTGTGGTGTGGAAAAACAAATTTGTTTTTATGTCCTCTTCTC
CCTTTCCATCTTTCAGCATAGACTTAACTCCTTTAATCCCAGGCATCTGTTGGGACCTGACCCCTAGTCATTGGT
TACCAGTGTGTCAGGCAATCTGGACTTTCCAGTGATGCCACTGAGATGGCACCTGTCAAAAGAGCAGTGGTTCCA
TTTCTAGATTGTGGATCTTCAGATAAATTCTGCCATTTTCATTTCACTTCCTGAAAGTCAGAGTCGGCTTGTGAA
AAGTTGTTAAACAACATGCTAAATGTGAAATGTCAACCCTCACTCTAAACTTTCCCTGTTCAGAGCATGAGATGA
AGACTTCTTTGGGTTTTATAGCGGCTTTCTGATTTTTCGTAGTCCATTGAAGAAGGGAGTTTGAAAGTTGTTGTA
TACTGTTAACAATTGTCTGCCCATGTCCTGCCTGAAATACCA

FIGURE 30

MPKRKAEGDAKGGKAKVKDEPQRRSARLSAKPAPPKPEPKPKKTPAKKAEKVPKGKKGKADVDTHGHLGTKALWC
GKTNLFLCPLLPFHLSA

FIGURE 31

TAGCTAGGCAGGAAGTCGGCGCGGGCGGCGCGGACAGTATCTGTGGGTACCCGGAGCACGGAGATCTCGCCGGCT
TTACGTTCACCTCGGTGTCTGCAGCACCCTCCGCTTCCTCTCCTAGGCGACGAGACCCAGTGGCTAGAAGTTCAC
C**ATG**TCTATTCTCAAGATCCATGCCAGGGAGATCTTTGACTCTCGCGGGAATCCCACTGTTGAGGTTGATCTCTT
CACCTCAAAAGGTCTCTTCAGAGCTGCTGTGCCCAGTGGTGCTTCAACTGGTATCTATGAGGCCCTAGAGCTCCG
GGACAATGATAAGACTCGCTATATGGGGAAGGGTGTCTCAAAGGCTGTTGAGCACATCAATAAAACTATTGCGCC
TGCCCTGGTTAGCAAGAAACTGAACGTCACAGAACAAGAGAAGATTGACAAACTGATGATCGAGATGGATGGAAC
AGAAAATAAATCTAAGTTTGGTGCGAACGCCATTCTGGGGGTGTCCCTTGCCGTCTGCAAAGCTGGTGCCGTTGA
GAAGGGGGTCCCCCTGTACCGCCACATCGCTGACTTGGCTGGCAACTCTGAAGTCATCCTGCCAGTCCCGGCGTT
CAATGTCATCAATGGCGGTTCTCATGCTGGCAACAAGCTGGCCATGCAGGAGTTCATGATCCTCCCAGTCGGTGC
AGCAAACTTCAGGGAAGCCATGCGCATTGGAGCAGAGGTTTACCACAACCTGAAGAATGTCATCAAGGAGAAATA
TGGGAAAGATGCCACCAATGTGGGGGATGAAGGCGGGTTTGCTCCCAACATCCTGGAGAATAAAGAAGGCCTGGA
GCTGCTGAAGACTGCTATTGGGAAAGCTGGCTACACTGATAAGGTGGTCATCGGCATGGACGTAGCGGCCTCCGA
GTTCTTCAGGTCTGGGAAGTATGACCTGGACTTCAAGTCTCCCGATGACCCCAGCAGGTACATCTCGCCTGACCA
GCTGGCTGACCTGTACAAGTCCTTCATCAAGGACTACCCAGTGGTGTCTATCGAAGATCCCTTTGACCAGGATGA
CTGGGGAGCTTGGCAGAAGTTCACAGCCAGTGCAGGAATCCAGGTAGTGGGGGATGATCTCACAGTGACCAACCC
AAAGAGGATCGCCAAGGCCGTGAACGAGAAGTCCTGCAACTGCCTCCTGCTCAAAGTCAACCAGATTGGCTCCGT
GACCGAGTCTCTTCAGGCGTGCAAGCTGGCCCAGGCCAATGGTTGGGGCGTCATGGTGTCTCATCGTTCGGGGGA
GACTGAAGATACCTTCATCGCTGACCTGGTTGTGGGGCTGTGCACTGGGCAGATCAAGACTGGTGCCCCTTGCCG
ATCTGAGCGCTTGGCCAAGTACAACCAGCTCCTCAGAATTGAAGAGGAGCTGGGCAGCAAGGCTAAGTTTGCCGG
CAGGAACTTCAGAAACCCCTTGGCCAAG**TAA**GCTGTGGGCAGGCAAGCCCTTCGGTCACCTGTTGGCTACACAGA
CCCCTCCCCTCGTGTCAGCTCAGGCAGCTCGAGGCCCCCGACCAACACTTGCAGGGGTCCCTGCTAGTTAGCGCC
CCACCGCCGTGGAGTTCGTACCGCTTCCTTAGAACTTCTACAGAAGCCAAGCTCCCTGGAGCCCTGTTGGCAGCT
CTAGCTTTGCAGTCGTGTAATTGGCCCAAGTCATTGTTTTTCTCGCCTCACTTTCCACCAAGTGTCTAGAGTCAT
GTGAGCCTCGTGTCATCTCCGGGGTGGCCACAGGCTAGATCCCCGGTGGTTTTGTGCTCAAAATAAAAAGCCTCA
GTGACCCATGAG

FIGURE 32

MSILKIHAREIFDSRGNPTVEVDLFTSKGLFRAAVPSGASTGIYEALELRDNDKTRYMGKGVSKAVEHINKTIAP
ALVSKKLNVTEQEKIDKLMIEMDGTENKSKFGANAILGVSLAVCKAGAVEKGVPLYRHIADLAGNSEVILPVPAF
NVINGGSHAGNKLAMQEFMILPVGAANFREAMRIGAEVYHNLKNVIKEKYGKDATNVGDEGGFAPNILENKEGLE
LLKTAIGKAGYTDKVVIGMDVAASEFFRSGKYDLDFKSPDDPSRYISPDQLADLYKSFIKDYPVVSIEDPFDQDD
WGAWQKFTASAGIQVVGDDLTVTNPKRIAKAVNEKSCNCLLLKVNQIGSVTESLQACKLAQANGWGVMVSHRSGE
TEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLLRIEEELGSKAKFAGRNFRNPLAK

FIGURE 33

TGGTCCCAAGGCGCGTGCTTTGCAGCAGATGTGTGACCTGGCGTTCCCCTGAGTGCTCGGAAAATGGCCTTGTCT
CCGGTCGTTCCCGTTCAGGAGCAGAATTTTCCCACTGTAAAAAACCGAGCAAGTCTGGATAAGTGAGGCTGGCTC
CATGTATCCAGAATCAACGACGGGCTCCCCGGCTCGGCTCTCGCTGCGGCAGACGGGCTCCCCCGGGATGATCTA
CAGTACTCGGTATGGGAGTCCCAAAAGACAGCTCCAGTTTTACAGGAACCTGGGCAAGTCTGGCCTGCGGGTCTC
CTGCCTGGGACTTGGAACATGGGTGACCTTCGGAGGCCAGATCACCGATGAGATGGCAGAGCAGCTCATGACCTT
GGCCTATGATAATGGCATCAACCTCTTCGATACAGCAGAAGTCTACGCAGCCGGCAAGGCTGAAGTGGTACTGGG
AAACATCATTAAGAAGAAAGGATGGAGGCGGTCCAGCCTCGTCATCACCACCAAGATCTTCTGGGGCGGAAAGGC
GGAGACGGAGCGGGGCCTGTCCAGGAAGCACATAATCGAAGGTCTGAAAGCTTCCCTGGAGCGACTGCAGCTGGA
GTACGTGGATGTGGTGTTTGCCAACCGCCCGGACCCCAACACCCCGATGGAAGAGACCGTCCGCGCCATGACCCA
CGTCATCAACCAGGGGATGGCCATGTACTGGGGCACGTCACGCTGGAGCTCCATGGAGATCATGGAGGCCTACTC
CGTGGCCCGGCAGTTCAACCTGACCCCGCCCATCTGCGAGCAGGCTGAGTACCACATGTTCCAGCGTGAGAAAGT
GGAGGTGCAGCTGCCGGAGCTGTTCCACAAGATAGGAGTGGGCGCCATGACCTGGTCCCCTCTGGCCTGTGGCAT
TGTTTCTGGCAAGTACGACAGTGGCATCCCACCCTACTCAAGAGCCTCCTTGAAGGGCTACCAGTGGCTGAAGGA
CAAGATCCTCAGTGAGGAGGGCCGGCGCCAGCAAGCCAAGCTGAAGGAGCTGCAGGCCATCGCCGAGCGCCTGGG
CTGCACCCTGCCCCAGCTGGCCATAGCCTGGTGCCTGAGGAATGAGGGAGTCAGCTCCGTGCTCCTGGGGGCCTC
CAATGCGGACCAGCTCATGGAGAACATTGGGGCAATACAGGTCCTTCCGAAACTGTCATCTTCCATTATCCACGA
GATTGATAGTATTTTGGGCAATAAACCCTACAGCAAAAAGGACTACAGATCCTAAGCCGCCCCCGCCCGCCTGCT
CGGACAGTTTCCGTTCCCTCCTAGTCTCTGTTCGCTCGCTTAAGCTGTTTTGAAGCCAAGTGAAGAGTGTGGTTT
GCATCCAAGAGAAAACACCACACTGTGATGTCATCGGGAAATGATCTCCCAAGTCGCTGCCAGACACCACCCACT
GCTTCGCCGGACAATGTCGAAGTCCAGTCTGTGCCGGGGAAGGCACTGGTTAGGAAGGATGTTCAAACGGTCCCA
CCCAAGCCTGTCACCTCTGCTCATCCTCCAAGACCACCCAGCTTTCTCCCAGCCACAGCCAAGATTCCCAAAGTC
AAGGCCCAAAGATTTCCAAGGTTCCCAAAGTCAAGGCCAGGCCAAGGCCTGGTTGGGTCCTTGGGGCGGGCAGGG
CCAGCCTCTCCTCTGCTGAGAATCCCCACTTGGTGTAGGGGGAGAGGGGAAAGGGGTCTGGCCCATCGAGGGGCC
CCTTCTGCCAGGGCCTTGGTTGCTGGGGCAGGGCCTCCCCACTGGGGGTCTTCCTCCACCTCCCACTTTCCAAGG
GCTCCAGGAATCTGGGGCCTGACCACAGATTCCTCTCCCATCCTTTTCTGCTCCAACCTGCCCCACTGGGTCCCG
GCAGGGGCCATGCCTACCAAGCTCGAGCTGGCCCTTGACCCCCACCCACCCCCACCCTTGCTGGCAGGGGCAGGG
ACCCCAGGGGGATTGACTCTGCAGTTTGGGAGCCACAAAAAGCGTAGCGGTGTGATTTCTAGCTCAGCCTCCCAC
CGTCTTCCTCCTACACACCAATGATGAGCCTCATGCCAGTGAGGCCCGGAGCGCTTGGGAGGGGTCCCAGTGGGG
CAGGCCCCTCTGTCTGGCCACCCCTCTGTCCTGGCCCCGGAAGGCCCTGTGGTCATGTGCTCCTAGCTGCACGGT
GGCTGCTGGCCACACCACGGCAAGTGGCAGCAGGGGCCGGCCCTGTGCACAAGGATGCACTCCTCTCGGCCCCTG
TAGACTTTCTCTAAAGCCGCCCGCCAGCCCAGGCCGCTGCTCTGCACCGAGCTGGTGGGCTTGGGTTTTGTGGAG
CGCATGCTTGGACCCTTTCAGTAAGGAAGGGTCTTTGGGGTTTTCTGTGCCCATGACTTGGGGGCTGCACCCCCA
CAGCACCCCCACAATGTAGGAAAAGACCTCAGGGAACCTCTCCCTGGAAAGACGGGCAGGGCTGGTTAGCCCCTC
CCACTGCCTGACACCTGGGACAGGCTGGGCAGAGGGGAGAGAGGGCAGGACAGGCCAGAGTGACGCCCCCGTGCA
GCTTGGGCCGGAGGGCAAGGGATGCCAGTAAGTCTGCAGGTGCGGGGTGCCACCTACAGGCCCAGGCCTGTGTCC
CAAGCAGTACCCAGGCTTTGCAGACCACGCGGGGCAGGGCTCCACTGAAGCCACCCCCACCCCTCGCCAGCTAGC
TCCATAGGGAAGCCTGTGTCTCCTGCCCCCAGGGCGCACCCTCAGTGCAGGCACCTCTGTTCCCGCTTTGCCCCT
GGAGGAGCCACTATTCCAGAAGGCTCCACCCTGCCGTCCTGCGGGAGCCTGCTGTCCAGTCCTGGCCGGGCCAAG
GCCTGGGAAACTGTGAAAGTCAGAAAGGCCAGCGGGGAGAGGCTGGGGCGAGGGGAGGAGGGGGATCAGCTTCTG
CTATTACCGACCCCCCTTCATGCTGCCCCTGGCGCCTAGAACCCTTGCCCCTCCTCATAGACCAAGTCCCGGGGG
TCTCCACTCAGTCCTGCTGCCTGCTTCACCAGAAGCAGCCCTGTGAGTGTGGGGTGGGGAAGTCCCTTCCCAACG
GAGGTCCCAGCCTATGGCCCTGGGCCCAGGTGGGGGTCGCCTGCTTCCTTCCCGGACAGGGTCCTGCAG

FIGURE 34

CCTTTCTAACTCCGCTGCCGCC**ATG**GCTCCTGTGAAAAAGCTTGTGGTGAAGGGGGGCAAAAAAAAGAAGCAAGT
TCTGAAGTTCACTCTTGATTGCACCCACCCTGTAGAAGATGGAATCATGGATGCTGCCAATTTTGAGCAGTTTTT
GCAAGAAAGGATCAAAGTGAACGGAAAAGCTGGGAACCTTGGTGGAGGGGTGGTGACCATCGAAAGGAGCAAGAG
CAAGATCACCGTGACATCCGAGGTGCCTTTCTCCAAAAGGTATTTGAAATATCTCACCAAAAAATATTTGAAGAA
GAATAATCTACGTGACTGGTTGCGCGTAGTTGCTAACAGCAAAGAGAGTTACGAATTACGTTACTTCCAGATTAA
CCAGGACGAAGAAGAGGAGGAAGACGAGGAT**TAA**ATTTCATTTATCTGGAAAATTTTGTATGAGTTCTTGAATAA
AACTTGGGAACCAAAATGGTGGTTTATCCTTGTATCTCTGCAGTGTGGATTGAACAGAAAATTGGAAATCATAGT
CAAAGGGCTTCCCTTGGTTCGCCACTCATTTATTTGTAACTTGACTTCT

FIGURE 35

MAPVKKLVVKGGKKKKQVLKFTLDCTHPVEDGIMDAANFEQFLQERIKVNGKAGNLGGGVVTIERSKSKITVTSE
VPFSKRYLKYLTKKYLKKNNLRDWLRVVANSKESYELRYFQINQDEEEEEDED

FIGURE 36A

CGCGCTCGCGGGGGGCGGTGGCGCCCGGCACAGAGGGGTTAAGGGGGCGGTGCAGACGTCTCCCCGCCCATCCCG
CCCCTCGAGAGCCGCGGCGCCCCGCCCTATTTATAGCAGCGGTGCCTAGCGCGCCGCGTCTCTCCGCAGGCCCCG
GCCGCGGCGTCCTCGACAACCTATCGAAGGCGCC**ATG**GAGCGACCGGCGCCCCTGGCCGTGCTTCCCTTCTCGGA
CCCCGCGCACGCCCTGAGCCTGCTGCGCGGCCTGAGCCAGCTGCGCGCCGAGCGCAAGTTCCTGGACGTGACCCT
GGAGGCGGCGGGCGGGCGCGACTTCCCGGCGCACCGTGCGGTGCTGGCCGCCGCCAGCCCCTACTTCCGCGCCAT
GTTCGCGGGGCAGCTGCGCGAGAGCCGCGCCGAGCGGGTGCGCCTGCACGGAGTGCCTCCCGACATGCTGCAGCT
GCTGCTGGACTTCAGCTACACGGGCCGCGTGGCGGTAAGCGGCGACAACGCTGAGCCGCTGCTGCGCGCCGCCGA
CCTGCTGCAGTTCCCGGCCGTGAAGGAGGCGTGCGGGGCCTTCCTGCAGCAGCAGCTCGACCTGGCCAACTGCCT
GGACATGCAGGACTTCGCTGAGGCCTTCAGCTGCTCGGGACTGGCGAGCGCGGCGCAGCGGTTCATTCTGCGCCA
CGTGGGCGAGCTGGGCGCCGAGCAGCTGGAGCGGCTGCCACTGGCGCGCCTGCTGCGCTACCTGCGGGACGACGG
GCTGTGTGTGCCCAAGGAGGAGGCCGCCTACCAGCTGGCGCTGCGCTGGGTCCGCGCTGACCCGCCGCGCCGCGC
CGCGCACTGGCCGCAGCTGCTGGAGGCCGTGCGCCTGCCCTTCGTGCGCCGCTTCTACCTGTTGGCGCACGTCGA
GGCCGAGCCGCTGGTGGCGCGCTGCCCACCCTGCCTGCGCCTGCTGCGCGAGGCGCGCGACTTCCAGGCGGCGCG
CTACGACCGCCACGACCGCGGGCCCTGTCCCCGAATGCGTCCTCGCCCGTCCACCGGTCTCGCCGAGATCCTCGT
GCTCGTGGGCGGCTGCGACCAGGACTGTGACGAGCTGGTCACTGTCGACTGCTACAACCCGCAGACGGGTCAGTG
GCGCTACCTGGCCGAGTTCCCAGACCACCTGGGCGGAGGCTACAGCATCGTGGCGCTGGGCAATGACATCTACGT
GACGGGTGGGTCCGATGGCTCCCGGCTCTATGACTGCGTGTGGAGGTACAACTCAAGCGTGAATGAGTGGGCGGA
GGTGGCGCCCATGCTGAAGGCCCGCGAGTACCACAGCTCCTCTGTGCTGGACGGACTGCTGTACGTGGTGGCCGC
CGACAGCACCGAGCGCTATGACCACACCACTGACTCCTGGGAGGCCCTGCAGCCCATGACCTACCCCATGGACAA
CTGCTCCACCACTGCGTGCCGTGGCCGGCTCTATGCCATCGGCTCCCTGGCTGGCAAGGAGACCATGGTGATGCA
GTGCTACGACCCGGACACCGACCTGTGGTCGCTGGTGGACTGCGGCCAGCTCCCGCCCTGGTCCTTCGCCCCCAA
GACTGCGACTCTAAACGGACTCATGTACTTTGTCAGGGATGACTCCGCTGAGGTGGACGTGTACAACCCGACGAG
GAACGAATGGGACAAGATCCCGTCCATGAATCAGGTAAATTTTCAGGCGGGCCAGCATTGGAAGCACAGGCTGGT
CCTGATTTTGCAACCCAAGTGTCATCGTGATGAGTGTTTGGGATCCACAGCCATGATGGATGGGTCTCATCTCAA
T**TAA**TAGAAGGCTGCTCTTACCCTTATTTTGCACTTAAGGCTCACTGAGACACAGATGTTAAGTAATACCCTATG
ATTACACAGCTTAGTACACATTTGAGCAGTGTTTATTGAGTATCTGCTGTGAGCCAGAGAGCAGAAGGAAGTGAG
GGAGCAAGGCATACAGTCATCTGGGGACACCTGTTCCAGAGAGGGACAGCAGGTACAGAGGCCCTGCAGCAGGGC
ACCCTGGCGTGTTCTTAGATACACCAGCAGCCCATGTGGCCGGAGCAGAGTCAGCATGAGGTCTGTGACCTACCT
TTTTTATTTTTGAGACAGGGTCTTGCTCTGTCACCCAGGCTGGAGTGCAGTGGTACAATCATGGCTCACTGCAGC
CTCCACCTCCTTGACTCGCAGTCCTCCCACCGCACCTTCCTGAATAGCTGAGACTACAGGCGTGTGCCACCACAC
CCAGTAATTTTTTTTCTCATATGTAGATACAAAAGGATATTCTTAAAATTTTTATAGAGACAGGGTCTTGCTGTG
TTACCCAGGCTGGTCTCACACTCCTGGCCTCAAGTGACCCTCCTGTCTCAGCCTCCCAAAGTGCTAGGATTATAG
GCGTGAACCACCACGCCCAGCTGGTTCCTGAGGAAGTCAGTGTGGGAATACTTTTTTTTTTTTATACGGAGTCT
CGCTCTGTCACCCAGGCTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAAGCTCCATCTCCCAGGTTCACGCCA
TTCTCCCGCCTCAACCTCCCGAGTAGCTGGGACTACAGGTACCCACCACCACGCCCAGCTAATTTTGTTTGTGTA
TTTTTAGTAGAGACGGGATTTCACTGTGTTAGCCAGGATGGTCTGGATCTCCTGACCTTGTGATCTGCCTGGCTC
AGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCATGCCCAGCCCACTGTGGGAATACTTGTGTTGAGCAC
TTGCTGTGTGTTCTGAATAGGACAACCAGGGTCCACCCCTTCTCTCTGGGCTTGTTGAGAAGAGGGGTGCCCAGC
CTGACAGTGATGGGACAGGGAGGCTTCAGTGCCATTTGGCCATGTGAGCAGTGTTAGTCTGAGGTACACATCATA
TTGCCTACAGCCTTCTTTCCTGTGTGTCTGTTAACATTTCCAAACCTACACTCCGTGACATCCAGCCTCACAGCT
TACATCACAGCTTAATGTCCTGGCATTTAAGAGACCCAGCGTTCTGTTTTCCCCGCAGTAAGCTGCACATAGTCA
TAGCGAATTTGGGAAAGATGGAAGGAATCATCCAGCCTCGCGGTTCAGAGCCCAGCTCTGCCACTGTCAGCCATG
CAAGCCTCAGTTTTCCCATCTGTAACATGGGGAGAACAGCACTGCTCAGCCCAGAGGGCCACTGCAGAGATTCTG
AGAGAGAACGTAGGAAGCGCTGCTCGGCACGACCTGCACACGGGGAGGCCTGGCGCTGCAGCGGGCACCCTCATC
ACCATAGGGAAGGCCCAGCTGCCTCCGGGGAGGCCCGTTCTCCTAGGCAGGGTGTTGGAAAGGGGTTGGCCTCTC
TGCTGCTTTCTGGGAGAGCCAAGGCCACCCCTCTGGGGTACTGACAGGGCATGCCTTGTCTCCAGTGGTTCCCCA
GGTGGGGCCCTGCCCTACCCTCTCCTCTGACCTCCACTCACTCATCCCTTTGGCCCACAGGTACATGTGGGGGGC
AGCCTGGCCGTCCTTGGGGGGAAGCTGTACGTCTCTGGGGATACGACAATACATTTGAACTCTCGGACGTGGTA

FIGURE 36B

GAGGCCTATGACCCAGAGACTCGCGCGTGGAGCGTGGTGGGGCGGCTCCCAGAACCCACCTTCTGGCATGGCAGT
GTCAGCATCTTCCGCCAGTTCATGCCCCAGACCTTCTCGGGTGGGCGTGGCTTCGAGTTGGACAGTGGCAGCGAT
GACATGGACCCAGGCCGACCCCGGCCGCCGCGGACCCCGATGAGCTGCACTAGCCCCAGTCTGGCCCGGCACGG
GCCTCGGTGCAGGTAACTGGCACCTCTGCGGGGCAGTGCCCCACTCCTTTGTGCACAAGGACACGTTGGGCTCAC
AGGAGGAGCACAGGCTCTTGGGTGGCGAAGCCAGCCCAGGATCCATTACCTGGAAGGTTTCTGTACCTTGAGAGC
CTGAATCAGAGGCCGTCGGGAACGCCCTCCCTGCAGTTGAGGAAGAGCCACTTTCCTGCCAGCACATGTTTCTGG
GTCTTGGAGGTCACCCCCACCCCGCGGATCACAGCTCACCCACGCGGCGCACACCCCTCCTGCCGTTGTCATCTG
CACCTACTTGTTCCCACCTTGGGAGAGGACGATGACTTGGGAGGGACGCGTGAAGGGAGAAGGGGTCCTCCCATG
AGGCTGAGGATGGCCTGAACCTGGAGCAGCGGACCAGGCAGACGGGCTGAAGTGGGGTCCCAAATTCCATGTCCA
GAGGTGTGGGGAGCCTGCCTCCCTAGCTCCTGGCCCCTGCCAGGGGCTTACATCAAAACACCTCAGAGGGCTGCC
CTCCAGAGGCTGCACCCAGAACAGTGGGACATGAGCAGGGGTGTGGGCTTGGAGGGTGAAGAGGATGTGGTCCTA
TCAGATGCTGGGCCTCCTCAGCCATAGCCCCCTGCTCCTACCCCCTGACTGGCTCTTGCGTCCTCACCTCTCACC
CTCTCCTTCCCGGGAGGCCCTGGGAGGTGATCATTGACACCCAGCCAAGCAGACAGCTGCGGGTGCCCAAGCCCT
TGCTGGGCCTGCGCGTGAGGAGTCCCACTGCTTCTAAAGGAAGTCCTGGGCAGGAGGTGGCTTTGGTGGTTGGTT
CCAAAGTTGAAAATGCTTGCAGTTTGACCTTAGAAGAAGTGGGAAGAAGAAGGAGCTCTACAGGGTCAGCTTTGT
TTGATTTGTCCAGTCTAAGAAGTCCCATTGCCAAAGCTTTCTGCAGGAGGGTGAATGCCGCAGCTTGGCAGCCCC
TGGGTTTCTCTTGGAAATGGTCAGTTTCCCCTCAAAGTACCCAAAGTAGCCTTGGCTTGAGTTTTTGTCCTTGCC
TCCTTTTTAGAGAAGAGGGCATTTAGACTGCATTTTCCTGGTTAAAGAAGGTTAAAGCAAATGTTTATTGCCTTT
TCTAGTGAACTAACTCGTAGAGATGTTCTCAGCAGGAAGACAGTCTTAGCACTGTCACTTAGCAGATTGCACTTA
AGTCCCTTGTGCTGGCCAGATGGCGTGGCTGGTTGCCTTAATATGTCCCAGGACCCCTGACAGGGCTGCCTGGCC
TCTCCCTCGTGCTCCTCAAGAGCCCAGTCCATACACTGTGGATGTCATTGCTGTCGGGTTAGGAAGTCTTGTCCT
AGAACGCCCTGGCTGGTATGACCACAGTTCATGGCGGCTCTTCTCGCTTGGGTCATGGTCATCTTCCAGCACCTG
CTGTGCTGGGAAGGCCGAGGATGGGGGCCCAGCACTGTCCAGGCCTGCTGGGGCCTGGCTGGGAGTCCTGTGGGC
AGCATGGAACATGCAGCTGGGCTTCCTGTGACCAGGCACCCTCTGGCACTGTTGCTTGCCCTGTGCCCTGGACCT
TTTCCTGCCCTTCTCCTTCCTCTGCTCCCTTGGGGCTACCCCTTGGCCCCTCCTGGTCTGTGCAAACTCCCTCAG
GGAGCCCCCCTGCCCTGTAGCTCTCGCTTAACTTCCTAGGGGCTGCTGAGCCCACCCAGAGGTTGTTGGAGTTCA
GCGGGGCAGCTTGTCTCCCTTGTCAGCAGGGGCGTAAGGGCTGGGTTTGGCCATACAAGGTTGGCTACGCCCTCA
ATCCCTGACCGTTCCAGGCACTGAGCTGGGCACCCACGGAAGGACATGCTGTCCAGACTGTGATGACTGCCAGCA
CAGGGCATCTCGGGCTTGGCTGGTCTGCGAGGCCTTGCCCCTGTGGAACTCTGGGTTCCTGTTTTCTCAGTCTTT
TTTGCGGCTTTGCTGTGGTTGGCAGCTGCCGTACTCCAGGCTTGTGTCGGCCACTCAGATGAGGGCTGTGGTGCG
AGCCAGTGCAGGAGAGCTGCGCTTGGGATTGTGCCCTCTCCTGTGTCTGTCCTCCGGACCTACCCAGGTCTCCAC
CATCAGGACCCTGTCTTTGGGTTTAGAAGACCAAGTATGGGGAAAACCAGGCACCAGCCTCTGCAGCAATGGGTC
CCTCTAGCCTGTGGACACCAGCTGGGGGATCCAGGGTCAGGCCCCCTCCTCTCCCCAGTTTCCCTCTGCTGTGGG
TTCTGGGCTGTCATGTCTCCACCACTTAAGGATGTCTTTACACTGACTTCAGGATAGATGTTGGGATGCCTGGGC
ATGGCCACATGTTACATGTACAGAACTTTGTCTACAGCACAAATTAAGTTATATAAACACAGTGACTGGTATTTA
ATGCTGATCTACTATAAGGTATTCTATATTTATATGACTTCAGAGACGCGTATGTAATAAAGGACGCCCTCCCTC
CAGTGTCCACATCCAGTTCACCCCAGAGGGTCGGCAGGTTGACATATTTATTTTTGTCTATTCTGTAGGCTTCC
ATGTCCAGAATCCTGCTTAAGGTTTTAGGGTACCTTCAGTACTTTTTGCAATAAAAGTATTTCCTATCCATTTGG

FIGURE 37

MERPAPLAVLPFSDPAHALSLLRGLSQLRAERKFLDVTLEAAGGRDFPAHRAVLAAASPYFRAMFAGQLRESRAE
RVRLHGVPPDMLQLLLDFSYTGRVAVSGDNAEPLLRAADLLQFPAVKEACGAFLQQQLDLANCLDMQDFAEAFSC
SGLASAAQRFILRHVGELGAEQLERLPLARLLRYLRDDGLCVPKEEAAYQLALRWVRADPPRRAAHWPQLLEAVR
LPFVRRFYLLAHVEAEPLVARCPPCLRLLREARDFQAARYDRHDRGPCPRMRPRPSTGLAEILVLVGGCDQDCDE
LVTVDCYNPQTGQWRYLAEFPDHLGGGYSIVALGNDIYVTGGSDGSRLYDCVWRYNSSVNEWAEVAPMLKAREYH
SSSVLDGLLYVVAADSTERYDHTTDSWEALQPMTYPMDNCSTTACRGRLYAIGSLAGKETMVMQCYDPDTDLWSL
VDCGQLPPWSFAPKTATLNGLMYFVRDDSAEVDVYNPTRNEWDKIPSMNQVNFQAGQHWKHRLVLILQPKCHRDE
CLGSTAMMDGSHLN

FIGURE 38A

CCCGCGGCCGAGCCGGCGCGGGCCCCCGCACCTCCCCCGCTCGCGCGGCCTCGAGTCCAGAAGACCCGCCTCCAC
ACACCGGGGCCGCCGCCGCGGAGCCTCATGGGGGTTGGAGTCCCCAAGGTTTCCTTTGTGCGCAGTATTGGCGGG
GCCTTGGACTACCACTCCCACAAGGCACCGCGCCCGCCTCCCGCGCCACGCCCCCTCGCCGCTGGCTTCCAGTCG
CCACCCAGACTACATTTCCCGACAGGCCTCCCGGCTCTCCCGCCCTCCCTCCCGAGACACGAGCCGAACTGGGCG
TCAGGTCGGGGAGCCGGTCGGGTTCCCGCTCACCGCCGCCGCCGCCGCCCCCTGCAGCCACTCTCCCGCCTCTAC
CGCCGCGGGAGCTGCATCGTCCACTCCGGTCGGCGGTGGAACCGCCAGTCCGGGGTCACAGAGCTTGAGAAGCGA
CGCGCTGAGCCCCCCATCACCTCCAGCCCGGGCGACCCCTCCCGGGTCCGCCCTCGCCCTGCGCAGCCGCCCGAG
CCCCCAGCCCCGGGCGGCCCCGCTCCAGCATCCCAGCTCCTGCACTCTCGCAGCCGCCGCCGCCCCCCGCCCGGA
ACATGGACTCTGACTCTTGCGCCGCCGCCTTCCACCCGGAGGAATACTCCCCCAGTTGCAAGAGGCGCAGGACCG
TGGAAGACTTCAACAAATTCTGCACCTTTGTCTTGGCCTATGCTGGCTACATCCCTTATCCGAAGGAGGAACTCC
CTTTAAGGAGCAGCCCCAGCCCTGCTAACAGCACTGCTGGTACCATTGACAGCGACGGCTGGGACGCGGGTTTCT
CAGACATCGCGTCCTCAGTGCCCTTGCCAGTCTCTGACCGCTGCTTTAGCCACCTGCAGCCTACTCTCTTGCAGC
GAGCCAAGCCCAGTAACTTCCTGCTGGACAGAAAGAAAACGGACAAGCTGAAGAAGAAGAAGAAGAGGAAGCGCA
GGGACAGTGATGCGCCTGGGAAAGAGGGGTACAGGGGGGGCTTGCTGAAGCTGGAAGCCGCTGACCCCTACGTGG
AGACCCCCACGAGTCCCACCTTGCAGGATATCCCCCAGGCTCCCAGCGACCCCTGCTCGGGCTGGGACTCCGATA
CTCCCTCGAGTGGATCTTGTGCCACTGTGTCACCTGATCAGGTCAAAGAAATAAAAACTGAAGGCAAACGGACTA
TCGTCCGGCAGGGAAAGCAGGTGGTGTTCCGAGATGAGGACAGCACTGGCAATGATGAGGACATCATGGTGGACT
CAGATGACGATTCCTGGGACCTCGTGACCTGCTTCTGCATGAAGCCATTTGCCGGCCGCCCCATGATCGAGTGTA
ATGAGTGCCACACCTGGATTCACCTGTCCTGTGCGAAAATCCGGAAATCCAATGTTCCAGAAGTGTTTGTCTGCC
AAAAGTGCCGGGACTCCAAGTTTGACATCCGCCGTTCCAACCGCTCGCGGACGGGCTCCCGGAAGCTGTTCCTGG
ACTGACTGCTGGCTGGCGAGGAGGCTGCGAGCGTGGAATCGGAAGCGACCGCGGGCTTTTTTGCCCTTCTCTTAG
TTGAGCACAGAACCCTCAGCTCTGGTGCGGGCAGATCCCTGCCATTTAGGTGCCTAAGCAAAAGGACAGGCTGTC
CAAGGTAGAAACTGTACATAGCCGGTGACCGAATGCGACCTTTGCCAGCCAGAGCTGCTGCCAGAGCTGCGTTCC
CTGCAGTGGAGGTGGACTGGACACCCACGTGCAGCGGGTTTGGCTCATTTGAAAATGAGGGTCCGTGGTAGCTGT
GCGTTTTGCTATCATTGCTAAGAGATTCCCGCTGATTGGGCTCAGTGCCAGCTGTTATTCTGCTTCCACTGTGTT
GGGGAGAGGTGTTCGGTTTCCCCAGCCTGTTAATGAACAGCCATACGTGTAAGCTTTTTCTTGAGTGTTAAGTCT
TTTACCAAAAGTGTCTGTACAGCAGCCATCCAAGTTGCCCCTACTTAGTGGCTTGCCCTCTGCCTGCCTCAGCTG
CTGCCTGACCGGCTGGGGGAGGCACTGGCGGGAGGCCTCGGGCTCCCCTGGAAGGGCGCTGGGCTGGCGGGTCAG
CTGGTGGTTCTTAGGTTTCCTTCTGTTTGTTAAAAGGGACAATGTGGCCACTTCTCTGTGGAAAGGGAGTTGGTT
GGGGGGTTGAGATGGCCCGTGTTCATAACTCAGTTTCCTGTTTTGCACGATGTAAAAACCCTGTCTTTTTGCACG
ATACAGCCAAAAGTATTGGCTGATTTCTTGCTGAGTGCCCTCTTAGTTGGTGTGTGAGGTCTTGGTGGGCTCAGG
CCAGCTGTTTGCGAGTGTGGGAACTCATAGGTTCTGTCTTTGTCTCTTCCTTTCACCTCATTCTGGTAGCAGCAT
AAAGGTTAGGCAATCACTGGGACCCGCATGGTGTTCCTCCAAAGAATAGGGTAAAGGAGAGCTGGGAGGGAGCCC
TCTCCGTTGGGTGACTCTTGTGTGCCCTTTAGACAGGCTGGCCTGCCGGTTCCACAGGGTACAGTTAGGACTTGA
GTCTTTCTTTTTCTGTTTTGAGTTGGTGAGTGAGTGATAGGGTAACATGGGCCTTCAGGATGACCCCTTGGAACT
GTGCCGAGTTCCTTAAATCTCAGCTGGGATCCTGGACCTGGGAGGCCCCTGTGAGGGCCAGCTCTGGAAAAACCT
GGGAGTTGATGCCGGAGGCTGTGGAAGAACTCTGCTCGAGGGCAGGGTGCCCTGGAACACTGGTAGTTCTGGGGC
TGGGAGGGAGAGGGGCTCCGGCTTTCTCTGAAATGAACACTGCTCTTCAGCAGTTCAAGTACTTGTTCTCAAAAC
ATTTTCTAATTGATTGGTAGGTTTTCATAAGCATTGTTTCTTTAAGGCATGGAAAGGGAAGAATGCTCAAGCAAG
TCATGTTTGTTTTCAGTGGGATGGGCCCGCGTTCTCACTGCTGGGGGCTTCCCCTTCATGTGGCACCTTTGTGCC
AGGCCACCAGGCAGACTCTTCCCACCTTCTCCCACTGAAGCACCAAGGGGGCTTGAACCGTAATTTGGCTAATCAG
AGGCATTTTTTTTGTCCTAGTATCTTTCACACTTGTCCAACCGTCTTATTTTTTTAAAAGTTCTGTTGCTTGTAT
TAACACGAAACTAGAGAGAAATAGTTTCTGAAGCCAGTTTATTGTGAAGATCCCCAAGGGGGAGGTTCGGTAGAG
AAAAATAGTAAGCTGGTTTAGAAACTGACGAGGGCAAACAGCCAGGACGCATTGGAGAGGAATTTGCCAAAGATC
TACCCTGAGATAACGCCTGTCCAGTGTCTTCACCACGTGAATAACCAGCGCTCCAAAGTGTTTTTCTGCTTTGAA
AAAAAAAAATTCCACAAGCTTTTAAAGGTGCATTTAAGAATCCATGTGACTTTAGAATGGAACTGCCGGCCCTGG
CAACTGTCACGTGTGCTAGAAGGTTCGATGCCTCTGGAATGCATGTGATACTCATCTCCATTTTGTTTCCTTGAT
TGCATTTTTGTTCTTTAGCAGATCTGTCCCTGTGGGTGGTGTCTAAGAAGTCGGACACCTTGGTTTTTGTGTTA

FIGURE 38B

GATTGAGCTGGGCAGCTGCAATCAGCTTCTTTATATGCAAATTAGGCACGACCCATCTGTGGTTCCTGGTTGGTG
GCTAATGAAGTGAGGGGAGGGAGGGATGTCACCCCAAAAGTAGGCCCTCCCATTGGCTTTGGCCAGGCCAGACAC
TTCACATCGTTTACATGGTTCTGTGTAATTTTAAAGTTTATGTGTATAAAGCGAAGCTGTTTCTGTGAAACTGTA
TATTTTGTAAATAAATATATTGCTACTTTGAGGTTCATGATTCAAGGTTCAGGCGATTGCGTTCTGTGCTGAAGG
A

FIGURE 39

MDSDSCAAAFHPEEYSPSCKRRRTVEDFNKFCTFVLAYAGYIPYPKEELPLRSSPSPANSTAGTIDSDGWDAGFS
DIASSVPLPVSDRCFSHLQPTLLQRAKPSNFLLDRKKTDKLKKKKKRKRRDSDAPGKEGYRGGLLKLEAADPYVE
TPTSPTLQDIPQAPSDPCSGWDSDTPSSGSCATVSPDQVKEIKTEGKRTIVRQGKQVVFRDEDSTGNDEDIMVDS
DDDSWDLVTCFCMKPFAGRPMIECNECHTWIHLSCAKIRKSNVPEVFVCQKCRDSKFDIRRSNRSRTGSRKLFLD

FIGURE 40

GACGGCTCCGGGCCGCCAGGGGCCGCTGTGGCGCAGCCGGGCTGGCCCGCGCTGTCCCTGACGCGGATCACTGGC
CCCTCTTGAGCACGGCCTTGCCGGTTTGGCGGGGTGAAAGGTTGCGAAGATGGCGACGGCCTTGAGCGAGGAGGA
GCTGGACAATGAAGACTATTACTCGTTGCTGAACGTGCGCAGGGAGGCCTCTTCTGAAGAGCTGAAAGCTGCCTA
CCGGAGGCTCTGTATGCTCTACCATCCAGACAAGCACAGAGACCCAGAGCTCAAGTCACAGGCGGAACGACTGTT
TAACCTTGTTCACCAGGCTTATGAAGTGCTTAGTGACCCCCAAACCAGGGCCATCTATGATATATATGGGAAGAG
AGGACTGGAAATGGAAGGATGGGAGGTTGTGGAAAGGAGGAGAACCCCTGCTGAAATTCGAGAGGAGTTTGAGCG
GCTGCAGAGAGAGAGAGAGAAGAGAGGAGATTGCAGCAGCGAACCAATCCCAAGGGAACGATCAGCGTTGGAGTAGA
TGCCACCGACCTTTTTGATCGCTATGATGAGGAGTATGAAGATGTGTCCGGCAGTAGCTTTCCGCAGATTGAAAT
TAATAAAATGCACATATCCCAGTCCATTGAGGCACCCTTGACAGCGACAGACACAGCCATCCTCTCTGGAAGCCT
CTCAACCCAGAATGGAAATGGAGGAGGTTCCATTAACTTTGCGCTCAGACGAGTAACTTCGGCAAAGGGATGGGG
AGAGTTGGAATTTGGAGCTGGAGACCTACAGGGGCCTTTGTTCGGTCTCAAGCTGTTCCGTAATCTCACACCAAG
ATGCTTTGTGACAACAAACTGTGCTCTGCAGTTTTCATCCCGTGGAATCCGACCCGGCCTGACCACTGTCCTAGC
TCGGAACCTAGACAAGAACACCGTGGGCTACCTGCAGTGGCGATGGGGTATCCAGTCAGCCATGAACACTAGCAT
CGTCCGAGACACTAAAACCAGCCACTTCACTGTGGCCCTGCAGCTGGGAATCCCTCACTCCTTTGCACTGATCAG
CTATCAGCACAAATTCCAAGATGACGATCAGACTCGTGTGAAAGGATCCCTCAAAGCAGGCTTCTTTGGGACGGT
GGTGGAGTACGGAGCTGAGAGGAAGATCTCCAGGCACAGCGTTTTGGGTGCAGCTGTCAGCGTTGGAGTTCCACA
GGGTGTTTCTCTCAAAGTCAAGCTCAACAGGGCCAGTCAGACATACTTCTTCCCTATTCACTTGACGGACCAGCT
TCTGCCCAGCGCCATGTTCTATGCCACCGTGGGGCCTCTAGTGGTCTACTTTGCCATGCACCGTCTGATCATCAA
ACCATACCTCAGGGCTCAGAAAGAGAAGGAATTGGAGAAGCAGAGGGAAAGCGCCGCCACCGATGTGCTGCAGAA
GAAGCAAGAGGCGGAGTCCGCTGTCCGGCTGATGCAGGAATCTGTCCGAAGGATAATTGAGGCAGAAGAGTCCAG
AATGGGCCTCATCATCGTCAATGCCTGGTACGGGAAGTTTGTCAATGACAAGAGCAGGAAGAGCGAGAAGGTGAA
GGTGATTGACGTGACTGTGCCCCTGCAGTGCCTGGTGAAGGACTCGAAGCTCATCCTCACGGAGGCCTCCAAGGC
TGGGCTGCCTGGCTTTTATGACCCGTGTGTGGGGGAAGAGAAGAACCTGAAAGTGCTCTATCAGTTCCGGGGCGT
CCTGCATCAGGTGATGGTGCTGGACAGTGAGGCCCTCCGGATACCAAAGCAGTCCCACAGGATCGATACAGATGG
ATAAACTGCCAAGAACCAGATTTTTAAAAGGCCGCAAAAAATCTTTTCCTGGGAGTCTACAAATTTGGAAATGAA
AAAACCCAGACATCAGATGTTTTTATTTTATATTATTATTATAGAAGGTGGTACCATTATCAATTATGTGAAGGG
ACATGCAGACACCCCAGCTTTTGAGGGTGCTGGGGGTAGGACTGAGGCAGCCCCACTGGGAACCAGACTGCAGCC
TGGCCCATGGCTGTTTTCCCAAGGATCAGTTCCTGGAGGGAAGGGCTCTGGCCCTGACTCCGCTGTGTCCCGAGC
ACACGTGCTGACCGCAGCCCGCCGCCCTGTAGTTCTTGGCTGGGTCTGGAGGTGTCTGTGGAGCACCCTGCCCTC
ACCACAGGAGCGTGAGCCACTTCTGCAGTCCACGCTGAACATGGGAAACAACCTGAAAAGCAGGCAGGCCTCCCG
GTCAGGGAGCCTCTGCTGTGCTGGCTTCCCATGACCACCTCCTCTTGCTGAAATATTACTGCTTGAATCTGGAGC
AGATTGCGGGTTTATAAAACTGCTTTTTATCTGAGAACAAACGGGTTTGGAAATTAGTCGTCTTTTTTCCCCACT
CCCAGAGCTGCTCAAGTCATTCCACCGGCCCCCTCGGCTTGGGACAGGGTAGTGTAACTCCCGATCCCAGGGCCT
AGCCCTGACACAGGTGGCTTCCCGTATCCCGGTGGGAAAACGCCCTGCCACCAGCGGGCTTGAGCTGGCCTGTGT
CCCTCCACCGCCTGCACCACCCACCTCCAGAGTGCAGTGCTGGGCAAGGGCAGCTCAAGAGGACAGGACCAGGCG
CTTGGCAAGACATCAGACACACCCAACCCAAAGGCGTGGACCCCAGGCCCGGCCCGTGGTACCCAGCAGGTGGCA
CTGCAGCTCCCCGCTCCTGCAGGTCCAGCGTCCTCACAGGAACACCAGGGCCTGTGCTCCGGAGCCTTCCTTCAG
ACCCTTCCTCCACGTGCCCACTTGGGATGCAGAATGCAGCGGAGCTAGGACCCCCTCCACGGCCTGGACCTCGGC
TGCAGTAAAGTTACGTGAGGCCTGTCTCTCGGGGCCTGGAAGTGGCAGCCATCAGTTGCTCTTGCTGACCCCTCG
GAGCAAGCGCCGCACAGGTGGTGGCTGAGACAGCTGGCGCGGGGGGCCCCAAGCTGCGCCGGCCTCCAGCCCACC
CACAGCTGTTGCTGAAGTCAGGCCTCCCTCCCCAGCACTGGTATCTGAGTAACGGCTAAGAACCTCCTTCCTCTG
GTTTTGAAAAGCAGTTCGGGTTGTCCAATTCTGTAACATTCATCTCCATTTTTTAAAAAGGTTTCTCTGACGGCC
CCACGGCCCGAGCCGCGGTGAGCGTCGTGTTGCATGAGCCTGGGCCCCGGGCTTCCCGTGCGCCTCTGCCGCAGG
TGCTTCTGGGCACCCATCCTCTGCGTTTCATTTGCAGTCGACTGTACAGAAGGCACTCACCACAATAAACCTTTC
CTGAAAGC

FIGURE 41

TGCGAGGCAGAGTGCTAGCGGGAGCGCGAGCCAGCAAGAGGCGCCTGCGCGATGTCCGGGCCCCTGAGCCCGCGG
CGCTGAGCCAGCCGGGACGGACATGCGCGGGAGGGCGCCGCGGGGCAGCCGCCGCTCCTCCGGGGGAATGAAAGC
TACTGGTTGATTTTAAAGTGCCTGGGCCTCACAGGTTTGGAGATGTCCCAGAATAAGGCACAATGTCAATAGCAG
GAGTTGCTGCTCAGGAGATCAGAGTCCCATTAAAAACTGGATTTCTACATAATGGCCGAGCCATGGGGAATATGA
GGAAGACCTACTGGAGCAGTCGCAGTGAGTTTAAAAACAACTTTTTAAATATTGACCCGATAACCATGGCCTACA
GTCTGAACTCTTCTGCTCAGGAGCGCCTAATACCACTTGGGCATGCTTCCAAATCTGCTCCGATGAATGGCCACT
GCTTTGCAGAAAATGGTCCATCTCAAAAGTCCAGCTTGCCCCCTCTTCTTATTCCCCCAAGTGAAAACTTGGGAC
CACATGAAGAGGATCAAGTTGTATGTGGTTTTAAGAAACTCACAGTGAATGGGGTTTGTGCTTCCACCCCTCCAC
TGACACCCATAAAAAACTCCCCTTCCCTTTTCCCCTGTGCCCCTCTTTGTGAACGGGGTTCTAGGCCTCTTCCAC
CGTTGCCAATCTCTGAAGCCCTCTCTCTGGATGACACAGACTGTGAGGTGGAATTCCTAACTAGCTCAGATACAG
ACTTCCTTTTAGAAGACTCTACACTTTCTGATTTCAAATATGATGTTCCTGGCAGGCGAAGCTTCCGTGGGTGTG
GACAAATCAACTATGCATATTTTGATACCCCAGCTGTTTCTGCAGCAGATCTCAGCTATGTGTCTGACCAAAATG
GAGGTGTCCCAGATCCAAATCCTCCTCCACCTCAGACCCACCGAAGATTAAGAAGGTCTCATTCGGGACCAGCTG
GCTCCTTTAACAAGCCAGCCATAAGGATATCCAACTGTTGTATACACAGAGCTTCTCCTAACTCCGATGAAGACA
AACCTGAGGTTCCCCCCAGAGTTCCCATACCTCCTAGACCAGTAAAGCCAGATTATAGAAGATGGTCAGCAGAAG
TTACTTCGAGCACCTATAGTGATGAAGACAGGCCTCCCAAAGTACCGCCAAGAGAACCTTTGTCACCGAGTAACT
CGCGCACACCGAGTCCCAAAAGCCTTCCGTCTTACCTCAATGGGGTCATGCCCCCGACACAGAGCTTTGCCCCTG
ATCCCAAGTATGTCAGCAGCAAAGCACTGCAAAGACAGAACAGCGAAGGATCTGCCAGTAAGGTTCCTTGCATTC
TGCCCATTATTGAAAATGGGAAGAAGGTTAGTTCAACACATTATTACCTACTACCTGAACGACCACCATACCTGG
ACAAATATGAAAAATTTTTAGGGAAGCAGAAGAAACAAATGGAGGCGCCCAAATCCAGCCATTACCTGCTGACT
GCGGTATATCTTCAGCCACAGAAAAGCCAGACTCAAAAACAAAAATGGATCTGGGTGGCCACGTGAAGCGTAAAC
ATTTATCCTATGTGGTTTCTCCTTAGACCTTGGGGTCATGGTTCAGCAGAGGTTACATAGGAGCAAATGGTTCTC
AATTTTCCAGTTTGATTGAAGTGCAGAGAAAAATCCCTTAGATTGCAAAATAAAATAGTTGAACTCTCTGTCTTC
ATGTGGAAGGTTTAGAGCAGTTGTGAGATGCTGTTATGCTGAGAAACCCTGACTTTGTTAGTGTTGGAAAAAAGT
CTTACAAGTCTATAATTTAAAGATGTGATGGTGGGGAGGGGAGGATGGGGAAGCTTTTTATATATGCATACATTA
CATACCTATATATAAACTTGTGGTATAACCATAGACCATAGCTGCAGGTTAACCAATTAGTTACTATCGTAGAGT
AATATATATTCAGAATAATAAACTCAAGCTGGAGAAATGAGTCCTGATAGACTGAAAATTGAGCAAATGGAAGAA
GATACAGTATTGTTTAGATCAGAATCATTAAAAAATATTTTTGTTTAGTAAGTTTGAAGATTTCTGGCTTTTAGG
CCTTTTCTATTTTGTTCCATTTATTTTTGCAGGCAATCTTTTCCATGGAGGGCAGGGTATCCATTCTTTACCATG
GGTGTACCTGCTTAGGTTAAAAATCATACCAAGGCCTCATACTTCCAGGTTTCATGTTGCGTCTTGTTGAGGGAG
GGAGAGCAGGTTACTTGGCAACCATATTGTCACCTGTACCTGTCACACATCTTGAAAAATAAAACGATAATAGAA
CTAGTGACTAATTTTCCCTTACAGTTCCTGCTTGGTCCCACCCACTGAAGTAGCTCATCGTAGTGCGGGCCGTAT
TAGAAGCAGTGGGGTACGTTAGACTCAGATGGAAAAGTATTCTAGGTGCCAGTGTTAGGATGTCAGTTTTACAAA
ATAATGAAGCAATTAGCTATGTGATTGAGAGTTATTGTTTGGGGATGTGTGTTGTGGTTTTGCTTTTTTTTTTTT
AGACTGTATTAATAAACATACAACACAAGCTGGCCTTGTGTTGCTGGTTCCTATTCAGTATTTCCTGGGGATTGT
TTGCTTTTTAAGTAAAACACTTCTGACCCATAGCTCAGTATGTCTGAATTCCAGAGGTCACATCAGCATCTTTCT
GCTTTGAAAACTCTCACAGCTGTGGCTGCTTCACTTAGATGCAGTGAGACACATAGTTGGTGTTCCGATTTTCAC
ATCCTTCCATGTATTTATCTTGAAGAGATAAGCACAGAAGAGAAGGTGCTCACTAACAGAGGTACATTACTGCAA
TGTTCTCTTAACAGTTAAACAAGCTGTTTACAGTTTAAACTGCTGAATATTATTTGAGCTATTTAAAGCTTATTA
TATTTTAGTATGAACTAAATGAAGGTTAAAACATGCTTAAGAAAAATGCACTGATTTCTGCATTATGTGTACAGT
ATTGGACAAAGGATTTTATTCATTTTGTTGCATTATTTGAATATTGTCTTTTCATTTTAATAAAGTTATAATAC
TTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 42

GAATTCGGCACGAGATAAAA**<u>ATG</u>**GCTTCCAAAAGAGCTCTGGTCATCCTGGCTAAAGGAGCAGAGGAAATGGAGA
CGGTCATCCCTGTAGATGTCATGAGGCGAGCTGGGATTAAGGTCACCGTTGCAGGCCTGGCTGGAAAAGACCCAG
TACAGTGTAGCCGTGATGTGGTCATTTGTCCTGATGCCAGCCTTGAAGATGCAAAAAAAGAGGGACCATATGATG
TGGTGGTTCTACCAGGAGGTAATCTGGGCGCACAGAATTTATCTGAGTCTGCTGCTGTGAAGGAGATACTGAAGG
AGCAGGAAAACCGGAAGGGCCTGATAGCCGCCATCTGTGCAGGTCCTACTGCTCTGTTGGCTCATGAAATAGGTT
GTGGAAGTAAAGTTACAACACACCCTCTTGCTAAAGACAAAATGATGAATGGAGGTCATTACACCTACTCTGAGA
ATCGTGTGGAAAAAGACGGCCTGATTCTTACAAGCCGGGGGCCTGGGACCAGCTTCGAGTTTGCGCTTGCAATTG
TTGAAGCCCTGAATGGCAAGGAGGTGGCGGCTCAAGTGAAGGCTCCACTTGTTCTTAAAGAC**<u>TAG</u>**AGCAGCGAAC
TGCGACGATCACTTAGAGAAACAGGCCGTTAGGAATCCATTCTCACTGTGTTCGCTCTAAACAAAACAGTGGTAG
GTTAATGTGTTCAGAAGTCGCTGTCCTTACTACTTTTGCGGAAGTATGGAAGTCACAACTACACAGAGATTTCTC
AGCCTACAAATTGTGTCTATACATTTCTAAGCCTTGTTTGCAGAATAAACAGGGCATTTAGCAAACTAAAAAAAA
AAAAAAAAAAACTCGAG

FIGURE 43

MASKRALVILAKGAEEMETVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDVVICPDASLEDAKKEGPYDVVVLPGG
NLGAQNLSESAAVKEILKEQENRKGLIAAICAGPTALLAHEIGCGSKVTTHPLAKDKMMNGGHYTYSENRVEKDG
LILTSRGPGTSFEFALAIVEALNGKEVAAQVKAPLVLKD

FIGURE 44

CTCTAAAGCGCCGCAGCTGCCAAA**ATG**TCTACAGGTCCAACTGCTGCCACTGGCAGTAATCGAAGACTTCAGCAG
ACACAAAATCAAGTAGATGAGGTGGTGGACATAATGCGAGTTAACGTGGACAAGGTTCTGGAAAGAGACCAGAAG
CTCTCTGAGTTAGACGACCGTGCAGACGCACTGCAGGCAGGCGCTTCTCAATTTGAAACGAGCGCAGCCAAGTTG
AAGAGGAAATATTGGTGGAAGAATTGCAAGATGTGGGCAATCGGGATTACTGTTCTGGTTATCTTCATCATCATC
ATCATCGTGTGGGTTGTCTCTTCA**TGA**AGAACCAGCGGAACTCAAAACTGCTGTTCAAGAAACCTCTTCAAGACT
TTTGACTTAGAACCTGCTATATTATCAAGCTTACCTACTGTTATCTCTAAAATTTTTTTGTGTTAATGTAAAGT
TGAATTTCTAGGAAACGTGCCTTTGTTTTTTAATATGCACTCCAAATTAGAAGGCCGGCCCCGTCCACATTTTGC
ACAGTGCCTTTACAGATTTACGTATGGGCTGATGAAGAGGCCTTCTTAAGTTCCAGAGTGCTATAATCTAGATGT
AATGTTGTCACTAATTAATTGCCATTACTCCCCTTTAG

FIGURE 45

MSTGPTAATGSNRRLQQTQNQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKN
CKMWAIGITVLVIFIIIIIVWVVSS

FIGURE 46

GCTGCGGGTCTTTCCCTCACTCGTCCTCCGCGCGTCGCCGCTCTTCGGTTCTGCTCTGTCCGCCGCCATGGCCCA
AGCTGACATCGCGCTGATCGGATTGGCCGTCATGGGCCAGAACTTAATTCTGAACATGAATGACCACGGCTTTGT
GGTCTGTGCTTTTAATAGGACTGTCTCCAAAGTTGATGATTTCTTGGCCAATGAGGCAAAGGGAACCAAAGTGGT
GGGTGCCCAGTCCCTGAAAGAGATGGTCTCCAAGCTGAAGAAGCCCCGGCGGATCATCCTCCTGGTGAAGGCTGG
GCAAGCTGTGGATGATTTCATCGAGAAATTGGTACCATTGTTGGATACTGGTGACATCATCATTGACGGAGGAAA
TTCTGAATATAGGGACACCACAAGACGGTGCCGAGACCTCAAGGCCAAGGGAATTTTATTTGTGGGGAGCGGAGT
CAGTGGTGGAGAGGAAGGGGCCCGGTATGGCCCATCGCTCATGCCAGGAGGGAACAAAGAAGCGTGGCCCCACAT
CAAGACCATCTTCCAAGGCATTGCTGCAAAAGTGGGAACTGGAGAACCCTGCTGTGACTGGGTGGGAGATGAGGG
AGCAGGCCACTTCGTGAAGATGGTGCACAACGGGATAGAGTATGGGGACATGCAGCTGATCTGTGAGGCATACCA
CCTGATGAAAGACGTGCTGGGCATGGCGCAGGACGAGATGGCCCAGGCCTTTGAGGATTGGAATAAGACAGAGCT
AGACTCATTCCTGATTGAAATCACAGCCAATATTCTCAAGTTCCAAGACACCGATGGCAAACACCTGCTGCCAAA
GATCAGGGACAGCGCGGGGCAGAAGGGCACAGGGAAGTGGACCGCCATCTCCGCCCTGGAATACGGCGTACCCGT
CACCCTCATTGGAGAAGCTGTCTTTGCTCGGTGCTTATCATCTCTGAAGGATGAGAGAATTCAAGCTAGCAAAAA
GCTGAAGGGTCCCCAGAAGTTCCAGTTTGATGGTGATAAGAAATCATTCCTGGAGGACATTCGGAAGGCACTCTA
CGCTTCCAAGATCATCTCTTACGCTCAAGGCTTTATGCTGCTAAGGCAGGCAGCCACCGAGTTTGGCTGGACTCT
CAATTATGGTGGCATCGCCCTGATGTGGAGAGGGGGCTGCATCATTAGAAGTGTATTCCTAGGAAAGATAAAGGA
TGCATTTGATCGAAACCCGGAACTTCAGAACCTCCTACTGGACGACTTCTTTAAGTCAGCTGTTGAAAACTGCCA
GGACTCCTGGCGGCGGGCAGTCAGCACTGGGGTCCAGGCTGGCATTCCCATGCCCTGTTTTACCACTGCCCTCTC
CTTCTATGACGGGTACAGACATGAGATGCTTCCAGCCAGCCTCATCCAGGCTCAGCGGGATTACTTCGGGGCTCA
CACCTATGAACTCTTGGCCAAACCAGGGCAGTTTATCCACACCAACTGGACAGGCCATGGTGGCACCGTGTCATC
CTCGTCATACAATGCCTGATCATGCTGCTCCTGTCACCCTCCACGATTCCACAGACCAGGACATTCCATGTGCCT
CATGGCACTGCCACCTGGCCCTTTGCCCTATTTTCTGTTCAGTTTTTTAAAAGTGTTGTAAGAGACTCCTGAGGA
AGACACACAGTTTATTTGTAAAGTAGCTCTGTGAGAGCCACCATGCCCTCTGCCCTTGCCTCTTGGGACTGACCA
GGAGCTGCTCATGTGCGTGAGAGTGGGAACCATCTCCTTGCGGCAGTGGCTTCCGCGTGCCCCGTGTGCTGGTGC
GGTTCCCATCACGCAGACAGGAAGGGTGTTTGCGCACTCTGATCAACTGGAACCTCTGTATCATGCGGCTGAATT
CCCTTTTTCCTTTACTCAATAAAAGCTACATCAGACTG

FIGURE 47

MAQADIALIGLAVMGQNLILNMNDHGFVVCAFNRTVSKVDDFLANEAKGTKVVGAQSLKEMVSKLKKPRRIILLV
KAGQAVDDFIEKLVPLLDTGDIIIDGGNSEYRDTTRRCRDLKAKGILFVGSGVSGGEEGARYGPSLMPGGNKEAW
PHIKTIFQGIAAKVGTGEPCCDWVGDEGAGHFVKMVHNGIEYGDMQLICEAYHLMKDVLGMAQDEMAQAFEDWNK
TELDSFLIEITANILKFQDTDGKHLLPKIRDSAGQKGTGKWTAISALEYGVPVTLIGEAVFARCLSSLKDERIQA
SKKLKGPQKFQFDGDKKSFLEDIRKALYASKIISYAQGFMLLRQAATEFGWTLNYGGIALMWRGGCIIRSVFLGK
IKDAFDRNPELQNLLLDDFFKSAVENCQDSWRRAVSTGVQAGIPMPCFTTALSFYDGYRHEMLPASLIQAQRDYF
GAHTYELLAKPGQFIHTNWTGHGGTVSSSSYNA

FIGURE 48

CGCCGCTCCGGCCTCCCGCGACTTCTCGAAGGTGGGCAGGTCCCACCTTGTGGAGG**ATG**GAGGTGACCGGGGACG
CCGGGGTACCAGAATCTGGCGAGATCCGGACTCTAAAGCCGTGTCTGCTGCGCCGCAACTACAGCCGCGAACAGC
ACGGCGTGGCCGCCTCCTGCCTCGAAGACCTGAGGAGCAAGGCCTGTGACATTCTGGCCATTGATAAGTCCCTGA
CACCAGTCACCCTTGTCCTGGCAGAGGATGGCACCATAGTGGATGATGACGATTACTTTCTGTGTCTACCTTCCA
ATACTAAGTTTGTGGCATTGGCTAGTAATGAGAAATGGGCATACAACAATTCAGATGGAGGTACAGCTTGGATTT
CCCAAGAGTCCTTTGATGTAGATGAAACAGACAGCGGGGCAGGGTTGAAGTGGAAGAATGTGGCCAGGCAGCTGA
AAGAAGATCTGTCCAGCATCATCCTCCTATCAGAGGAGGACCTCCAGATGCTTGTTGACGCTCCCTGCTCAGACC
TGGCTCAGGAACTACGTCAGAGTTGTGCCACCGTCCAGCGGCTGCAGCACACACTCCAACAGGTGCTTGACCAAA
GAGAGGAAGTGCGTCAGTCCAAGCAGCTCCTGCAGCTGTACCTCCAGGCTTTGGAGAAAGAGGGCAGCCTCTTGT
CAAAGCAGGAAGAGTCCAAAGCTGCCTTTGGTGAGGAGGTGGATGCAGTAGACACGGGTATCAGCAGAGAGACCT
CCTCGGACGTTGCGCTGGCGAGCCACATCCTTACTGCACTGAGGGAGAAGCAGGCTCCAGAGCTGAGCTTATCTA
GTCAGGATTTGGAGTTGGTTACCAAGGAAGACCCCAAAGCACTGGCTGTTGCCTTGAACTGGGACATAAAGAAGA
CGGAGACTGTTCAGGAGGCCTGTGAGCGGGAGCTCGCCCTGCGCCTGCAGCAGACGCAGAGCTTGCATTCTCTCC
GGAGCATCTCAGCAAGCAAGGCCTCACCACCTGGTGACCTGCAGAATGCTAAGCGAGCCAGACAGGATCCCACA**T**
AGCAGCAGCGGGAAGTGTGCCAAGGAAGCTCTGTGGCGTTGTGTTATTGGTAGACACCCTCAGCCTCATCATTTG
ACTACCTATGTACTACTCTACCCCCTGCCTTAGAGCACCTTCCAGAGAAGCTATTCCAGGTCTCAACATACGCCG
TTCCACCAATTTTTTTTTTAGCCCCACCAGCTTCAGGACTTCTGCCAATTTTGAATGATATAGCTGCACCAACAA
TATCCCGCCTCCTCTAATTACATATGATGTTCTCTGTTCAAAAGTAATTGGCAGTGATTGGCCAGGCGCAGTGGC
TCACGCCTGTAATCCCAGCACTGGGAGGCCGAGGGGGGCGGATCGTGAAGTCAGGAGATCGAGACCATCCTGGCT
AACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAAAAATTAGCCAGCCATGGTGGCGGGCGCCTGTAATCCC
AGCTACTTGGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAGGCAGAGCTTGCAGTGAGCTGAGATTGCGCC
ACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAA

FIGURE 49

MEVTGDAGVPESGEIRTLKPCLLRRNYSREQHGVAASCLEDLRSKACDILAIDKSLTPVTLVLAEDGTIVDDDDY
FLCLPSNTKFVALASNEKWAYNNSDGGTAWISQESFDVDETDSGAGLKWKNVARQLKEDLSSIILLSEEDLQMLV
DAPCSDLAQELRQSCATVQRLQHTLQQVLDQREEVRQSKQLLQLYLQALEKEGSLLSKQEESKAAFGEEVDAVDT
GISRETSSDVALASHILTALREKQAPELSLSSQDLELVTKEDPKALAVALNWDIKKTETVQEACERELALRLQQT
QSLHSLRSISASKASPPGDLQNPKRARQDPT

FIGURE 50

CGGCGGAGCTGGTCCCGTTGTGCTGCGGCGCCGCGCGGCCTGCAGTCCCGGGCCCGCGCCCCGCGCCGCCCGCCC
GCCCGCC**ATG**GAGCCCGGCCCCGACGGCCCCGCCGCCTCCGGCCCCGCCGCCATCCGCGAGGGCTGGTTCCGCGA
GACCTGCAGCCTGTGGCCCGGCCAGGCCCTGTCGCTGCAGGTGGAGCAGCTGCTCCACCACCGGCGCTCGCGCTA
CCAGGACATCCTCGTCTTCCGCAGTAAGACCTATGGCAACGTGCTGGTGTTGGACGGTGTCATCCAGTGCACGGA
GAGAGACGAGTTCTCCTACCAGGAGATGATCGCCAACCTGCCTCTCTGCAGCCACCCCAACCCGCGAAAGGTGCT
GATCATCGGGGGCGGAGATGGAGGTGTCCTGCGGGAGGTGGTGAAGCACCCCTCCGTGGAGTCCGTGGTCCAGTG
TGAGATCGACGAGGATGTCATCCAAGTCTCCAAGAAGTTCCTGCCAGGCATGGCCATTGGCTACTCTAGCTCGAA
GGTGACCCTACATGTGGGTGACGGTTTTGAGTTCATGAAACAGAATCAGGATGCCTTCGACGTGATCATCACTGA
CTCCTCAGACCCCATGGGCCCCGCCGAAAGTCTCTTCAAGGAGTCCTATTACCAGCTCATGAAGACAGCCCTCAA
GGAAGATGGTGTCCTCTGCTGCCAGGGCGAGTGCGAGTGGCTGCACCTGGACCTCATCAAGGAGATGCGGCAGTT
CTGCCAGTCCCTGTTCCCCGTGGTGGCCTATGCCTACTGCACCATCCCCACCTACCCCAGCGGCCAGATCGGCTT
CATGCTGTGCAGCAAGAACCCGAGCACGAACTTCCAGGAGCCGGTGCAGCCGCTGACACAGCAGCAGGTGGCGCA
GATGCAGCTGAAGTACTACAACTCCGACGTGCACCGCGCCGCCTTTGTGCTGCCCGAGTTTGCCCGCAAGGCCCT
GAATGATGTGAGC**TGA**GCCCAGGCGCCACCACTGATGCCACCCAGGACCTCGGACCTTGGAGCCTGCGGGGTGCC
TCGGCCCCTCCAGCCCCGGGCCGGACCTCCTGCTGGCTCTCGCCCACCAACCAAGTGTTACAAGCCCCAGAATGC
TGCCCGGCCTGCCCTGCTGGGCGGACTGTCTGTGTGTCTGTCTCTCTGGCGTTCCACCTCCAAGCCTATACCAGC
TGTGTACAGCGCCATCTCTCTGCCTTCTGTTGCCCCCG

FIGURE 51

MEPGPDGPAASGPAAIREGWFRETCSLWPGQALSLQVEQLLHHRRSRYQDILVFRSKTYGNVLVLDGVIQCTERD
EFSYQEMIANLPLCSHPNPRKVLIIGGGDGGVLREVVKHPSVESVVQCEIDEDVIQVSKKFLPGMAIGYSSSKVT
LHVGDGFEFMKQNQDAFDVIITDSSDPMGPAESLFKESYYQLMKTALKEDGVLCCQGECEWLHLDLIKEMRQFCQ
SLFPVVAYAYCTIPTYPSGQIGFMLCSKNPSTNFQEPVQPLTQQQVAQMQLKYYNSDVHRAAFVLPEFARKALND
VS

FIGURE 52

AGGCGCAGGCGCAGGCGAGGGGCTGGGTGGCGGTTGAGACAGCGGCGGTACTGGGAGGCGTAGGTGAGGGTCGCG
AGGCTGCCCGAGCTTCTGAGCGAGCGCGGTGCTTTTGGGAACGCGGGACGGGCGATCTGCGGCGCCAGGAGCTGG
GCCGAGGCGCGGCGGCGCGGCTGCCGGCTGCCCTGTGAATGGGAAGTTACGCGAAGTCCACCCAGCGTTTCTGAG
GCAATCTGAAGGCAAATCCTGTTTAGACCCAGGCGAAGGTTCCCGGTGACCCGGGCTCTCACCAGCCAATTGTCC
CTTGCCGTCCTCCTGAGGGTGCCTGGAGCTTAAGCACTGTGTGCTCTTGGCCTCCACACTGGGG**ATG**CCGCTGAC
TCCCACTGTCCAGGGCTTCCAGTGGATTCTCCGAGGCCCTGATGTAGAAACTTCCCCATTGGGTGCACCAAGAGC
AGCCTCACATGGTGTGGGC**TGA**CATCAAGAGCTGCCAGATCCAACAGGAAGATGGCCAATCTTTCCTAAGCTGCT
CACCTTACAAGAAAACGAATCGTACTGCTAAGAATTCAAACTTCAGCAGTCATGGGGAGCCTTGGAAGGAGCCCG
AATCACTGATGGAATTGGACAGTGCATGGAGATGGTTCAGCAGGACAAGGGTAAGTGCAGGGGCAAGTCCAGGTC
ATACTGAGAGACAACGAGTGGCGCTGACAGAGACAGACAAAGATAAAATCAAAAGTTTGTGCTTCATCTTCAAAA
ACTCAAACTAATAACAAACTTGGCCTT

FIGURE 53

MPLTPTVQGFQWILRGPDVETSPLGAPRAASHGVG

FIGURE 54

CTGCGCCCGCGACGGAGGCGCGCTTCAAAGCGCAGGCGCGGGGAGGGGGTGGGGGAGGAGGGAAAGCGGCGAGTA
AGATGGAAGATGAGGAGGTCGCTGAGAGCTGGGAAGAGGCGGCAGACAGCGGGGAAATCCAAATCTCCTCCCAAA
GTGCCCATTGTGATTCAGGACGATAGCCTTCCCGCGGGGCCCCCTCCACAGATCCGCATCCTCAAGAGGCCCACC
AGCAACGGTGTGGTCAGCAGCCCCAACTCCACCAGCAGGCCCACCCTTCCAGTCAAGTCCCTAGCACAGCGAGAG
GCCGAGTACGCCGAGGCCCGGAAGCGGATCCTGGGCAGCGCCAGCCCCGAGGAGGAGCAGGAGAAACCCATCCTC
GACAGGCCAACCAGGATCTCCCAACCCGAAGACAGCAGGCAGCCCAATAATGTGATCAGACAGCCTTTGGGTCCT
GATGGGTCTCAAGGCTTCAAACAGCGCAGATAAATGCAGGCAAGAAAAGATGCCGCCGTTGCTGCCGTCACCGCC
TCCTGGGTCGTCCGCCACGGGTTGCACTGCCGTGGCAGACAGCTGGACTTGAGCAGAGGGAACGACCTGACTTAC
TTGCACTGTGATCCCCCTTGCTCCGCCCACTGTGACCTTGAACCCCATGCACTGTGACCTCCCCCCTTCTCCCCC
TTCCCACTGTGATTGGCACATCGACAAGGGCTGTCCCAAGTCAATGGAAAGGGAAAGGGTGGGGGTTAGGGGAAG
GTTGGGGGGACCCAGCAAGGACTCAGAGAGTCAGACAGTGCCACTTGGCCACTTGGGGTAAAGCCAGTGCCAGCA
ATAACAGTTTATCATGCTCATTAATTTGGGATTTCAAAACACAAATGAAAACTCACACCCACCCACCCCCAAGTG
CATGTCTCCATCACTTAAAAAGTAAGTTCCATTTGAAAATATCCTTTCTTTTTTTTTTCTTCCTATTTTTGTTTG
TTTATACAAATATCTGATTTGCAAGAAAAAGTGCATGGGAGGGGTTTAGTGGTTTAATGAATTTTTAATTAAGA
AAGGGTAGTTTGGTAGTCTACTTAAAAATGTTTCTGGGAAATTCACTAGAAACATTAACCAATAGGATTTTGGTG
AGCTTAGCTTCTGTATTCCTACTGCCGCCCAGAAAAGGGGCAGGGCTCTGCAGCCGCCAGGACAGACGAGCACCC
CATGCCTATACCTCCCTCCCCGAGCTAAGTCCCAGGGCATCTGGGCCTTGCCTGGAGACTGGGCTAGCTCTGTAG
GCTCGGAGAGCCTGGGGAGGGTGCCAACCCCACCTCTAGTATTTTGGGAGATAGGGAAAGTGAACCGACTTCCCC
TTCCCATACCCCTCAGGGTGGTTCCCTACCAGCCAGGCTTACTACTTCTAGAAGAAAGCAGAGTGCCAGGGAGTG
AGATTGCATCCCTGGGCTTAGAAGTGACGGAGAGAAGACTTGTTTAGTATTTTGCCATCAGCACAAGGAAAACCA
GGAGAGAGTCTGCCTCCAGGACTCTGAGCCTTCTGCCTCGTATGTTCAGAAGGTGGATAGGTCTTCCCACTCCAG
CATGGCTTGAACTCTTAGGGGTCTGCAGTGCTCCATCTCCATTGGTGGCCCCAGCTCAGTAACTATACCTGGTAC
ATTTCCTGTGTGCAATCAGTACCTTGAAGGCAGAACATTCTGAATAAAGTTGGAAAAAGAACA

FIGURE 55

CCACCTGGCACTGCCCACCACCCTGTAGCAGTGTGCCAGCAGGAGAGTCTGTCCTTTGCAGAGCTGCCCGCCCTG
AAGCCCCCGAGCCCAGTGTGTCTGGACCTTTTCCCTGTTGCCCCAGAGGAGCTTCGGGCTCCTGGCAGCCGCTGG
TCCCTGGGGACCCCTGCCCCTCTCCAAGGGTTGCTATGGCCATTATCCCCAGGAGGCTCAGATACAGAGATCACC
AGCGGGGGGATGCGGCCCAGCAGGGCTGGCAGCTGGCCACACTGTCCTGGTGCCCAGCCCCCAGCTCTGGAGGGA
CCCTGGAGTCCCCGACACACACAGCCACAGCGCCGGGCCAGCCACGGCTCGGAGAAGAAGTCTGCCTGGCGCAAG
ATGCGGGTGTACCAGCGTGAAGAGGTCCCCGGCTGCCCCGAGGCCCACGCTGTCTTCCTAGAGCCTGGCCAGGTA
GTGCAAGAGCAGGCCCTGAGCACAGAGGAGCCCAGGGTGGAGTTGTCTGGGTCCACCCGAGTGAGCCTCGAAGGT
CCTGAGCGGAGGCGCTTCTCGGCATCGGAGCTGATGACCCGGCTGCACTCTTCTCTGCGCCTGGGGCGGAATTCA
GCAGCCCGGGCACTCATCTCTGGGTCAGGCACCGGAGCAGCCCGGGAAGGGAAAGCATCTGGAATGGAGGCTCGA
AGTGTAGAGATGAGCGGGGACCGGGTGTCGCGGCCAGCCCCTGGTGACTCACGAGAGGGCGATTGGTCCGAGCCC
AGGCTAGACACACAGGAAGAGCCGCCTTTGGGGTCCAGGAGCACCAACGAGCGGCGCCAGTCTCGATTCCTCCTT
AACTCCGTCCTCTATCAGGAATACAGCGACGTGGCCAGCGCCCGCGAACTGCGGCGGCAGCAGCGCGAGGAGGAG
GGCCCGGGGGACGAGGCCGAGGGCGCAGAGGAGGGGCCGGGGCCGCCGCGGGCCAACCTCTCCCCCAGCAGCTCC
TTCCGGGCGCAGCGCTCGGCGCGAGGCTCCACCTTCTCGCTGTGGCAGGATATCCCCGACGTACGCGGCAGCGGC
GTCCTGGCCACGCTGAGCCTGCGGGACTGCAAGCTGCAGGAGGCCAAGTTTGAGCTGATCACCTCCGAGGCCTCC
TACATCCACAGCCTGTCGGTGGCTGTGGGCCACTTCTTAGGCTCTGCCGAGCTGAGCGAGTGTCTGGGGGCGCAG
GACAAGCAGTGGCTGTTTTCCAAACTGCCCGAGGTCAAGAGCACCAGCGAGAGGTTCCTGCAGGACCTGGAGCAG
CGGCTGGAGGCAGATGTGCTGCGCTTCAGCGTGTGCGACGTGGTGCTGGACCACTGCCCGGCCTTCCGCAGAGTC
TACCTGCCCTATGTCACCAACCAGGCCTACCAGGAGCGCACCTACCAGCGCCTGCTCCTGGAGAACCCCAGGTTC
CCTGGCATCCTGGCTCGCCTGGAGGAGTCTCCTGTGTGCCAGCGTCTGCCCCTTACCTCCTTCCTTATCCTGCCC
TTCCAGAGGATCACCCGCCTCAAGATGTTGGTGGAGAACATCCTGAAGCGGACAGCACAGGGCTCTGAAGACGAA
GACATGGCCACCAAGGCCTTCAATGCGCTCAAGGAGCTGGTGCAGGAGTGCAATGCTAGTGTACAGTCCATGAAG
AGGACAGAGGAACTCATCCACCTGAGCAAGAAGATCCACTTTGAGGGCAAGATTTTCCCGCTGATCTCTCAGGCC
CGCTGGCTGGTTCGGCATGGAGAGTTGGTAGAGCTGGCACCACTGCCTGCAGCACCCCCTGCCAAGCTGAAGCTG
TCCAGCAAGGCAGTCTACCTCCACCTCTTCAATGACTGCTTGCTGCTCTCTCGGCGGAAGGAGCTAGGGAAGTTT
GCCGTTTTCGTCCATGCCAAGATGGCTGAGCTGCAGGTGCGGGACCTGAGCCTGAAGCTGCAGGGCATCCCCGGC
CACGTGTTCCTCCTCCAGCTCCTCCACGGGCAGCACATGAAGCACCAGTTCCTGCTGCGGGCCCGGACGGAAAGT
GAGAAGCAGCGATGGATCTCAGCCTTGTGCCCCTCCAGCCCCCAGGAGGACAAGGAGGTCATCAGTGAGGGGGAA
GATTGCCCCCAGGTTCAGTGTGTTAGGACATACAAGGCACTGCACCCAGATGAGCTGACCTTGGAGAAGACTGAC
ATCCTGTCAGTGAGGACCTGGACCAGTGACGGCTGGCTGGAAGGGGTCCGCCTGGCAGATGGTGAGAAGGGGTGG
GTGCCCCAGGCCTATGTGGAAGAGATCAGCAGCCTCAGCGCCCGCCTCCGAAACCTCCGGGAGAATAAGCGAGTC
ACAAGTGCCACCAGCAAACTGGGGGAGGCTCCTGTGTGATGGGCAGCCATGGCCTAGGACCCCACCTCCATGCCT
GGCTCCTGGATGGTCCTGGAGGGGCCTGCAGTGTCTCCATTCCCCAAGCTGCTCCTGCTGGCACTTCGCTTCTGT
GGCCTTGGCATTGAGGGCACAGGCTGGACACAGGAATGGGGGCGCCTCCAGAGGGTCTCTCCGTCCTCATGCTCC
TCAGTGTCCACACTTCAAGGCCAAGGATAGTTTCTTCCTCTGACATGGGGACCATAACAGGTGATCACTGATACC
TGGCAAAGACTGGGGCCCTCTCCTTTCTATGTCCTCAATCCTGCCTGACTCTTGGTCCTTCTGGCAGGGACCTGG
CTGGGGAACGTTCTGGTGCTGATGGTGCTGGGACCTATATGTATATTTATATATATCTGGGGTCTTGTCTACCAC
CTCC

FIGURE 56

MDCGPPATLQPHLTGPPGTAHHPVAVCQQESLSFAELPALKPPSPVCLDLFPVAPEELRAPGSRWSLGTPAPLQG
LLWPLSPGGSDTEITSGGMRPSRAGSWPHCPGAQPPALEGPWSPRHTQPQRRASHGSEKKSAWRKMRVYQREEVP
GCPEAHAVFLEPGQVVQEQALSTEEPRVELSGSTRVSLEGPERRRFSASELMTRLHSSLRLGRNSAARALISGSG
TGAAREGKASGMEARSVEMSGDRVSRPAPGDSREGDWSEPRLDTQEEPPLGSRSTNERRQSRFLLNSVLYQEYSD
VASARELRRQQREEEGPGDEAEGAEEGPGPPRANLSPSSSFRAQRSARGSTFSLWQDIPDVRGSGVLATLSLRDC
KLQEAKFELITSEASYIHSLSVAVGHFLGSAELSECLGAQDKQWLFSKLPEVKSTSERFLQDLEQRLEADVLRFS
VCDVVLDHCPAFRRVYLPYVTNQAYQERTYQRLLLENPRFPGILARLEESPVCQRLPLTSFLILPFQRITRLKML
VENILKRTAQGSEDEDMATKAFNALKELVQECNASVQSMKRTEELIHLSKKIHFEGKIFPLISQARWLVRHGELV
ELAPLPAAPPAKLKLSSKAVYLHLFNDCLLLSRRKELGKFAVFVHAKMAELQVRDLSLKLQGIPGHVFLLQLLHG
QHMKHQFLLRARTESEKQRWISALCPSSPQEDKEVISEGEDCPQVQCVRTYKALHPDELTLEKTDILSVRTWTSD
GWLEGVRLADGEKGWVPQAYVEEISSLSARLRNLRENKRVTSATSKLGEAPV

FIGURE 57A

GAAGTTGCGCGCAGGCCGGCGGGCGGGAGCGGACACCGAGGCCGGCGTGCAGGCGTGCGGGTGTGCGGGAGCCGG
GCTCGGGGGGATCGGACCGAGAGCGAGAAGCGCGGCATGGAGCTCCAGGCAGCCCGCGCCTGCTTCGCCCTGCTG
TGGGGCTGTGCGCTGGCCGCGGCCGCGGCGGCGCAGGGCAAGGAAGTGGTACTGCTGGACTTTGCTGCAGCTGGA
GGGGAGCTCGGCTGGCTCACACACCCGTATGGCAAAGGGTGGGACCTGATGCAGAACATCATGAATGACATGCCG
ATCTACATGTACTCCGTGTGCAACGTGATGTCTGGCGACCAGGACAACTGGCTCCGCACCAACTGGGTGTACCGA
GGAGAGGCTGAGCGTATCTTCATTGAGCTCAAGTTTACTGTACGTGACTGCAACAGCTTCCCTGGTGGCGCCAGC
TCCTGCAAGGAGACTTTCAACCTCTACTATGCCGAGTCGGACCTGGACTACGGCACCAACTTCCAGAAGCGCCTG
TTCACCAAGATTGACACCATTGCGCCCGATGAGATCACCGTCAGCAGCGACTTCGAGGCACGCCACGTGAAGCTG
AACGTGGAGGAGCGCTCCGTGGGGCCGCTCACCCGCAAAGGCTTCTACCTGGCCTTCCAGGATATCGGTGCCTGT
GTGGCGCTGCTCTCCGTCCGTGTCTACTACAAGAAGTGCCCCGAGCTGCTGCAGGGCCTGGCCCACTTCCCTGAG
ACCATCGCCGGCTCTGATGCACCTTCCCTGGCCACTGTGGCCGGCACCTGTGTGGACCATGCCGTGGTGCCACCG
GGGGGTGAAGAGCCCCGTATGCACTGTGCAGTGGATGGCGAGTGGCTGGTGCCCATTGGGCAGTGCCTGTGCCAG
GCAGGCTACGAGAAGGTGGAGGATGCCTGCCAGGCCTGCTCGCCTGGATTTTTTAAGTTTGAGGCATCTGAGAGC
CCCTGCTTGGAGTGCCCTGAGCACACGCTGCCATCCCCTGAGGGTGCCACCTCCTGCGAGTGTGAGGAAGGCTTC
TTCCGGGCACCTCAGGACCCAGCGTCGATGCCTTGCACACGACCCCCCTCCGCCCCACACTACCTCACAGCCGTG
GGCATGGGTGCCAAGGTGGAGCTGCGCTGGACGCCCCCTCAGGACAGCGGGGGCCGCGAGGACATTGTCTACAGC
GTCACCTGCGAACAGTGCTGGCCCGAGTCTGGGGAATGCGGGCCGTGTGAGGCCAGTGTGCGCTACTCGGAGCCT
CCTCACGGACTGACCCGCACCAGTGTGACAGTGAGCGACCTGGAGCCCCACATGAACTACACCTTCACCGTGGAG
GCCCGCAATGGCGTCTCAGGCCTGGTAACCAGCCGCAGCTTCCGTACTGCCAGTGTCAGCATCAACCAGACAGAG
CCCCCCAAGGTGAGGCTGGAGGGCCGCAGCACCACCTCGCTTAGCGTCTCCTGGAGCATCCCCCCGCCGCAGCAG
AGCCGAGTGTGGAAGTACGAGGTCACTTACCGCAAGAAGGGAGACTCCAACAGCTACAATGTGCGCCGCACCGAG
GGTTTCTCCGTGACCCTGGACGACCTGGCCCCAGACACCACCTACCTGGTCCAGGTGCAGGCACTGACGCAGGAG
GGCCAGGGGGCCGGCAGCAAGGTGCACGAATTCCAGACGCTGTCCCCGGAGGGATCTGGCAACTTGGCGGTGATT
GGCGGCGTGGCTGTCGGTGTGGTCCTGCTTCTGGTGCTGGCAGGAGTTGGCTTCTTTATCCACCGCAGGAGGAAG
AACCAGCGTGCCCGCCAGTCCCCGGAGGACGTTTACTTCTCCAAGTCAGAACAACTGAAGCCCCTGAAGACATAC
GTGGACCCCCACACATATGAGGACCCCAACCAGGCTGTGTTGAAGTTCACTACCGAGATCCATCCATCCTGTGTC
ACTCGGCAGAAGGTGATCGGAGCAGGAGAGTTTGGGGAGGTGTACAAGGGCATGCTGAAGACATCCTCGGGGAAG
AAGGAGGTGCCGGTGGCCATCAAGACGCTGAAAGCCGGCTACACAGAGAAGCAGCGAGTGGACTTCCTCGGCGAG
GCCGGCATCATGGGCCAGTTCAGCCACCACAACATCATCCGCCTAGAGGGCGTCATCTCCAAATACAAGCCCATG
ATGATCATCACTGAGTACATGGAGAATGGGGCCCTGGACAAGTTCCTTCGGGAGAAGGATGGCGAGTTCAGCGTG
CTGCAGCTGGTGGGCATGCTGCGGGGCATCGCAGCTGGCATGAAGTACCTGGCCAACATGAACTATGTGCACCGT
GACCTGGCTGCCCGCAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCTGACTTTGGCCTGTCCCGCGTG
CTGGAGGACGACCCCGAGGCCACCTACACCACCAGTGGCGGCAAGATCCCCATCCGCTGGACCGCCCCGGAGGCC
ATTTCCTACCGGAAGTTCACCTCTGCCAGCGACGTGTGGAGCTTTGGCATTGTCATGTGGGAGGTGATGACCTAT
GGCGAGCGGCCCTACTGGGAGTTGTCCAACCACGAGGTGATGAAAGCCATCAATGATGGCTTCCGGCTCCCCACA
CCCATGGACTGCCCCTCCGCCATCTACCAGCTCATGATGCAGTGCTGGCAGCAGGAGCGTGCCCGCCGCCCCAAG
TTCGCTGACATCGTCAGCATCCTGGACAAGCTCATTCGTGCCCCTGACTCCCTCAAGACCCTGGCTGACTTTGAC
CCCCGCGTGTCTATCCGGCTCCCCAGCACGAGCGGCTCGGAGGGGGTGCCCTTCCGCACGGTGTCCGAGTGGCTG
GAGTCCATCAAGATGCAGCAGTATACGGAGCACTTCATGGCGGCCGGCTACACTGCCATCGAGAAGGTGGTGCAG
ATGACCAACGACGACATCAAGAGGATTGGGGTGCGGCTGCCCGGCCACCAGAAGCGCATCGCCTACAGCCTGCTG
GGACTCAAGGACCAGGTGAACACTGTGGGGATCCCCATCTGAGCCTCGACAGGGCCTGGAGCCCCATCGGCCAAG
AATACTTGAAGAAACAGAGTGGCCTCCCTGCTGTGCCATGCTGGGCCACTGGGGACTTTATTTATTTCTAGTTCT
TTCCTCCCCCTGCAACTTCCGCTGAGGGGTCTCGGATGACACCCTGGCCTGAACTGAGGAGATGACCAGGGATGC
TGGGCTGGGCCCTCTTTCCCTGCGAGACGCACACAGCTGAGCACTTAGCAGGCACCGCCACGTCCCAGCATCCCT
GGAGCAGGAGCCCCGCCACAGCCTTCGGACAGACATATGGGATATTCCCAAGCCGACCTTCCCTCCGCCTTCTCC
CACATGAGGCCATCTCAGGAGATGGAGGGCTTGGCCCAGCGCCAAGTAAACAGGGTACCTCAAGCCCCATTTCCT
CACACTAAGAGGGCAGACTGTGAACTTGACTGGGTGAGACCCAAAGCGGTCCCTGTCCCTCTAGTGCCTTCTTTA
GACCCTCGGGCCCCATCCTCATCCCTGACTGGCCAAACCCTTGCTTTCCTGGGCCTTTGCAAGATGCTTGGTTGT

FIGURE 57B

GTTGAGGTTTTTAAATATATATTTTGTACTTTGTGGAGAGAATGTGTGTGTGTGGCAGGGGGCCCCGCCAGGGCT
GGGGACAGAGGGTGTCAAACATTCGTGAGCTGGGGACTCAGGGACCGGTGCTGCAGGAGTGTCCTGCCCATGCCC
CAGTCGGCCCCATCTCTCATCCTTTTGGATAAGTTTCTATTCTGTCAGTGTTAAAGATTTTGTTTTGTTGGACAT
TTTTTTCGAATCTTAATTTATTATTTTTTTTATATTTATTGTTAGAAAATGACTTATTTCTGCTCTGGAATAAAG
TTGCAGATGATTCAAACCG

FIGURE 58

GGTGGGCTGTAGGAATGAGGAGGAACTTAGGGAGAAACAGCTAGTGGGGAGGTAGGGCCTGGGGGAGCCGCCCCT
TGCCCCAAGAGAAGGAGCCAGAACCCCCGGATCTGCATGCAAGGCCTGCTCCATGCCTCGCTCACAGCAGCCCAT
CCCACAGCCCGCCCCGGTGGGGCAGGCAACATCAAGACCCTAGGAGACGCCTATGAGTTTGCGGTGGACGTGAGA
GACTTCTCACCTGAAGACATCATTGTCACCACCTCCAACAACCACATCGAGGTGCGGGCTGAGAAGCTGGCGGCT
GACGGCACCGTCATGAACACCTTCGCTCACAAGTGCCAGCTGCCGGAGGACGTGGACCCGACGTCGGTGACCTCG
GCTCTGCGGGAGGACGGCAGCCTCACTATCCGGGCACGGCGTCACCCGCATACAGAACACGTCCAGCAGACCTTC
CGGACGGAGATCAAAATCTGAGTGCCTCTCCCTTCCCTTTCCCTGTCCCCCCGCCCCACGCCTGCCAGCAAAGCC
TCGCTAACCCCATTACAACAGCTCCAGGACATCTCAGCCCAGGTTCTAGCCCCCACGCACCCCAGACCCCAGGTG
GACCATCCTCCCAAACTAGGGCCCTCCACTCTATCCAGGGCAGGCCAGGGACTCCCTGGCCTGACACATGATGCC
CAGATTTCAGATTTGGCCTCCGTCACTTAATCCAGAGTACAGGGGCTGGGGTCAGGGAAGGAAGATCTAAAGAAC
CCACTGTGGGTCAGGGGAATGGACCAGCAGGACATATGGGCAAGCTCTGCAGGACAGACAGGCAGACAAACCCT
CTGATCTATGA

FIGURE 59

GCTCGTGTTAAATCTAGAACCGTAGCCAGACATGGGACTGGAGGACGAGCAAAAGATGCTTACCGAATCCGGAGA
TCCTGAGGAGGAGGAAGAGGAAGAGGAGGAATTAGTGGATCCCCTAACAACAGTGAGAGAGCAATGCGAGCAGTT
GGAGAAATGTGTAAAGGCCCGGGAGCGGCTAGAGCTCTATGATGAGCATGTATCCTCTCGATCACATACAGAAGA
GGATTGCACGGAGGAGCTCTTTGACTTCTTGCATGCAAAGGACCATTGCGTGGCCCACAAACTCTTTAACAACTT
GAAATAAATGTGTGGACTTAATTCACCCCAGCCTTCATCATCTGGGCATCAGAATATTTCCTTATGGTTTCGGAT
GTACCATTTGTTTCTTATTTGTGTAACTGTAAGTTCACATGAACCTCGTGGGTTTTGGCTTAGGCTGGTAGCTTC
TATGTAATTCGCAGTGATTCCATCTAAATAAAAGTTCTGTGATCTGC

FIGURE 60

CTTACAGAACTCCCACGGACACACC**ATG**ATAAGGACGCTGCTGCTGTCCACTTTGGTGGCTGGAGCCCTCAGTTG
TGGGGACCCCACTTACCCACCTTATGTGACTAGGGTGGTTGGCGGTGAAGAAGCGAGGCCCAACAGCTGGCCCTG
GCAGGTCTCCCTGCAGTACAGCTCCAATGGCAAGTGGTACCACACCTGCGGAGGGTCCCTGATAGCCAACAGCTG
GGTCCTGACGGCTGCCCACTGCATCAGCTCCTCCAGGACCTACCGCGTGGGGCTGGGCCGGCACAACCTCTACGT
TGCGGAGTCCGGCTCGCTGGCAGTCAGTGTCTCTAAGATTGTGGTGCACAAGGACTGGAACTCCAACCAAATCTC
CAAAGGGAACGACATTGCCCTGCTCAAACTGGCTAACCCCGTCTCCCTCACCGACAAGATCCAGCTGGCCTGCCT
CCCTCCTGCCGGCACCATTCTACCCAACAACTACCCCTGCTACGTCACGGGCTGGGGAAGGCTGCAGACCAACGG
GGCTGTTCCTGATGTCCTGCAGCAGGGCCGGTTGCTGGTTGTGGACTATGCCACCTGCTCCAGCTCTGCCTGGTG
GGGCAGCAGCGTGAAAACCAGTATGATCTGTGCTGGGGGTGATGGCGTGATCTCCAGCTGCAACGGAGACTCTGG
CGGGCCACTGAACTGTCAGGCGTCTGACGGCCGGTGGCAGGTGCACGGCATCGTCAGCTTCGGGTCTCGCCTCGG
CTGCAACTACTACCACAAGCCCTCCGTCTTCACGCGGGTCTCCAATTACATCGACTGGATCAATTCGGTGATTGC
AAATAAC**TAA**CCAAAAGAAGTCCCTGGGACTGTTTCAGACTTGGAAAGGTCACAGAAGGAAAATAATATAATAAA
GTGACAACTATGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAA

FIGURE 61

MIRTLLLSTLVAGALSCGDPTYPPYVTRVVGGEEARPNSWPWQVSLQYSSNGKWYHTCGGSLIANSWVLTAAHCI
SSSRTYRVGLGRHNLYVAESGSLAVSVSKIVVHKDWNSNQISKGNDIALLKLANPVSLTDKIQLACLPPAGTILP
NNYPCYVTGWGRLQTNGAVPDVLQQGRLLVVDYATCSSSAWWGSSVKTSMICAGGDGVISSCNGDSGGPLNCQAS
DGRWQVHGIVSFGSRLGCNYYHKPSVFTRVSNYIDWINSVIANN

FIGURE 62

CGGACGCGTGGGCCCGGCCAAGGCGAGTGCCGCGCGGGCCACC**ATG**GCCACGGACGAGCTGGCCACCAAGCTGAG
CCGGCGGCTGCAGATGGAGGGCGAGGGCGGCGGCGAGACCCCGGAGCAGCCCGGGCTGAACGGGGCAGCGGCGGC
GGCGGCGGGGGCACCCGACGAGGCGGCCGAGGCGCTGGGCAGCGCGGACTGCGAGCTGAGCGCCAAGCTGCTGCG
GCGCGCAGACCTCAACCAGGGCATCGGCGAGCCCCAGTCGCCCAGCCGCCGCGTCTTCAACCCCTACACCGAGTT
CAAGGAGTTCTCCAGGAAGCAGATCAAGGACATGGAGAAGATGTTCAAGCAGTATGATGCCGGGCGGGACGGCTT
CATCGACCTGATGGAGCTAAAACTCATGATGGAGAAACTTGGGGCCCCTCAGACCCACCTGGGCCTGAAAAACAT
GATCAAGGAGGTGGATGAGGACTTTGACAGCAAGCTGAGCTTCCGGGAGTTCCTCCTGATCTTCCGCAAGGCGGC
GGCCGGGGAGCTTCAGGAGGACAGCGGGCTGTGCGTGCTGGCCCGCCTCTCTGAGATCGACGTCTCCAGTGAGGG
TGTCAAGGGGGCCAAGAGCTTCTTTGAGGCCAAGGTCCAGGCCATCAACGTGTCCAGCCGCTTCGAGGAGGAGAT
CAAGGCAGAGCAGGAGGAAAGGAAGAAGCAGGCGGAGGAGATGAAGCAGCGGAAAGCGGCCTTCAAGGAGCTGCA
GTCCACCTTTAAG**TAG**CGGGGGCTGCAGCCGACCGCCCTGCTCCGGCCCCAGTGTGGTGGGCGAGGGTGGCGCAT
GGGAGGCCGAGCCTGAATCCTTGCCTGTGTCTGACGGGACCACTACTAAAAACCTAAAAATATCTGTGAATGGAG
CAAGTTCAGGGGTCTTATGGAGGTGGCCCGGCCCCTCCCCGCTCCCTTCCACTCTGCACGAGGCCGCCACACCGG
CGCTGGCTCCCTGCCCGGCCCGGCCCTCCCTGGCAATCCCTGGGCTCTCTTGCACCCCTAACTGCCCCCTGCCTG
CTCCGGCACTGCCCCAGGCCCAGCTCCTGGCCCTAGGTCCCTCCCAGCCCCATGTGCCTGCCGCCTGCCCTCCAC
ACATCCCTGTCCCCCCAACCCGGGAACCCCTGCCCTCCTCCAGCAGGCCGCACCGCCCCTGGGGCCCCCTGCCAG
CCCCTTCCCAGGCTGGGAGACAGCAGAAGAGATAGAATCAGGGCTGCCCCCACAGAGTGGGACCCAAGGGGCTAA
TTGGAGGCACGAGGGGACCCCTCCCCAGGGCCTTTTCCTCCTCTGCGTCTTCCATCTACTGAAATGGGAGAGGGG
GTGGGGAGCTTCTGTTCTGGTGAAGGGACCCGGGCAGGCCCCCAGCACCCCATGCTGACTTGGAGAACCCCAGAT
CTCTGGGGCCCAGCCAGGCAGGGTGTGGGGGCAGCTGTGCCAATCTACCTCACAGGCCCACCCCCTGCCGGGCAT
GCCGTGGGATCATGGGCAGGGAAGGCTCTGGGGGTCGGAGACACCGCTGCTTAGCACCCCCAGCCAGAACACCCT
GAGGGTCTCGGGGCTCTGGAGAGAGTGGGGCGGGAGGAAGAATTGGCACCTTCCTAGGGAAGGAGACGAGCGCTT
CGCCTTGATTCTCCGAGAAGCCTCCGAGAAGTGCTTTAAGTGTGTTTGCATGCGCCAGGCGGTGGGCAGCGGGGG
CCTGTCCAGCCCTCTCCCGCCATCCTTCCCCAAGTGACGTCCACTGCCTTGTCACCAGCGACCTGCCTGTCATGC
CCACCCCCTGAGGAAGCATGGGGACCCTAACACCCTGGTGCCCTGCACCAGACAGGCCGTGGTCAGGCCCAGGCC
ACCGGCCGGGTTCTGCCACAGCTTCCCACGTGCTTGCTGACATGCGTGTGCCTGTGTGTGGTGTCTGTTGCTGTG
TCGTGAAACTGTGACCATCACTCAGTCCAAACAAGTGAGTGGCCCTCGAGGCCACAGTTATGCAACTTTCAGTGT
GTGTCATAACGACGTCACTGCTTTTTAAACTCGATAACTCTTTATTTAGTAAAATGCCCAGGAGTCCTGGAAGC
TACGCGGACTTGCAGAGGTTTTATTTTTTGGCCTTAGAATCTGCAGAAATTAGGAGGCACCGAGCCCAGCGCAGC
AGCCTCGGACCCGGATTGCGTTTGCCTTAGCGGATATGTTTATACAGATGAATATAAAATGTTTTTTTCTTTGGG
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 63

MATDELATKLSRRLQMEGEGGGETPEQPGLNGAAAAAAGAPDEAAEALGSADCELSAKLLRRADLNQGIGEPQSP
SRRVFNPYTEFKEFSRKQIKDMEKMFKQYDAGRDGFIDLMELKLMMEKLGAPQTHLGLKNMIKEVDEDFDSKLSF
REFLLIFRKAAAGELQEDSGLCVLARLSEIDVSSEGVKGAKSFFEAKVQAINVSSRFEEEIKAEQEERKKQAEEM
KQRKAAFKELQSTFK

FIGURE 64

GCCTCCCACTTGGTTGCTCGTACGCGGCTAGTGGGTCCTCAGTGGATGTAGGCTGGGCGCCGCGATGTTGGACGG
GACACCGGCGGAGAGCGACCTCGGGGTTAAGGGGTGGGGCTGACGTCAGGAGCCAAGATGGCGGCGGTGGTCGCC
CTCTCCTTGAGGCGCCGGTTGCCGGCCACAACCCTTGGCGGAGCCTGCCTGCAGGCCTCCCGAGGAGCCCAGACA
GCTGCAGCCACAGCTCCCCGTATCAAGAAATTTGCCATCTATCGATGGGACCCAGACAAGGCTGGAGACAAACCT
CATATGCAGACTTATGAAGTTGACCTTAATAAATGTGGCCCCATGGTATTGGATGCTTTAATCAAGATTAAGAAT
GAAGTTGACTCTACTTTGACCTTCCGAAGATCATGCAGAGAAGGCATCTGTGGCTCTTGTGCAATGAACATCAAT
GGAGGCAACACTCTAGCTTGCACCCGAAGGATTGACACCAACCTCAATAAGGTCTCAAAAATCTACCCTCTTCCA
CACATGTATGTGATAAAGGATCTTGTTCCCGATTTGAGCAACTTCTATGCACAGTACAAATCCATTGAGCCTTAT
TTGAAGAAGAAGGATGAATCTCAGGAAGGCAAGCAGCAGTATCTGCAGTCCATAGAAGAGCGTGAGAAACTGGAC
GGGCTCTACGAGTGCATTCTCTGTGCCTGCTGTAGCACCAGCTGCCCCAGCTACTGGTGGAACGGAGACAAATAT
CTGGGGCCTGCAGTTCTTATGCAGGCCTATCGCTGGATGATTGACTCCAGAGATGACTTCACAGAGGAGCGCCTG
GCCAAGCTGCAGGACCCATTCTCTCTATACCGCTGCCACACCATCATGAACTGCACAAGGACCTGTCCTAAGGGT
CTGAATCCAGGGAAAGCTATTGCAGAGATCAAGAAAATGATGGCAACCTATAAGGAGAAGAAAGCTTCAGTTTAA
CTGTTTCCATGCTAAACATGATTTATAACCAGCTCAGAGCTGAACATAATTTATATCTAATTTGAGTTCCTTTAA
AGATCTTGGTTTTCCATGAATACAGCATGTATAATAAAAATTTTAAGAAATAAATGTTATTCTACTTTATTAACA
AAAAA

FIGURE 65

MAAVVALSLRRRLPATTLGGACLQASRGAQTAAATAPRIKKFAIYRWDPDKAGDKPHMQTYEVDLNKCGPMVLDA
LIKIKNEVDSTLTFRRSCREGICGSCAMNINGGNTLACTRRIDTNLNKVSKIYPLPHMYVIKDLVPDLSNFYAQY
KSIEPYLKKKDESQEGKQQYLQSIEEREKLDGLYECILCACCSTSCPSYWWNGDKYLGPAVLMQAYRWMIDSRDD
FTEERLAKLQDPFSLYRCHTIMNCTRTCPKGLNPGKAIAEIKKMMATYKEKKASV

FIGURE 66

AGTGTTGGGGTTGGCGGCCACAGCTAAGTCCAACACCAGCATGTCGCTGCAGAGAATCGTGCGTGTGTCCCTGGA
GCATCCCACCAGCGCGGTGTGTGTGGCTGGCGTGGAGACCCTCGTGGACATTTATGGGTCAGTGCCTGAGGGCAC
AGAAATGTTTGAGGTCTATGGGACGCCTGGCGTGGACATCTACATCTCTCCCAACATGGAGAGGGGCCGGGAGCG
TGCAGACACCAGGCGGTGGCGCTTTGACGCGACTTTGGAGATCATCGTGGTCATGAACTCCCCCAGCAATGACCT
CAACGACAGCCATGTTCAGATTTCCTACCACTCCAGCCATGAGCCTCTGCCCCTGGCCTATGCGGTGCTCTACCT
CACCTGTGTTGACATCTCTCTGGATTGCGACCTGAACTGTGAGGGAAGGCAGGACAGGAACTTTGTAGACAAGCG
GCAGTGGGTCTGGGGGCCCAGTGGGTATGGCGGCATCTTGCTGGTGAACTGTGACCGTGATGATCCGAGCTGTGA
TGTCCAGGACAATTGTGACCAGCACGTGCACTGCCTGCAAGACCTGGAAGACATGTCTGTCATGGTCCTGCGGAC
GCAGGGCCCTGCAGCCCTCTTTGATGACCACAAACTTGTCCTCCATACCTCCAGCTATGATGCCAAACGGGCACA
GGTCTTCCACATCTGCGGTCCTGAGGATGTGTGTGAGGCCTATAGGCATGTGCTGGGCCAAGATAAGGTGTCCTA
TGAGGTACCCCGCTTGCATGGGGATGAGGAGCGCTTCTTCGTGGAAGGCCTGTCCTTCCCTGATGCCGGCTTCAC
AGGACTCATCTCCTTCCATGTCACTCTGCTGGACGACTCCAACGAGGATTTCTCGGCATCCCCTATCTTCACTGA
CACTGTGGTGTTCCGAGTGGCACCCTGGATCATGACGCCCAGCACTCTGCCACCCCTAGAGGTGTATGTGTGCCG
TGTGAGGAACAACACGTGTTTTGTGGATGCGGTGGCAGAGCTGGCCAGGAAGGCCGGCTGCAAGCTGACCATCTG
CCCACAGGCCGAGAACCGCAACGACCGCTGGATCCAGGATGAGATGGAGCTGGGCTACGTTCAGGCGCCGCACAA
GACCCTCCCGGTGGTCTTTGACTCCCCAAGGAATGGGGAACTGCAGGATTTCCCTTACAAAAGAATCCTGGGTCC
AGATTTTGGTTACGTGACTCGGGAACCACGCGACAGGTCTGTGAGTGGCCTGGACTCCTTTGGGAACCTGGAGGT
CAGCCCTCCAGTGGTGGCCAATGGGAAAGAGTACCCCCTGGGGAGGATCCTCATTGGGGGCAACCTGCCTGGGTC
AAGTGGCCGCAGGGTCACCCAGGTGGTGCGGGACTTCCTCCATGCCCAGAAGGTGCAGCCCCCCGTGGAGCTCTT
TGTGGACTGGTTGGCCGTGGGCCATGTGGATGAGTTTCTGAGCTTTGTCCCTGCCCCCGATGGGAAGGGCTTCCG
GATGCTCCTGGCCAGCCCTGGGGCCTGCTTCAAGCTCTTCCAGGAAAAGCAGAAGTGTGGCCACGGGAGGGCCCT
CCTGTTCCAGGGGGTTGTTGATGATGAGCAGGTCAAGACCATCTCCATCAACCAGGTGCTCTCCAATAAAGACCT
CATCAACTACAATAAGTTTGTGCAGAGCTGCATCGACTGGAACCGTGAGGTGCTGAAGCGGGAGCTGGGCCTGGC
AGAGTGTGACATCATTGACATCCCACAGCTCTTCAAGACCGAGAGGAAAAAAGCAACGGCCTTCTTCCCTGACTT
GGTGAACATGCTGGTGCTGGGGAAGCACCTGGGCATCCCCAAGCCCTTTGGGCCCATCATCAATGGCTGCTGCTG
CCTGGAGGAGAAGGTGCGGTCCCTGCTGGAGCCGCTGGGCCTCCACTGCACCTTCATTGATGACTTCACTCCATA
CCACATGCTGCATGGGGAGGTGCACTGTGGCACCAATGTGTGCAGAAAGCCCTTCTCTTTCAAGTGGTGGAACAT
GGTGCCCTGAGACAGCTCCCACCCACCATCCTGTCCCCCTGGGGCGGGCATTGGCCCAGGTGGTGGAGACAGAGA
CAGGCCCCTGAACGATAAGCACCAAGAGACCCCAAGGCTCCAGATGGAACACTGAGGGTGACCGTCCCTCTCAGA
AGCCTTTTCCCTGGAAGTGTCCATGCCTCACCTGCAACCCATGTGGTTCTCAGACTTGAATCTTCTCGGCCCCCC
AAAAAGAAGGACCTCATTTCTTATAGCCTCTCCTGTGATTCAACACAACCCATGGAGATGTCCCCTTCTCACTCT
GAAATCATCCATTTGGGGACAAATCCACATTGGGGTCTAGAAACATCCACGTATCTCATCAGCCATCTTGTCCTG
TGCATCCTAACAGAGGAAGGATCCATGATTCTGCTTTGGTCCAATTGCTTCCTCTCTGCAGAGGAACAACCCTAA
AACCAGACCACTCCACGCAGGACAGGCAGGAGAGATTCTTCCTAAAGCCTCCCCCATAAAAAGGGAGCTGTGGAT
CCACTTAGATCAGGGCGGAACCATCTTTCACCCGGCCAAGCTCCTGCCCAGATGTTGACCCTCACCCAGCGTGAG
CTGTCACATAGTAGGAGCTTCTAGATGCATGTGGAAGCAATGAGAGTTGTCCCTTAGCCTTATAAACTCCCCATG
ATCTGACATGCAGAAATCCAGCCTTGTCCAGAATCCTCCTGGAATTTCTTGGAGACGAAAGTATCTGGGGGATTG
TTGGGTACTAGGGAGACTGGGTACAAGGGTGAAAAGTAGTTCCCATAATACACATGGTTGACTATGGTGATCCAC
CTTGTGATGGTTAATATTAGGTGTCTGGAGAAGGTTGCTTCATTGGCCCTGGGACTTCTCTCTGCAGGAGGAGAG
AACGCTGCCTCTCCTCTGGATTGGTCTCAGGCTCTCTGTTGGCCTTTGGTCAGCGTTTCCACATCCTGCTCTGCT
GCAGGAGAGGGGGCTAAGGGGCTGGATCCACCAAGGCAGCTCACAGCGGGAAAACTCTGGGAATGAACCACTGAA
TTCAGGGGATGGGGGTGGGGGGGCGGTTCTCGAGGTGTGTGCCAGCTACACGTGTGTTCTGTATGGGTCCAGCTG
CGTTTCCATCACTCGCTAATAAATCAACAGAAACAC

FIGURE 67

AGCCAGAGGGACGAGCTAGCCCGACGATGGCCCAGGGGACATTGATCCGTGTGACCCCAGAGCAGCCCACCCATG
CCGTGTGTGTGCTGGGCACCTTGACTCAGCTTGACATCTGCAGCTCTGCCCCTGAGGACTGCACGTCCTTCAGCA
TCAACGCCTCCCCAGGGGTGGTCGTGGATATTGCCCACGGCCCTCCAGCCAAGAAGAAATCCACAGGTTCCTCCA
CATGGCCCCTGGACCCTGGGGTAGAGGTGACCCTGACGATGAAAGTGGCCAGTGGTAGCACAGGCGACCAGAAGG
TTCAGATTTCATACTACGGACCCAAGACTCCACCAGTCAAAGCTCTACTCTACCTCACCGGGGTGGAAATCTCCC
TGTGCGCAGACATCACCCGCACCGGCAAAGTGAAGCCAACCAGAGCTGTGAAAGATCAGAGGACCTGGACCTGGG
GCCCTTGTGGACAGGGTGCCATCCTGCTGGTGAACTGTGACAGAGACAATCTCGAATCTTCTGCCATGGACTGCG
AGGATGATGAAGTGCTTGACAGCGAAGACCTGCAGGACATGTCGCTGATGACCCTGAGCACGAAGACCCCCAAGG
ACTTCTTCACAAACCATACACTGGTGCTCCACGTGGCCAGGTCTGAGATGGACAAAGTGAGGGTGTTTCAGGCCA
CACGGGGCAAACTGTCCTCCAAGTGCAGCGTAGTCTTGGGTCCCAAGTGGCCCTCTCACTACCTGATGGTCCCCG
GTGGAAAGCACAACATGGACTTCTACGTGGAGGCCCTCGCTTTCCCGGACACCGACTTCCCGGGGCTCATTACCC
TCACCATCTCCCTGCTGGACACGTTCAACCTGGAGCTCCCCGAGGCTGTGGTGTTCCAAGACAGCGTGGTCTTCC
GCGTGGCGCCCTGGATCATGACCCCCAACACCCAGCCCCCGCAGGAGGTGTACGCGTGCAGTATTTTTGAAAATG
AGGACTTCCTGAAGTCAGTGACTACTCTGGCCATGAAAGCCAAGTGCAAGCTGACCATCTGCCCTGAGGAGGAGA
ACATGGATGACCAGTGGATGCAGGATGAAATGGAGATCGGCTACATCCAAGCCCCACACAAAACGCTGCCCGTGG
TCTTCGACTCTCCAAGGAACAGAGGCCTGAAGGAGTTTCCCATCAAACGCGTGATGGGTCCAGATTTTGGCTATG
TAACTCGAGGGCCCCAAACAGGGGGTATCAGTGGACTGGACTCCTTTGGGAACCTGGAAGTGAGCCCCCCAGTCA
CAGTCAGGGGCAAGGAATACCCGCTGGGCAGGATTCTCTTCGGGGACAGCTGTTATCCCAGCAATGACAGCCGGC
AGATGCACCAGGCCCTGCAGGACTTCCTCAGTGCCCAGCAGGTGCAGGCCCCTGTGAAGCTCTATTCTGACTGGC
TGTCCGTGGGCCACGTGGACGAGTTCCTGAGCTTTGTGCCAGCACCCGACAGGAAGGGCTTCCGGCTGCTCCTGG
CCAGCCCCAGGTCCTGCTACAAACTGTTCCAGGAGCAGCAGAATGAGGGCCACGGGGAGGCCCTGCTGTTCGAAG
GGATCAAGAAAAAAAAACAGCAGAAAATAAAGAACATTCTGTCAAACAAGACATTGAGAGAACATAATTCATTTG
TGGAGAGATGCATCGACTGGAACCGCGAGCTGCTGAAGCGGGAGCTGGGCCTGGCCGAGAGTGACATCATTGACA
TCCCGCAGCTCTTCAAGCTCAAAGAGTTCTCTAAGGCGGAAGCTTTTTTCCCCAACATGGTGAACATGCTGGTGC
TAGGGAAGCACCTGGGCATCCCCAAGCCCTTCGGGCCCGTCATCAACGGCCGCTGCTGCCTGGAGGAGAAGGTGT
GTTCCCTGCTGGAGCCACTGGGCCTCCAGTGCACCTTCATCAACGACTTCTTCACCTACCACATCAGGCATGGGG
AGGTGCACTGCGGCACCAACGTGCGCAGAAAGCCCTTCTCCTTCAAGTGGTGGAACATGGTGCCCTGAGCCCATC
TTCCCTGGCGTCCTCTCCCTCCTGGCCAGATGTCGCTGGGTCCTCTGCAGTGTGGCAAGCAAGAGCTCTTGTGAA
TATTGTGGCTCCCTGGGGGCGGCCAGCCCTCCCAGCAGTGGCTTGCTTTCTTCTCCTGTGATGTCCCAGTTTCCC
ACTCTGAAGATCCCAACATGGTCCTAGCACTGCACACTCAGTTCTGCTCTAAGAAGCTGCAATAAAGTTTTTTTA
AGTCACTTTGTAC

FIGURE 68A

GGAAGCTCGTATTTACATTTTAAGTGTATCTGGTGAGTGGGCTGGAGCCCTCGTCTGGGCCGGAAAAAAAAAAGC
CCTCCGATCCGTCTTTTAGTTGCTTCTCTTCCTTTTTCTCTCCGGTTTCTCATCACTCCAACCAGCCGCGACCA
TGCCCAGGAAGAAGGCGGCGGCGGCGGCCTGGGAGGAGCCGAGCTCGGGCAACGGCACTGCCCGCGCCGGGCCCA
GGAAACGCGGCGGCCCGGCGGGCAGGAAGCGCGAGCGGCCCGAGCGCTGCAGTAGCAGCAGCGGCGGCGGCAGCA
GCGGCGACGAGGACGGCCTGGAGCTCGACGGGGCCCCCGGCGGGGGCAAGCGCGCGGCGCGGCCGGCGACAGCAG
GCAAGGCGGGCGGCGCGGCCGTGGTCATCACCGAACCCGAGCACACCAAGGAGCGCGTCAAACTTGAAGGGTCAA
AGTGCAAAGGGCAGCTTTTGATTTTTGGGGCAACCAACTGGGACTTGATTGGTCGAAAAGAAGTGCCTAAACAGC
AAGCTGCTTACCGCAATCTCGGTCAGAATTTGTGGGGGCCCCACAGATATGGGTGCCTGGCGGGGGTCCGGGTGC
GGACAGTGGTCTCGGGCTCGTGTGCTGCACACAGCCTCCTCATCACCACGGAAGGGAAGCTGTGGAGCTGGGGTC
GAAATGAGAAGGGGCAGCTGGGACATGGTGACACCAAGAGAGTAGAAGCCCCTAGACTCATCGAGGGTCTTAGCC
ACGAAGTGATTGTGTCTGCAGCATGTGGGCGGAACCACACCTTGGCCTTGACGGAAACGGGCTCCGTGTTTGCGT
TTGGGGAAAACAAGATGGGGCAGCTGGGCCTTGGCAACCAGACAGACGCTGTTCCCAGCCCCGCGCAGATAATGT
ACAACGGCCAGCCAATTACCAAAATGGCCTGTGGGGCTGAATTCAGTATGATAATGGACTGCAAAGGAAACCTCT
ATTCCTTTGGGTGCCCTGAATATGGTCAGCTGGGACACAACTCAGATGGGAAGTTCATCGCCCGGGCACAGCGGA
TAGAGTACGACTGTGAACTAGTTCCCCGGCGAGTGGCCATCTTCATTGAGAAGACGAAAGATGGACAGATTCTGC
CTGTACCAAACGTGGTTGTACGAGACGTGGCCTGTGGCGCTAACCACACGCTGGTCCTGGACTCCCAGAAGCGAG
TCTTCTCCTGGGGCTTTGGTGGCTATGGCCGGCTGGGCCACGCAGAGCAGAAGGATGAGATGGTCCCCCGCCTGG
TGAAGCTGTTTGACTTCCCTGGGCGTGGGGCTTCCCAGATCTATGCTGGTTACACCTGCTCCTTTGCTGTCAGTG
AAGTGGGTGGTCTGTTTTTCTGGGGGGCCACCAACACCTCCCGTGAATCTACCATGTACCCAAAAGCAGTGCAGG
ACCTCTGCGGCTGGAGAATTCGGAGCCTGGCTTGTGGGAAGAGCAGCATCATTGTGGCCGCCGATGAGAGCACCA
TCAGCTGGGGTCCGTCACCGACCTTTGGGGAACTGGGCTACGGGGACCACAAGCCCAAGTCTTCCACTGCAGCCC
AGGAGGTAAAGACTCTGGATGGCATTTTCTCAGAGCAGGTCGCCATGGGCTACTCACACTCCTTGGTGATAGCAA
GAGATGAAAGTGAGACTGAGAAAGAGAAGATCAAGAAACTGCCAGAATACAACCCCCGAACCCTCTGATGCTCCC
GGAGACTCCTCCGACTCCACACCTCTCGCGGCAGCTGTCATTTCCATGTGCACTGGGACGGGAAGTCAAACGAGG
AATTTAAAAAAGCAAAAGTTGACCGAAGGTGCATTTTTGTTTAGACTCCCTGAGGTTCCGTTTTACACATGATCC
AACGTTAACTACCTTTTTTTCTGTATGCTTTCCAAAGTCCTTTTTTTTCCCTTAATGTTGAATTAAAATACTTGC
TCATAGTTGATTTACCATTCCTACAAAAGAGGCAGAAACTTTGAGCAATCTAGGTTTTTTTTTTTTTTAAGTTTT
TTCTTTCTTCCTTTCCTGAATACACTCCCCAAAACACCCCTTTCCAGTTACAATTAGCATCGTGATCCAAGCAGA
TGCCACATGGAAGAGGAATCGCCATTTACTCAGAAAAAATGTCCCTTACAGGAACCGGCAGCAGCTAGGCAGTCA
CCGGCCCGCCTCCATCCAAAATCACGCTCGCGTGCTTCGGAAGCATCCGGGTCACTCCTTCTCCGCTTTTTCTTG
CAGATGGGCCTAGGCCGGTGTCGGTTCTGTTTCTCCCCTTGGCTGCCTGTACGCCCACAGCCTTCTGGCTGCGAC
ATTATAGAATCGGCCGTGTCCCCCCTGGTGGGGGATTGGGGATCTGTGTTTAGCCATTTATATCTACTTTAGCTG
TTAAAGAGGTCCAAATGAAAATCAGGTGATTGTGGAACCATGGGGACTTGGGGGTGGGGCAGAGGTGGGAACATT
TGTATCAGTTGAGTCAGCTTGGTGGCTCCCTGTGGAGCCAGGGCTGAGCCTTGTCACGCGCACTCGCCAATTAAG
AGATGGACCAGCCAGCAGTCAAGTGCATTCTCCAGTCCTTGCAAGAAGGATCAGCCCTTTCTGTGCCAGCCTCGA
TCGCCTTGTGCTTTGGTCTCTTTTTCTCCCCCCCGCCTGGATCCTGCCTCGCGCGGGCCGTCCTGTTGCTGAGAC
TCGGGGTACCGTTCTGCTGACCCAGCTCCCTTTAGTCACGTTTGCTTGGCTCTGGTACCAAATAGTTGGGATTAC
CGAAGAGTCCCCTTCCTTGCGTGTCAGCACGGATGCTGTGACTGCCACCTGCGTCCTCGTCAAGTGCCCGAGCTC
GCCGCCGTGTGTGCTGCGCTGAGTGAGTTATGAGGTGCCTTTCCCGGAACCCTCCTCTCGCCTGGACCCAAGAGA
GGCGACAGCTGTGGCTGGGGCTCTTGGTTTCCAGAGGGTCTGGACTGGTTTGGGTGCTTTAAAATAGATATTTAG
TTCAGTGGTGCTTATGGGGGAGATGGGACTAGAACTTAAGTGTGAGACTTGGGTGGATGGGAAAGTTAAATATTG
GTCTCTTCAAGTTTTTTTTTTCTTTTGCTTTGTTACCACTTGTCACTGTCTCCATGTTAAAATGCCAAAAATGAT
GTAGTTGTTGTTGCTTTTTTCCCTATTTTCCACCCCAGTCGCTCCTTACCGTGACTCCTGCCCTTGGAGGGCATG
TAGCAGTGTCTGTCCTGCCAGTCCCAAGGCCCTGTGGGAGGAGACTGGCCTGCATCTCTCTAAGACTTAGTCTGA
CGCCACGCGCATCTCTTGTTCTGTGTTCAATCAGTAGTCCAGGGGAGAAGCTTCTGCTACTTCAGAGCTTTGCTA
AACTAACCTAATTTGTCCAAATCACCCCAAAACCACCATCTCTGACGTAAGCTTCCATGCGACAGCCTGATCCGT
TTCCCTGGACAGGTCTCTTTCCTGGAATGCAGCCCAGGCACCTGTGCTCCTGGCACCCTTGAGGTCTCTTCTTTG
AGCCGTGGTCACCGAGAGGGTTGAGGACGCAGCACCCGAGGTCCCAGCCTTTGCAGGAGCCTCCCTGGGCTTAGC

FIGURE 68B

TGGACTTAGATCTTCGGTGGCCTCATGTAAACGTGGCAGCCAGCCTCTTCTAGAACCCTAGCCCAGGGACTGGAG
CAGGAAAGGGACCTTCAAAGTGAAGACTGCCTTGTCCCGCAGCTCCTTCTGGCTTAGATTGAAACATGGGCTTCC
TAATGGGTTAAATCCTTTAAAACAAGGAGTTGTGGGGGAAGGGTGTCGTGCACTCCTAGAGAAAGGTACACAGTT
GCCCGGTTGGGAATGTGCTTGGCGCTGACCCTGCGGGCATCTGACTGGTCTTCCAGCTCAGGAAAAAGAATTTGA
AAGAGGCTTAGCGTGAAGGGGAATCAAAGAGGAGGTTGTGATTTGGTCGAAGGTGCCTGGTTTAGTGCTGTAATT
GTCTTATTATTTTTTTTATATATATATTTCTTGGAGTAAACATTTTAAAT

FIGURE 69

ATGAGTGATCAGCAGCTGGACTGTGCCTTGGACCTAATGAGGCGCCTGCCTCCCCAGCAAATCGAGAAAAACCTC
AGCGACCTGATCGACCTGGTCCCCAGTCTATGTGAGGATCTCCTGTCTTCTGTTGACCAGCCACTGAAAATTGCC
AGAGACAAGGTGGTGGGAAAGGATTACCTTTTGTGTGACTACAACAGAGATGGGGACTCCTATAGGTCACCATGG
AGTAACAAGTATGACCCTCCCTTGGAGGATGGGGCCATGCCGTCAGCTCGGCTGAGAAAGCTGGAGGTGGAAGCC
AACAATGCCTTTGACCAGTATCGAGACCTGTATTTTGAAGGTGGCGTCTCATCTGTCTACCTCTGGGATCTGGAT
CATGGCTTTGCTGGAGTGATCCTCATAAAGAAGGCTGGAGATGGATCAAAGAAGATCAAAGGCTGCTGGGATTCC
ATCCACGTGGTAGAAGTGCAGGAGAAATCCAGCGGTCGCACCGCCCATTACAAGTTGACCTCCACGGTGATGCTG
TGGCTGCAGACCAACAAATCTGGCTCTGGCACCATGAACCTCGGAGGCAGCCTTACCAGACAGATGGAGAAGGAT
GAAACTGTGAGTGACTGCTCCCCACACATAGCCAACATCGGGCGCCTGGTAGAGGACATGGAAAATAAAATCAGA
AGTACGCTGAACGAGATCTACTTTGGAAAAACAAAGGATATCGTCAATGGGCTGAGGTCTGTGCAGACTTTTGCA
GACAAATCAAAACAAGAAGCTCTGAAGAATGACCTGGTGGAGGCTTTGAAGAGAAAGCAGCAATGCTAAACCTCT
GTTTCATGCTAACCAGACACGCCGTGCACTCGTTAGATTCCTTTCTTAGAAAACTCGTTTTCTGCTCCCTTCCCT
CGTCCCTTCCCTCCCCGACAGGTCACATAACAGCTGCATCATTGACCGCACAGCGCCATCTCTCCCTGAGAATAA
AGCCGATAGCCACCTCCTCCGGCTCCGAGCCTGCTTCTGCCACACCTCGCTCTCAGTCTCTCCACATTTCCATAG
AGACCGTGTGGTTTTTGTTCACCCGGG

FIGURE 70

MSDQQLDCALDLMRRLPPQQIEKNLSDLIDLVPSLCEDLLSSVDQPLKIARDKVVGKDYLLCDYNRDGDSYRSPW
SNKYDPPLEDGAMPSARLRKLEVEANNAFDQYRDLYFEGGVSSVYLWDLDHGFAGVILIKKAGDGSKKIKGCWDS
IHVVEVQEKSSGRTAHYKLTSTVMLWLQTNKSGSGTMNLGGSLTRQMEKDETVSDCSPHIANIGRLVEDMENKIR
STLNEIYFGKTKDIVNGLRSVQTFADKSKQEALKNDLVEALKRKQQC

FIGURE 71

CCGCGTCTCGCGTAGTCTCCCGCGCCGCCGTCCACTGCGCGCTTCGCTCTCCGCCGCCCGAGGCCCGCGCGCTCG
CC**ATG**TCCCGGCCACCGCCACCGCGGGTCGCCTCGGTGCTGGGCACCATGGAGATGGGGCGCCGCATGGACGCGC
CCGCCAGCGCCGCGGCCGTGCGCGCCTTTCTGGAGCGCGGCCACACCGAACTGGACACGGCCTTCATGTACAGCG
ACGGCCAGTCCGAGACCATCCTGGGCGGCCTGGGGCTCGGGCTGGGCGGTGGCGACTGCAGAGTGAAAATTGCCA
CCAAGGCCAACCCTTGGGATGGAAAATCACTAAAGCCTGACAGTGTCCGGTCCCAGCTGGAGACGTCATTGAAGA
GGCTGCAGTGTCCCCAAGTGGACCTCTTCTACCTACACACACCTGACCACGGCACCCCGGTGGAAGAGACGCTGC
ATGCCTGCCAGCGGCTGCACCAGGAGGGCAAGTTCGTGGAGCTTGGCCTCTCCAACTATGCTAGCTGGGAAGTGG
CCGAGATCTGTACCCTCTGCAAGAGCAATGGCTGGATCCTGCCCACTGTGTACCAGGGCATGTACAACGCCACCA
CCCGGCAGGTGGAAACGGAGCTCTTCCCCTGCCTCAGGCACTTTGGACTGAGGTTCTATGCCTACAACCCTCTGG
CTGGGGGCCTGCTGACTGGCAAGTACAAGTATGAGGACAAGGACGGGAAACAGCCTGTGGGCCGCTTCTTTGGGA
ATAGCTGGGCTGAGACCTACAGGAATCGCTTCTGGAAGGAGCACCACTTCGAGGCCATTGCGTTGGTGGAGAAGG
CCCTGCAGGCCGCATATGGCGCCAGCGCCCCCAGTGTGACCTCGGCTGCCCTCCGGTGGATGTACCACCACTCAC
AGCTGCAGGGTGCCCACGGGGACGCGGTCATCCTGGGCATGTCCAGCCTGGAGCAGCTGGAGCAGAACTTGGCAG
CAACAGAGGAAGGGCCCCTGGAGCCGGCTGTCGTGGATGCCTTTAATCAAGCCTGGCATTTGGTTGCTCACGAAT
GTCCCAACTACTTCCGC**TAG**GCCCATCATGGCTCAGGCTGCCCAAGGCTTTTCTGTCACCTCTTTTGTTCTCTCA
CACTGACCAGTCTTGGCCTTAAGCTGACTTAGAAGGGTTTTTCTGAATTGTCTAGATCCATGCATTATTTTTCTA
GCTTCCTGCCTTGCTCCCTATTCACTTTACACTGTGAAAGGTGGGGGGTGAGTCCCACTTGAGCGCTTCCTGTTG
AATAAAGCAGGCACTTGACCTGGCTGTAGCCTAGGTCTTGAGTGAACCCCAAAAAA

FIGURE 72

MSRPPPPRVASVLGTMEMGRRMDAPASAAAVRAFLERGHTELDTAFMYSDGQSETILGGLGLGLGGGDCRVKIAT
KANPWDGKSLKPDSVRSQLETSLKRLQCPQVDLFYLHTPDHGTPVEETLHACQRLHQEGKFVELGLSNYASWEVA
EICTLCKSNGWILPTVYQGMYNATTRQVETELFPCLRHFGLRFYAYNPLAGGLLTGKYKYEDKDGKQPVGRFFGN
SWAETYRNRFWKEHHFEAIALVEKALQAAYGASAPSVTSAALRWMYHHSQLQGAHGDAVILGMSSLEQLEQNLAA
TEEGPLEPAVVDAFNQAWHLVAHECPNYFR

FIGURE 73

ACCGTCTTCCGCCGCACGTGGATTCAGCGCG**ATG**CCCAAATCCAAGCGCGACAAGAAAGTCTCCTTAACCAAAAC
TGCCAAGAAAGGCTTGGAATTGAAACAAAACCTGATAGAAGAGCTTCGGAAATGTGTGGACACCTACAAGTACCT
TTTCATCTTCTCTGTGGCCAACATGAGGAACAGCAAGCTGAAGGACATCCGGAACGCCTGGAAGCACAGCCGGAT
GTTCTTTGGCAAAAACAAGGTGATGATGGTGGCCTTGGGTCGGAGCCCATCTGATGAATACAAAGACAACCTGCA
CCAGGTCAGCAAAAGGTTGAGGGGTGAGGTGGGTCTCCTGTTCACCAACCGCACAAAGGAAGAGGTGAATGAGTG
GTTCACGAAATACACAGAAATGGACTACGCCCGAGCTGGTAACAAAGCAGCTTTCACTGTGAGCCTGGATCCAGG
GCCCCTGGAGCAGTTCCCCCACTCCATGGAGCCACAGCTCAGGCAGCTGGGCCTGCCCACCGCCCTCAAGAGAGG
TGTGGTGACTCTGCTGTCTGACTACGAGGTGTGCAAGGAGGGCGATGTGCTGACCCCAGAGCAGGCTCGCGTCCT
GAAGCTTTTTGGGTATGAGATGGCTGAATTCAAGGTGACCATCAAATACATGTGGGATTCACAGTCGGGAAGGTT
CCAGCAGATGGGAGACGACTTGCCAGAGAGCGCATCTGAGTCCACAGAAGAGTCAGACTCAGAAGATGATGAC**TG**
AAAGGGACTCGGGACTGAAGGTCTCCTGGAAGCTTCTGGGTCTCACTGGACCATCAGGACTGCTGCCGCCCCTCT
GGAGAGAGCAGCTTTTTATTTGTCTGTAGACAGGGAACATGATGGGCACTGACCTCCTGTAAAGAATAAAACTGT
GGGCCGGGCGCGGTGGCTCACGCCTGGAATCCCAGCACTTTGGGAAGCCGAGGTGGGCAGATCATAAGGTCAGGA
GATTAAGACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAATAGAAAAAAAAACTAGTTGGGCATAG
TGGCATGTGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCCGGGAGGTGGAGGTTG
CCGTGAGTTGAGATTGGACCACTGCTCTCCAGCCTGGGCAACAGAGTAAAACTCTGTCCC

FIGURE 74

MPKSKRDKKVSLTKTAKKGLELKQNLIEELRKCVDTYKYLFIFSVANMRNSKLKDIRNAWKHSRMFFGKNKVMMV
ALGRSPSDEYKDNLHQVSKRLRGEVGLLFTNRTKEEVNEWFTKYTEMDYARAGNKAAFTVSLDPGPLEQFPHSME
PQLRQLGLPTALKRGVVTLLSDYEVCKEGDVLTPEQARVLKLFGYEMAEFKVTIKYMWDSQSGRFQQMGDDLPES
ASESTEESDSEDDD

FIGURE 75

ATCGCTGGGCGACTGATTTCGAGTTTCCGGTCAGGTTAGGCCGGGGGGGTGCGGTCCTGGTCGGAAGGAGGTGGA
GAGTCGGGGGTCACCAGGCCTATCCTTGGCGCCACAGTCGGCCACCGGGGCTCGCCGCCGTCATGGAGAGCGGAG
GGCGGCCCTCGCTGTGCCAGTTCATCCTCCTGGGCACCACCTCTGTGGTCACCGCCGCCCTGTACTCCGTGTACC
GGCAGAAGGCCCGGGTCTCCCAAGAGCTCAAGGGAGCTAAAAAAGTTCATTTGGGTGAAGATTTAAAGAGTATTC
TTTCAGAAGCTCCAGGAAAATGCGTGCCTTATGCTGTTATAGAAGGAGCTGTGCGGTCTGTTAAAGAAACGCTTA
ACAGCCAGTTTGTGGAAAACTGCAAGGGGGTAATTCAGCGGCTGACACTTCAGGAGCACAAGATGGTGTGGAATC
GAACCACCCACCTTTGGAATGATTGCTCAAAGATCATTCATCAGAGGACCAACACAGTGCCCTTTGACCTGGTGC
CCCACGAGGATGGCGTGGATGTGGCTGTGCGAGTGCTGAAGCCCCTGGACTCAGTGGATCTGGGTCTAGAGACTG
TGTATGAGAAGTTCCACCCCTCGATTCAGTCCTTCACCGATGTCATCGGCCACTACATCAGCGGTGAGCGGCCCA
AAGGCATCCAAGAGACCGAGGAGATGCTGAAGGTGGGGGCCACCCTCACAGGGGTTGGCGAACTGGTCCTGGACA
ACAACTCTGTCCGCCTGCAGCCGCCCAAACAAGGCATGCAGTACTATCTAAGCAGCCAGGACTTCGACAGCCTGC
TGCAGAGGCAGGAGTCGAGCGTCAGGCTCTGGAAGGTGCTGGCGCTGGTTTTTGGCTTTGCCACATGTGCCACCC
TCTTCTTCATTCTCCGGAAGCAGTATCTGCAGCGGCAGGAGCGCCTGCGCCTCAAGCAGATGCAGGAGGAGTTCC
AGGAGCATGAGGCCCAGCTGCTGAGCCGAGCCAAGCCTGAGGACAGGGAGAGTCTGAAGAGCGCCTGTGTAGTGT
GTCTGAGCAGCTTCAAGTCCTGCGTCTTTCTGGAGTGTGGGCACGTTTGTTCCTGCACCGAGTGCTACCGCGCCT
TGCCAGAGCCCAAGAAGTGCCCTATCTGCAGACAGGCGATCACCCGGGTGATACCCCTGTACAACAGCTAATAGT
TTGGAAGCCGCACAGCTTGACCTGGAAGCACCCCTGCCCCCTTTTCAGGGATTTTTATCTCGAGGCCTTTGGAGG
AGCAGTGGTGGGGGTAGCTGTCACCTCCAGGTATGATTGAGGGAGGAATTGGGTAGAAACTCTCCAGACCCATGC
CTCCAATGGCAGGATGCTGCCTTTCCCACCTGAGAGGGGACCCTGTCCATGTGCAGCCTCATCAGAGCCTCACCC
TGGGAGGATGCCGTGGCGTCTCCTCCCAGGAGCCAGATCAGTGCGAGTGTGACTGAAAATGCCTCATCACTTAAG
CACCAAAGCCAGTGATCAGCAGCTCTTCTGTTCCTGTGTCTTCTGTTTTTTTCTGGTGAATCGTTGCTTGCTGTG
GACTTGGTGGAGGACTCAGAGGGGAGGAAAGGCTGGGCCCCGAGTACAACGGATGCCTTGGGTGCTGCCTCCGAA
GAGACTCTGCCGCAGCTTTTCTTCTTTTTCCTCATGCCCCGGGAAACAGTCTTTCTTCAGAATTGTCAGGCTGGG
CAGGTCAACTTGTGTTCCTTTCCCCTCACCTGCTTGCCTCCTTAACGCCTGCACGTGTGTGTAGAGGACAAAAGA
AAGTGAAGTCAGCACATCCGCTTCTGCCCAGATGGTCGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAA
GGGCAGTTGGTCAGGCAGGCCTCCTGGTTTCGCCACTGGCCCTGATTTGAACTCCTGCCACTTGGGAGAGCTCGG
GGTGGTCCCTGGTTTTCCCTCCTGGAGAATGAGGCGCAGAGGCCTCGCCTCCTGAAGGACGCAGTGTGGATGCCA
CTGGCCTAGTGTCCTGGCCTCACAGCTTCCTTGCAAGGCTGTCACAAGGAAAAGCAGCCGGCTGGCACCCTGAGC
ATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTCGCAGCTTTGACATCTTGGTGTACTCATGTCGCTTCTCCTT
GTGTTACCCCCTCCCAGTATTACCATTTGCCCCTCACCTGCCCTTGGTGAGCCTTTTAGTGCAAGACAGATGGGG
CTGTTTTCCCCCACCTCTGAGTAGTTGGAGGTCACATACACAGCTCTTTTTTTATTGCCCTTTTCTGCCTCTGAA
TGTTCATCTCTCGTCCTCCTTTGTGCAGGCGAGGAAGGGGTGCCCTCAGGGGCCGACACTAGTATGATGCAGTGT
CCAGTGTGAACAGCAGAAATTAAACATGTTGCAACC

FIGURE 76A

GCGGCAGAGCTCGGCGGCTGGGACTGGAGGACAGCGGTGGCGGAGGCGACTAGCGGCGGCGGGAGCGGCGCCGAG
AGGCCGTGCGGGACGCGGGCGCCAGGACCGGCCGAACGCAGAGGTTGATTCTTCACCACACTGAAACCATTAGGA
AAAATCCTTGTGGTTAACAGCAGAGGCTTCAGAGTGTAACCTGTACTCGGGCCTAGAAATTATTTAAAATGGCGA
CTGATACGTCTCAAGGTGAACTCGTCCATCCTAAGGCACTCCCACTTATAGTAGGAGCTCAGCTGATCCACGCGG
ACAAGTTAGGTGAGAAGGTAGAAGATAGCACCATGCCGATTCGTCGAACTGTGAATTCTACCCGGGAAACTCCTC
CCAAAAGCAAGCTTGCTGAAGGGGAGGAAGAAAAGCCAGAACCAGACATAAGTTCAGAGGAATCTGTCTCCACTG
TAGAAGAACAAGAGAATGAAACTCCACCTGCTACTTCGAGTGAGGCAGAGCAGCCAAAGGGGGAACCTGAGAATG
AAGAGAAGGAAGAAAATAAGTCTTCTGAGGAAACCAAAAAGGATGAGAAAGATCAGTCTAAAGAAAAGGAGAAGA
AAGTGAAAAAAACAATTCCTTCCTGGGCTACCCTTTCTGCCAGCCAGCTAGCCAGGGCCCAGAAACAAACACCGA
TGGCTTCTTCCCCACGTCCCAAGATGGATGCAATCTTAACTGAGGCCATTAAGGCATGCTTCCAGAAGAGTGGTG
CATCAGTGGTTGCTATTCGAAAATACATCATCCATAAGTATCCTTCTCTGGAGCTGGAGAGAAGGGGTTATCTCC
TTAAACAAGCACTGAAAAGAGAATTAAATAGAGGAGTCATCAAACAGGTTAAAGGAAAAGGTGCTTCTGGAAGTT
TTGTTGTGGTTCAGAAATCAAGAAAAACACCTCAGAAATCCAGAAACAGAAAGAATAGGAGCTCTGCAGTGGATC
CAGAACCACAAGTAAAATTGGAGGATGTCCTCCCACTGGCCTTTACTCGCCTTTGTGAACCTAAAGAAGCTTCCT
ACAGTCTCATCAGGAAATATGTGTCTCAGTATTATCCTAAGCTTAGAGTGGACATCAGGCCTCAGCTGTTGAAGA
ACGCTCTGCAGAGAGCAGTAGAGAGGGGCCAGTTAGAACAGATAACTGGCAAAGGTGCTTCGGGGACATTCCAGC
TGAAGAAATCAGGGGAGAAACCCCTGCTTGGTGGAAGCCTGATGGAATATGCAATCTTGTCTGCCATTGCTGCCA
TGAATGAGCCGAAGACCTGCTCTACCACTGCTCTGAAGAAGTATGTCCTAGAGAATCACCCAGGAACCAATTCTA
ACTATCAAATGCATTTGCTGAAAAAAACCCTGCAGAAATGCGAAAAGAATGGGTGGATGGAACAGATCTCTGGGA
AAGGGTTCAGTGGCACCTTCCAGCTCTGTTTCCCTATTATCCAGCCCAGGAGTTCTGTTTCCGAAGAAAGAGC
CAGATGATTCTAGAGATGAGGATGAAGATGAAGATGAGTCATCAGAAGAAGACTCTGAGGATGAAGAGCCGCCAC
CTAAGAGAAGGTTGCAGAAGAAAACCCCAGCCAAGTCCCCAGGGAAGGCCGCATCTGTGAAGCAGAGAGGGTCCA
AACCTGCACCTAAAGTCTCAGCTGCCCAGCGGGGGAAAGCTAGGCCCTTGCCTAAGAAAGCACCTCCTAAGGCCA
AAACGCCTGCCAAGAAGACCAGACCCTCATCCACAGTCATCAAGAAACCTAGTGGTGGCTCCTCAAAGAAGCCTG
CAACCAGTGCAAGAAAGGAAGTAAAATTGCCGGGCAAGGGCAAATCCACCATGAAGAAGTCTTTCAGAGTGAAAA
AGTAAATTTTATAGGAAAAAAGGGTATCATGATGAAATTCAAAATCTTATTTTCTAAGGTCAGTGTGCATTTGTT
TAGTTTTGATGCTTTTCAAATTACATTATTTTCCTCCCCTATGAACATTGTGGGGAGGGACTCTAAATAAACCAG
TTTAGGCATTTGCTAGCTTTAGGTGCTTTTATTGGTGCCTGCCCTTTTCCTTGTTCATTTTAATTTCTGCAATAA
TCCTGGACTTTCCTAAACTATGTAATGTATACTTGTCCTTTTTCTCTGCCTCCCCCAACCCCCTGTTGTTTTTAT
GGTCAGCTTTGCCTTTTTTTTTTCTTCCAATTTTATCTAAACAGTTGCAGAGATTTTTATATTTGTAGAAAGCAT
CAAGAACGGTATGCCAGTCAGGTCCTGGAAGTAAAATGGAGGCACAATATAGCACTGACTGAGTTGTAAAGCCTC
CTGCCTGGAGACTTCAGTTATAGCTGTAATAATTAATCTTATTTATAAAAGCCACTCCACTAACCTTTTCTCTCC
AACTGTAAACACAGAGACAGCTTTGGGAATAAGCCAAAAACAGGGTGATCTCATTAGATTTTGAAGATATATGAC
TCCTTTGGGCTACATTTCATATTGATCAATTTCTAGGTATTTTTCACTGGCCCAAAGTATTGCATTCCCTTAACA
GCAAGCACAAGTTCTCTATATCACTTGTTTTTTGTTGTTGTTGTTGTCGTCGTTGTTTTGAGACGGAGTCTT
GCTCAGGTGCCCCGGAGTGCAGTGGTGCAATCTCAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAATTCTC
CTGCTTCAGCCTCCCGAGTAGCTGGGATTACAGGTGTGTACCACCACGCCTGGCAATTTTTTTGTATTTTTAGTA
GAGATGGGGTTTCGCCGTGTTGGTCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCGCCTGCCTCGGCCTCC
CAAAGTGCTGGGATTACAGGAGTGAGCCACTGTGCCTGGCCTATCCCACTTGGTTTTTGACTGAAGGGGAAGTGT
AGAAATATATTGATTTGTGATTTCTGGTGTCACCTGTGTTACCAAAAATCAAAACAAATCTTTTTTATTTTTTAT
TATTATTATTATTTTTGAGACAGAGTCTCGCTCTGTCGCCCAGTGTGGAGTGCAGTGGTGTGATCTTGGCTCACT
GCAAACTCCGCCTCCCAGGTTCAAGCGATTCTCCCACCTCAGCCTCCTGAGTTGGGTCCTACAGGCGCACACGAC
CACGCCCAGCTAATTTTTTGTATTTTTAGTAGAGTTGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCT
GACCTCGTGATCCACTCACCTCAGCCTCCCAAAATCCTGGGGTTACAGATGTGAGCTACCACTCACGGCCCAAAT
CTTCTTGATCATATGTTTAAATATATTTTTTAATATTTGGAGCATGAGTTGTCACTTCTTGTTTGCCTTTTTTAT
AAGGAAATGTTGGAGAGTTACATCATTGCTAATGTAGAAATGTTAAGTGGAAAAATATACAGTTTGGTAAAATAA
ACTAGATTCTACATTTATTTGTGGGTTTTTTCCCCTCCTTTCTTTCCACAGCACTTTTGATATCAAGCAAGTGG
CTTCCTTTTTGAGATATTAAAAAAAAAAAGAAAAGGAAAAAAGTAAATGAAGCCCAACTACCTAACCCTTTCTTA

FIGURE 76B

TTTGTATTTGTTTTAGTATTGTGAAGTTGTGTTAAATAGTACTAGCTAGAAATACAAATTTCTGGTTATCATTTC
TCTTCCCTGTGGCACTTGACATTTTAATTGTCTTAAAGTTTTTGAAGTACATCTTCTGGCCCCTTGAGTACTGCC
AGAGGCAAAAGATGTTTGTTTCTTATTCATTCCACTTTTGTCTCCTGGGATCCCTTCTGTAGCCTAAAGTATGGC
TGGGAAATGGACTTGAGAAGATTGGCTTGAATTAGATCATAATCATGTGTGATCCCATCATGAATTCATTGGAAT
TTGTGTTGCATGTAAGGCAATCTTTCCTGTTGTAAATCTTCCTTTTTTAATGTACATATATTTTGAAAAATATGA
ATAAACATGAAATTTT

FIGURE 77

GGCGCCGAGTAGCCGGGCCGGGCCGGAGCGCGGGCGGCGGCGGAGGCAGCTGCGCCCGCGCCTCCTGCCCTCCCA
GGCCCCGCGCCCCGCGCCCGGGCCCCGGCGATGGTGACACATGCGGCGGCGGCGCGCCAGCGGCAGGACCATGGT
TGAGCGCGCCAGCAAGTTCGTGCTGGTGGTGGCGGGCCCGGTGTGCTTCATGCTCATCTTGTACCAGTACGCGGG
CCCAGGACTGAGCCTGGGCGCGCCCGGCGGCGGCGCGCCGCCCGACGACCTGGACCTGTTCCCCACGCCCGACCC
CCACTACGAGAAGAAGCACTACTTCCCGGTCCGCGAGCTGGAGCGCTCGCTGCGCTTCGACATGAAGGGCGACGA
CGTGATCGTCTTCCTGCACATCCAGAAGACGGGCGGCACCACCTTCGGCCGCCACCTCGTGCAGAACGTACGCCT
CGAGGTGCCGTGCGACTGCCGGCCCGGCCAGAAGAAGTGCACCTGCTACCGGCCCAACCGCCGCGAGACTTGGCT
CTTCTCCCGCTTCTCCACCGGCTGGAGCTGCGGGCTGCACGCCGACTGGACCGAGCTCACCAACTGCGTGCCCGG
CGTGCTGGACCGCCGCGACTCCGCCGCGCTGCGCACGCCCAGGAAGTTCTACTACATCACCCTGCTACGAGACCC
CGTGTCCCGCTACCTGAGCGAGTGGCGGCATGTGCAGAGGGGTGCCACGTGGAAGACGTCGTTGCACATGTGTGA
TGGGCGCACGCCCACGCCTGAGGGGCTGCCGCCCTGCTACGAGGGCACGGACTGGTCGGGCTGCACGCTACAGGA
GTTCATGGACTGCCCGTACAACCTGGCCAACAACCGCCAGGTGCGCATGCTGGCCGACCTGAGCCTGGTGGGCTG
CTACAACCTGTCCTTCATCCCCGAGGGCAAGCGGGCCCAGCTGCTGCTCGAGAGCGCCAAGAAGAACCTGCGGGG
CATGGCCTTCTTCGGCCTGACCGAGTTCCAGCGCAAGACGCAGTACCTGTTCGAGCGGACGTTCAACCTCAAGTT
CATCCGGCCCTTCATGCAGTACAACAGCACGCGGGCGGGCGGCGTGGAGGTGGATGAGGACACCATCCGGCGCAT
CGAGGAGCTCAACGACCTGGACATGCAGCTGTATGACTACGCCAAGGACCTCTTCCAGCAGCACTACCAGTACAA
GCGGCAGCTGGAGCGCAGGGAGCAGCGCCTGAGGAGCCGCGAGGAGCGTCTGCTGCACCGGGCCAAGGAGGCGCT
GCCGCGGGAGGACGCCGACGAGCCGGGCCGCGTGCCCACCGAGGACTACATGAGCCACATCATTGAGAAGTGGTA
GTGGCGGTGGTGGCCACGGGGAGGCCTCTTGGGGTGTGTGGGGGATAAAACAGGACAGACGACAGGTCCACCCAA
GACTGTCAAGGGATGAGCATCCCAAACCTGCTCCACAGAGGTAGCTGCGTCCTGAAAAAAAACACAGCAGGGACA
TAGTGGGGCTGGGCAGGGATGGGGCTTGAGAAATCAACAGGTGCAGCCCAGTGGGTCAGAGGAAAGCGTGCTCGA
AGGATGCCATGGTCAGGGCAGAGCCTCCAGAGCAGGTGTTGTGCCTGGAGCTGCTCTCCTGGCCTCCTTGGATTT
ATCGCAAAAACTGAAGGTTTGCGTGAGAGACGAGGACAGCGGAAAGTGGACCTGCCAGGCCGGGAGTGTGTCCCT
CACCAACTATGCACACAGCACTCGCTCTTAGCTCCTCTGTCCGGGCTACTAGGAGTGAGACCAGCTTCTGGCAAC
TGCCCCAGCTCCAGGCCATCCCATAGCTCCTCCTCTTCTGGCTGCCCCCAATGCCCCGAGGCCTGGGGAGCCCCC
AGCTCACCCATCTGTAGCTCCCTCAAAGTCAGGGCCCACCCCATCTGAGGCAGAGAAGACTCGAGTCCAGCCCCC
AGGAAGCCTGCTCCCCTCTCTGGCCCATGGTCCTGCTTCATGCTTTGGGTCAGGAGGCCAAAGCTGATGTTCAGG
CCCCACCCACTCCCTACAGTCCTCAGACC

FIGURE 78

AGAAACTCCCGGTGTGGCAGCTGAGATGGCCCAGGAAAGAACTATATTACCTTCAAAAAGAGAGGTACATGCGAT
GTTTGAGGTGGCATGAAGCTCAGTGGTGTTATATTGGAATGAGTGAGTGACCATCCTGGAGCCTTCCTGAAAGAG
GATTGGAACATCAGTTAACATCTGACCACTGCCAGCCCACCCCCTCCCACCCACGTCGATTGCATCTCTGGGCTC
CAGGGATAAAGCAGGTCTTGGGGTGCACCATGATTTCACCATTCTTAGTACTGGCCATTGGCACCTGCCTTACTA
ACTCCTTAGTGCCAGAGAAAGAGAAAGACCCCAAGTACTGGCGAGACCAAGCGCAAGAGACACTGAAATATGCCC
TGGAGCTTCAGAAGCTCAACACCAACGTGGCTAAGAATGTCATCATGTTCCTGGGAGATGGGATGGGTGTCTCCA
CAGTGACGGCTGCCCGCATCCTCAAGGGTCAGCTCCACCACAACCCTGGGGAGGAGACCAGGCTGGAGATGGACA
AGTTCCCCTTCGTGGCCCTCTCCAAGACGTACAACACCAATGCCCAGGTCCCTGACAGTGCCGGCACCGCCACCG
CCTACCTGTGTGGGGTGAAGGCCAATGAGGGCACCGTGGGGGTAAGCGCAGCCACTGAGCGTTCCCGGTGCAACA
CCACCCAGGGGAACGAGGTCACCTCCATCCTGCGCTGGGCCAAGGACGCTGGGAAATCTGTGGGCATTGTGACCA
CCACGAGAGTGAACCATGCCACCCCCAGCGCCGCCTACGCCCACTCGGCTGACCGGGACTGGTACTCAGACAACG
AGATGCCCCCTGAGGCCTTGAGCCAGGGCTGTAAGGACATCGCCTACCAGCTCATGCATAACATCAGGGACATTG
ACGTGATCATGGGGGGTGGCCGGAAATACATGTACCCCAAGAATAAAACTGATGTGGAGTATGAGAGTGACGAGA
AAGCCAGGGGCACGAGGCTGGACGGCCTGGACCTCGTTGACACCTGGAAGAGCTTCAAACCGAGATACAAGCACT
CCCACTTCATCTGGAACCGCACGGAACTCCTGACCCTTGACCCCCACAATGTGGACTACCTATTGGGTCTCTTCG
AGCCAGGGGACATGCAGTACGAGCTGAACAGGAACAACGTGACGGACCCGTCACTCTCCGAGATGGTGGTGGTGG
CCATCCAGATCCTGCGGAAGAACCCCAAAGGCTTCTTCTTGCTGGTGGAAGGAGGCAGAATTGACCACGGGCACC
ATGAAGGAAAAGCCAAGCAGGCCCTGCATGAGGCGGTGGAGATGGACCGGGCCATCGGGCAGGCAGGCAGCTTGA
CCTCCTCGGAAGACACTCTGACCGTGGTCACTGCGGACCATTCCCACGTCTTCACATTTGGTGGATACACCCCCC
GTGGCAACTCTATCTTTGGTCTGGCCCCCATGCTGAGTGACACAGACAAGAAGCCCTTCACTGCCATCCTGTATG
GCAATGGGCCTGGCTACAAGGTGGTGGGCGGTGAACGAGAGAATGTCTCCATGGTGGACTATGCTCACAACAACT
ACCAGGCGCAGTCTGCTGTGCCCCTGCGCCACGAGACCCACGGCGGGGAGGACGTGGCCGTCTTCTCCAAGGGCC
CCATGGCGCACCTGCTGCACGGCGTCCACGAGCAGAACTACGTCCCCCACGTGATGGCGTATGCAGCCTGCATCG
GGGCCAACCTCGGCCACTGTGCTCCTGCCAGCTCGGCAGGCAGCCTTGCTGCAGGCCCCCTGCTGCTCGCGCTGG
CCCTCTACCCCCTGAGCGTCCTGTTCTGAGGGCCCAGGGCCCGGGCACCCACAAGCCCGTGACAGATGCCAACTT
CCCACACGGCAGCCCCCCCCTCAAGGGGCAGGGAGGTGGGGGCCTCCTCAGCCTCTGCAACTGCAAGAAAGGGGA
CCCAAGAAACCAAAGTCTGCCGCCCACCTCGCTCCCCTCTGGAATCTTCCCCAAGGGCCAAACCCACTTCTGGCC
TCCAGCCTTTGCTCCCTCCCCGCTGCCCTTTGGCCAACAGGGTAGATTTCTCTTGGGCAGGCAGAGAGTACAGAC
TGCAGACATTCTCAAAGCCTCTTATTTTTCTAGCGAACGTATTTCTCCAGACCCAGAGGCCCTGAAGCCTCCGTG
GAACATTCTGGATCTGACCCTCCCAGTCTCATCTCCTGACCCTCCCACTCCCATCTCCTTACCTCTGGAACCCCC
CAGGCCCTACAATGCTCATGTCCCTGTCCCCAGGCCCAGCCCTCCTTCAGGGGAGTTGAGGTCTTTCTCCTCAGG
ACAAGGCCTTGCTCACTCACTCACTCCAAGACCACCAGGGTCCCAGGAAGCCGGTGCCTGGGTGGCCATCCTACC
CAGCGTGGCCCAGGCCGGGAAGAGCCACCTGGCAGGGCTCACACTCCTGGGCTCTGAACACACACGCCAGCTCCT
CTCTGAAGCGACTCTCCTGTTTGGAACGGCAAAAAAAAATTTTTTTTTCTCTTTTTGGTGGTGGTTAAAAGGGAA
CACAAAACATTTAAATAAAACTTTCCAAATATTTCCGAGG

FIGURE 79

GAACCGCCATCTTCCAGTAATTCGCCAAA**ATG**ACGAACACAAAGGGAAAGAGGAGAGGCACCCAATAGATGTTCT
CCAGGCCTTTTAGAAAACATGGAGTTGTTCCTTTGGCCACGTATATGCGAATCTATAAGAAAGGTGATATTGTAG
ACATCAAGGGAATGGGTACTGTTCAAAAAGGAACGCCCCACAAGTGTTACCATGGCAAAACTGGAAGAGTCTACA
ATGTTATCCAGTATGCTGCTAGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATG
TGCGTATTGAGCACATTAAGCACTCTGAGAGCCGAGATAGCTTCCTGAAACGCGTGAAGGAGAATGATCAGAAAA
AGAGAGAAGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCAGCCTGCTCCACCCAGCAAAGCACACTTTG
TGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCTCTATGAATTCACGGCA**TAA**TAGGTATTTAAAA
AAAAAAAAAGACCTCTGGGCTGT

FIGURE 80

DRTQRERGEAPNRMFSRPFRKHGVVPLATYMRIYKKGDIVDIKGMGTVQKGTPHKCYHGKTGRVYNVIQYAASIV
VNKQVKGKILAKRINVRIEHIKHSESRDSFLKRVKENDQKKREAKEKGTWVQLKRQPAPPSKAHFVRTNGKEPEL
LEPILYEFTA

FIGURE 81

GGCAGCCGAGGAGACCCCGCGCAGTGCTGCCAACGCCCCGGTGGAGAAGCTGAGGTCATCATCAGATTTGAAATA
TTTAAAGTGGATACAAAATTATTTCAGCA**ATG**CAGACAATTAAGTGTGTTGTTGTGGGCGATGGTGCTGTTGGTA
AAACATGTCTCCTGATATCCTACACAACAAACAAATTTCCATCGGAATATGTACCGACTGTTTTTGACAACTATG
CAGTCACAGTTATGATTGGTGGAGAACCATATACTCTTGGACTTTTTGATACTGCAGGGCAAGAGGATTATGACA
GATTACGACCGCTGAGTTATCCACAAACAGATGTATTTCTAGTCTGTTTTTCAGTGGTCTCTCCATCTTCATTTG
AAAACGTGAAAGAAAAGTGGGTGCCTGAGATAACTCACCACTGTCCAAAGACTCCTTTCTTGCTTGTTGGGACTC
AAATTGATCTCAGAGATGACCCCTCTACTATTGAGAAACTTGCCAAGAACAAACAGAAGCCTATCACTCCAGAGA
CTGCTGAAAAGCTGGCCCGTGACCTGAAGGCTGTCAAGTATGTGGAGTGTTCTGCACTTACACAGAAAGGCCTAA
AGAATGTATTTGACGAAGCAATATTGGCTGCCCTGGAGCCTCCAGAACCGAAGAAGAGCCGCAGGTGTGTGCTGC
TA**TGA**ACATCTCTCCAGAGCCCTTTCTGCACAGCTGGTGTCGGCATCATACTAAAAGCAATGTTTAAATCAAACT
AAAGATTAAAAATTAAAATTCGTTTTTGCAATAATGACAAATGCCCTGCACCTACCCACATGCACTCGTGTGAGA
CAAGGCCCATAGGTATGGCCCCCCCCTTCCCCCTCCCAGTACTAGTTAATTTTGAGTAATTGTATTGTCAGAAAA
GTGATTAGTACTATTTTTTTTTGTTGTTTCAAAAAAAAAATTTTTGTGTGTCTGTTTTTTTTTTTTTTTTTTTTT
GTTGTTTAAAAGGAAGGCATGCTTGTGGATGACTCTGTAACAGACTAATTGGAATTGTTGAAGCTGCTCCCTGGT
TCCACTCTGGAGAGTAATCTGGGACATCTTAGTGTTTTGTTTTGTTTTTTTCCCTCCTCTTTTTTTTGGGGGGGA
GTGTGTGTGGGGTTTGTTTTTTAGTCTTGTTTTTTTAATTCATTAACCAGTGGTTAGCCCTTAAGGGGAGGAGGA
CGGATTGATTCCACATTCCACTTCCTAGATCTAGTTTAGAAAACATGTTCCCCATCTGGTGCTCTTAGGAAGGAG
TATAGTAAATGCCTCATTTAATAACATACTCCTTTTTGAAAGTTGCCTTTTCTCTCCACCCTTGAGTAGATCCAG
TATTTGATGAAACTCATGAAAGTGGGTGGAGCCCATCTTGCCCCTCCTCTTTTCTAGGACGCACTATATGTGACT
GTGACTTTCAAGGACATTTGTTTGCCATTTGCTGATTTTTTTGGGAAGTTAATTTCTAACTTCTTTCACTGATAA
ATGAAGAAAAGTATTGCACCTTTGAAATGCACCAAATGAATTGAGTTTGTAATTAAAAAAATTTTTTTCCCTTTC
AGTCATTGTCTTATATGCTTAGCATAGATTTGCAGCTCAGTAGTATATGGTGTTCCTAGAATGCAGCTGAAGACC
TGTTATGTAGAGGAAATACGAGGGGTGGTGCTAGAAGACAGACATCTGTGGAATGATTCACATCCTCTCAAGTTA
GGAGGATGGAGGCCTGCTTCATTAAGAAGCTGGGGGTAGGGTGGGGGTGGGGAGAACACTTAACAACATGGGGAC
CAGTCAGGGGAATCCCCTTATTTCTGTTTTGCATATGAGGAACCCTAGAGCAGCCAGGTGAGGCTCTCTAGTTTA
ATAAAAATCATGGAAAGACTCTTAATGCAGACTCTTCTTAAGTGTTAATAGGGATTTTTTCAGCTTATTTTGGTT
GCAGTTTCCAATTTTTAAAAATGTTGAGGTAATCTTTCCCACCTTCCCAAACCTAATTCTTGTAGATGCATTAGT
GTTGAACCAATGCTTTCTCATGTCTCAATTCTTTGTATATGCATTCTTTTCAGATGTATTAAACAAACAAAAACC
CTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAA

FIGURE 82

MQTIKCVVVGDGAVGKTCLLISYTTNKFPSEYVPTVFDNYAVTVMIGGEPYTLGLFDTAGQEDYDRLRPLSYPQT
DVFLVCFSVVSPSSFENVKEKWVPEITHHCPKTPFLLVGTQIDLRDDPSTIEKLAKNKQKPITPETAEKLARDLK
AVKYVECSALTQKGLKNVFDEAILAALEPPEPKKSRRCVLL

FIGURE 83

CGCGCGCGCCATTTCTAGTCGTTTTCAAAGCGCCTCGCGCTGATTCTCACGGGCCCGGCTGCCGGCCCCCGCTCT
GCCCTGCATAATAAAATGGCTAATCAGGTGAATGGTAATGCGGTACAGTTAAAAGAAGAGGAAGAACCAATGGAT
ACTTCCAGTGTAACTCACACAGAACACTACAAGACACTGATAGAGGCAGGCCTCCCACAGAAGGTGGCAGAAAGA
CTTGATGAAATATTTCAGACAGGATTGGTAGCTTATGTCGATCTTGATGAAAGAGCAATTGATGCTCTCAGGGAA
TTTAATGAAGAAGGAGCTCTGTCTGTACTACAGCAGTTCAAGGAAAGTGACTTATCACATGTTCAGAACAAAAGT
GCATTTTTATGTGGAGTTATGAAGACCTACAGGCAGAGAGAGAAACAGGGGAGCAAGGTGCAAGAGTCCACAAAG
GGACCTGATGAAGCGAAGATCAAGGCCTTGCTTGAGAGAACTGGTTATACTCTGGATGTAACCACAGGACAGAGG
AAGTATGGTGGTCCTCCACCAGACAGTGTGTACTCTGGCGTGCAACCTGGAATTGGAACGGAGGTATTTGTAGGC
AAAATACCAAGGGATTTATATGAGGATGAGTTGGTGCCCCTTTTTGAGAAGGCCGGACCCATTTGGGATCTACGT
CTTATGATGGATCCACTGTCCGGTCAGAATAGAGGGTATGCATTTATCACCTTCTGTGGAAAGGAAGCTGCACAG
GAAGCCGTGAAACTGTGTGACAGCTATGAAATTCGCCCTGGTAAACACCTTGGAGTGTGCATTTCTGTGGCAAAC
AACAGACTTTTTGTTGGATCCATTCCGAAGAATAAGACTAAAGAAAACATTTTGGAAGAATTCAGTAAAGTCACA
GAGGGTTTGGTGGACGTTATTCTCTATCATCAACCCGATGACAAAAAGAAGAATCGGGGGTTCTGCTTCCTTGAA
TATGAGGATCACAAGTCAGCAGCACAAGCCAGACGCCGGCTGATGAGTGGAAAAGTAAAAGTGTGGGGAAATGTA
GTTACAGTTGAATGGGCTGACCCTGTGGAAGAACCAGATCCAGAAGTCATGGCTAAGGTAAAAGTTTTGTTTGTG
AGAAACTTGGCTACTACGGTGACAGAAGAAATATTGGAAAAGTCATTTTCTGAATTTGGAAAACTCGAAAGAGTA
AAGAAGTTGAAAGATTATGCATTTGTTCATTTTGAAGACAGAGGAGCAGCTGTTAAGGCTATGGATGAAATGAAT
GGCAAAGAAATAGAAGGGGAAGAAATTGAAATAGTCTTAGCCAAGCCACCAGACAAGAAAAGGAAAGAGCGCCAA
GCTGCTAGACAGGCCTCCAGAAGCACTGCGTATGAAGATTATTACTACCACCCTCCTCCTCGCATGCCACCTCCA
ATTAGAGGTCGGGGTCGTGGTGGGGGGAGAGGTGGATATGGCTACCCTCCAGATTACTACGGCTATGAAGATTAC
TATGATGATTACTATGGTTATGATTATCACGACTATCGTGGAGGCTATGAAGATCCCTACTACGGCTATGATGAT
GGCTATGCAGTAAGAGGAAGAGGAGGAGGAAGGGGAGGGCGAGGTGCTCCACCACCACCAAGGGGGAGGGGAGCA
CCACCTCCAAGAGGTAGAGCTGGCTATTCACAGAGGGGGGCACCTTTGGGACCACCAAGAGGCTCTAGGGGTGGC
AGAGGGGGTCCTGCTCAACAGCAGAGAGGCCGTGGTTCCCGTGGATCTCGGGGCAATCGTGGGGGCAATGTAGGA
GGCAAGAGAAAGGCAGATGGGTACAACCAGCCTGATTCCAAGCGTCGTCAGACCAACAACCAACAGAACTGGGGT
TCCCAACCCATCGCTCAGCAGCCGCTTCAGCAAGGTGGTGACTATTCTGGTAACTATGGTTACAATAATGACAAC
CAGGAATTTTATCAGGATACTTATGGGCAACAGTGGAAGTAGACAAGTAAGGGCTTGAAAATGATACTGGCAAGA
TACGATTGGCTCTAGATCTACATTCTTCAAAAAAAAAAATTGGCTTAACTGTTTCATCTTTAAGTAGCATTTTGC
TGCCATTTGTATTGGGCTGAAGAAATCACTATTGTGTATATACTCAAGTCTTTTTATTTTTCCTCTTTTCATAAA
TGCTCTTGGACATTATTGGGCTTGCAGAGTTCCCTTATTCTGGGGATTACAATGCTTTTATCGTTTCAGGCTTCA
TTTTAGCTTCAAAACAAGCTGGGCACACTGTTAAATCATGATTTTGCAGAACCTTTGGTTTTGGACAGTTTCATT
TTTTTGGATTTGGGATAGATTACATAGGAGTATGGAGTATGCTGTAAATAAAAATACAAGCTAGTGCTTTGTCTT
AGTAGTTTTAAGAAATTAAAGCAAACAAATTTAAGTTTTCTTGTATTGAAAATAACCTATGATTGTATGTTTTGC
ATTCCTAGAAGTAGGTTAACTGTGTTTTTAAATTGTTATAACTTCACACCTTTTTGAAATCTGCCCTACAAAATT
TGTTTGGCTTAAACGTCAAAAGCCGTGACAATTTGTTCTTTGATGTGATTGTATTTCCAATTTCTTGTTCATGTA
AGATTTCAATAAAACTAAAAAATCTATTCAAAACATTA

FIGURE 84

MANQVNGNAVQLKEEEEPMDTSSVTHTEHYKTLIEAGLPQKVAERLDEIFQTGLVAYVDLDERAIDALREFNEEG
ALSVLQQFKESDLSHVQNKSAFLCGVMKTYRQREKQGSKVQESTKGPDEAKIKALLERTGYTLDVTTGQRKYGGP
PPDSVYSGVQPGIGTEVFVGKIPRDLYEDELVPLFEKAGPIWDLRLMMDPLSGQNRGYAFITFCGKEAAQEAVKL
CDSYEIRPGKHLGVCISVANNRLFVGSIPKNKTKENILEEFSKVTEGLVDVILYHQPDDKKKNRGFCFLEYEDHK
SAAQARRRLMSGKVKVWGNVVTVEWADPVEEPDPEVMAKVKVLFVRNLATTVTEEILEKSFSEFGKLERVKKLKD
YAFVHFEDRGAAVKAMDEMNGKEIEGEEIEIVLAKPPDKKRKERQAARQASRSTAYEDYYYHPPPRMPPPIRGRG
RGGGRGGYGYPPDYYGYEDYYDDYYGYDYHDYRGGYEDPYYGYDDGYAVRGRGGGRGGRGAPPPPRGRGAPPPRG
RAGYSQRGAPLGPPRGSRGGRGGPAQQQRGRGSRGSRGNRGGNVGGKRKADGYNQPDSKRRQTNNQQNWGSQPIA
QQPLQQGGDYSGNYGYNNDNQEFYQDTYGQQWK

FIGURE 85

CGGACTGGCAGGGGGCAGGGAAGCTCAAAGATCTGGGGTGCTGCCAGGAAAAAGCAAATTCTGGAAGTTAATGGT
TTTGAGTGATTTTTAAATCCTTGCTGGCGGAGAGGCCCGCCTCTCCCCGGTATCAGCGCTTCCTCATTCTTTGAA
TCCGCGGCTCCGCGGTCTTCGGCGTCAGACCAGCCGGAGGAAGCCTGTTTGCAATTTAAGCGGGCTGTGAACGCC
CAGGGCCGGCGGGGGCAGGGCCGAGGCGGGCCATTTTGAATAAAGAGGCGTGCCTTCCAGGCAGGCTCTATAAGT
GACCGCCGCGGCGAGCGTGCGCGCGTTGCAGGTCACTGTAGCGGGACTTCTTTTGGTTTTCTTTCTCTTTGGGGC
ACCTCTGGACTCACTCCCCAGCATGAAGGCGCTGAGCCCGGTGCGCGGCTGCTACGAGGCGGTGTGCTGCCTGTC
GGAACGCAGTCTGGCCATCGCCCGGGGCCGAGGGAAGGGCCCGGCAGCTGAGGAGCCGCTGAGCTTGCTGGACGA
CATGAACCACTGCTACTCCCGCCTGCGGGAACTGGTACCCGGAGTCCCGAGAGGCACTCAGCTTAGCCAGGTGGA
AATCCTACAGCGCGTCATCGACTACATTCTCGACCTGCAGGTAGTCCTGGCCGAGCCAGCCCCTGGACCCCCTGA
TGGCCCCCACCTTCCCATCCAGACAGCCGAGCTCACTCCGGAACTTGTCATCTCCAACGACAAAAGGAGCTTTTG
CCACTGACTCGGCCGTGTCCTGACACCTCCAGGTGAGTATCTCCTCTCTTGGAGAGGGAGGTTTAAACGGCAAGT
CCTGGAGTTGGCAGACGTTTTGAAAAATTGCCACTCACTCGGTTTAGGGAAACTGAGGCCAGAGAGGGACAAGTG
ACTTGCCCATGGTTG

FIGURE 86

MKALSPVRGCYEAVCCLSERSLAIARGRGKGPAAEEPLSLLDDMNHCYSRLRELVPGVPRGTQLSQVEILQRVID
YILDLQVVLAEPAPGPPDGPHLPIQTAELTPELVISNDKRSFCH

FIGURE 87

TTCTCTTCCTGCTCTCCATC**ATG**GCGCAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAACTTCGCATCCGCA
AACTCTGTCTCAACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGTTGGAGCAGCTCA
CAGGGCAGACCCCTGTGTTTCCAAAGCTAGATACACTGTCAGATCCTTTGGCATCCGGAGAAATGAAAAGATTG
CTGTCCACTGCACAGTTCGAGGGGCCAAGGCAGAAGAAATCTTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGT
TAAGAAAAAACAACTTCTCAGATACTGGAAACTTTGGTTTTGGGATCCAGGAACACATCGATCTGGGTATCAAAT
ATGACCCAAGCATTGGTATCTACGGCCTGGACTTCTATGTGGTGCTGGGTAGGCCAGGTTTCAGCATCGCAGACA
AGAAGCGCAGGACAGGCTGCATTGGGGCCAAACACAGAATCAGCAAAGAGGAGGCCATGCGCTGGTTCCAGCAGA
AGTATGATGGGATCATCCTTCCTGGCAAA**TAA**ATTCCCGTTTCTATCCAAAAGAGCAATAAAAAGTTTTCAGTGA
AATGTGCAA

FIGURE 88

MAQDQGEKENPMRELRIRKLCLNICVGESGDRLTRAAKVLEQLTGQTPVFSKARYTVRSFGIRRNEKIAVHCTVR
GAKAEEILEKGLKVREYELRKNNFSDTGNFGFGIQEHIDLGIKYDPSIGIYGLDFYVVLGRPGFSIADKKRRTGC
IGAKHRISKEEAMRWFQQKYDGIILPGK

FIGURE 89

GGAAGTTCCGGCGGGGGCGGCCGAGGGGGAAGAGTGTGTCTGCGGGAGAAAGAGGAGAATCGCCCAAGCGGCCTC
GGAAGTCCCAGGGAGTGGAGGCCCCCGCCGTGGAGCCGTGTGGTGT<u>ATG</u>TGTGGTAACACCATGTCTGTGCCCCT
GCTCACCGATGCTGCCACCGTGTCTGGAGCTGAGCGGGAAACGGCCGCGGTTATTTTTTTACATGGACTTGGAGA
CACAGGGCACAGCTGGGCTGACGCCCTCTCCACCATCCGGCTCCCTCACGTCAAGTACATCTGTCCCCATGCGCC
TAGGATCCCTGTGACCCTCAACATGAAGATGGTGATGCCCTCCTGGTTTGACCTGATGGGGCTGAGTCCAGATGC
CCCAGAGGACGAGGCTGGCATCAAGAAGGCAGCAGAGAACATCAAGGCCTTGATTGAGCATGAAATGAAGAACGG
GATCCCTGCCAATCGAATCGTCCTGGGAGGCTTTTCACAGGGCGGGGCCCTGTCCCTCTACACGGCCCTCACCTG
CCCCCACCCTCTGGCTGGCATCGTGGCGTTGAGCTGCTGGCTGCCTCTGCACCGGGCCTTCCCCCAGGCAGCTAA
TGGCAGTGCCAAGGACCTGGCCATACTCCAGTGCCATGGGGAGCTGGACCCCATGGTGCCCGTACGGTTTGGGGC
CCTGACGGCTGAGAAGCTCCGGTCTGTTGTCACACCTGCCAGGGTCCAGTTCAAGACATACCCGGGTGTCATGCA
CAGCTCCTGTCCTCAGGAGATGGCAGCTGTGAAGGAATTTCTTGAGAAGCTGCTGCCTCCTGTC<u>TAA</u>CTAGTCGC
TGGCCCCAGTGCAGTACCCCAGCTCATGGGGGACTCAGCAAGCAAGCGTGGCACCATCTTGGATCTGAGCCGGTC
GAGCCCCTGTCCCCACCCTTCCTGACCTGTCCTTTTCCCACAGGCCTCTGGGGGCAGGTGGCAAGGCCTGGCCGG
GCCTTCCTTCCTGGCCTTAGCCACCTGGCTCTGTCTGCAGCAGGGGCAGGCTGCTTTCTTATCCATTTCCCTGGA
GGCGGGCCCCCCTGGCAGCAGTATTGGAGGGGCTACAGGCAGCTGGAGAAAGGGGCCCAGCCGCTGACCCACTCA
CTCAGGACCTCACTCACTAGCCCCGCTTTGGGCCCCCTCCTGTGACCTCAGGGTTTGGCCCATGGGGCCCCCCCA
GGCCCCTGCCCCAACTGATTCTGCCCAGATAATCGTGTCTCCTGCCTCCACTCAGCTGCTTCTCAGTCATGAATG
TGGCCATGGCCCCGGGGTCCCCTTGCTGCTGTGGGCTCCCTGTCCCTGGGCAGGAGTGCTGGTGAGGAGGTGGAG
CCTTTTGAGGGGGGCCTTCCCTCAGCTGTTTCCCCACACTGGGGGGCTGGGCCCTGCCTCCCCGTTACCCTCCTT
CCCTGCAGGCCTGGAGCCTGTAGGGCTGGACTGAGGTTCAGGTCTCCCCCCAGCTGTCTCACCCCCACTTTGTCC
CCACTCTAGAGCAGGGAGGCAGTGGGGGAGGAGTTGTGTCTCGTCTTCTGTCTCCATGTGGTTTTTGGGTGTTTT
TCTTGTTGTGTCCTGGATTCCGATAAAATTAAAGAAATTGCTTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 90

MCGNTMSVPLLTDAATVSGAERETAAVIFLHGLGDTGHSWADALSTIRLPHVKYICPHAPRIPVTLNMKMVMPSW
FDLMGLSPDAPEDEAGIKKAAENIKALIEHEMKNGIPANRIVLGGFSQGGALSLYTALTCPHPLAGIVALSCWLP
LHRAFPQAANGSAKDLAILQCHGELDPMVPVRFGALTAEKLRSVVTPARVQFKTYPGVMHSSCPQEMAAVKEFLE
KLLPPV

FIGURE 91

AGAAGGAGAAGGTCGGGTTGTAGAAGCTGGGGTGGCCGGCAGCTCGCTCATCGGTGTTCGTGGGCTTTGTCGGTC
CGTGCCTCGTCTCTCCCTGGAAAGGGAGGGAGGCTTCGACGTCGAGAGGGAGCCGCTGCCGCGTTAGTTCCGAGC
TTGAAGTCACTAGGACTTCTCTCAAACTTGTGTGCTGAGGAGACTCAGATGTTGGCCTCAGCTCCTAGGCTGAAC
TCAGCAGATCGGCCCATGAAAACTTCTGTATTGAGACAAAGGAAGGGATCTGTCAGAAAGCAACACTTGTTATCT
TGGGCTTGGCAGCAAGGAAGAGGACAGGTAGTGGAGATCCTGCAATCTGAAAAGCAGACTGAAAGGTGACAAAGA
AGCTGAAG**ATG**GGTGGTGGAGAGAGGTATAACATTCCAGCCCCTCAATCTAGAAATGTTAGTAAGAACCAACAAC
AGCTTAACAGACAGAAGACCAAGGAACAGAATTCCCAGATGAAGATTGTTCATAAGAAAAAAGAAAGAGGACATG
GTTATAACTCATCAGCAGCTGCCTGGCAGGCCATGCAAAATGGGGGGAAGAACAAAAATTTTCCAAATAATCAAA
GTTGGAATTCTAGCTTATCAGGTCCCAGGTTACTTTTTAAATCTCAAGCTAATCAGAACTATGCTGGTGCCAAAT
TTAGTGAGCCGCCATCACCAAGTGTTCTTCCCAAACCACCAAGCCACTGGGTCCCTGTTTCCTTTAATCCTTCAG
ATAAGGAAATAATGACATTTCAACTTAAAACCTTACTTAAAGTACAGGTA**TAA**AATAAGACAAATGTTTAAATTT
AGTTATGTTCACGGATAGTTGTCAATTGGTCTGAAACAAATTCGCTAGGGAATCTATTTGTGTAGAACTAATTAA
TGTAAAAAAAACAGACCATCTCGTGTTGTGTGCACTGTGATATAATGGTAGTATCAGTGCAACTTTAATGATTGT
ACTTGATATTAAGTGTTCTCAACTGAGTAACTTTTAAGTGGAAACCAAGTTTAGATTTGGGGAGTGGTAAAGGAA
TCAGCTTTTTCTATTGTTAGGGGAAGACAGTAATTTATCATTCATGGACCAGTAGATTGTTGAAAGTTGGTGAAT
CGGATTATAAGCTTCTAGCTAACACAAGGATTCAGAATTAGGTAAACATCTGAAGGTTTAGTATATTAGAAACAC
CCAAACCAGTAATATGCTAACCTGATGCACTGCTGAAAGAAAATGTGAATTTTTCGTAATAATTGCATTTTAGTG
AATTGTACAGTGGGTGGAAAGGGCATTTGGAGCTCATTAGAATGAGACATAGTACACCCCAATGGCCCTGTTTAT
TAAATGTAGTGGATTAAGTGTCTGTCAACAAATACACCAAAACCATTTTTTATAGAAACAGTATTTAATGGTCAC
TCAATAGCTTTCAAAATACATTTTTGTATTACAGCACTGCACAAGCTATTCTAATAGTGCTCTCGCCTCATCATT
CCTGCAAAGCTTGCTTTGGGGAGTTGGATAATGTGAAAATTTTAAGTACCTAGGGGAGAAAGAGCCATGTAAATA
TCTGTAATAAACTTGTAGCATATGTAAAGTTTTCTTGGCCTTTATCTTACAAAAATGGAGTATTTTAGTATGAAT
TTGCTGAATGTAAGACCGTGGACTGTTTTTATAATATGGCCTAATTTTAAAGGTCCAAAATAACTTGTTTTTAA
AGTTTGCCCTTGTGCTAAAGTGCCAGTGTATGTATGTTATACTTGATTTGGTTGTAAACTATATTTCAAAGTAAA
CCCTAGTGTAATAAGTTTTATAACTAAAAAGGTTTAAGCTGCTAAAACTATTTTTAAGAGATGTGAAATGCAGTA
TGGGACTATCTTTTTTTCCTCCTCTAAGCCCAAAGATTAACTAGAGTCCCTCCAACCTTATAGATTGTTGGCTTT
CACAATCTTATAACCTAGGATACAGGTAGTTTCGAGTATGGTGCCAGTGATGTTTTGTTTTTGTTTGGTCAAGGG
GTAGGTGCAACCCAATGGACCACTTATGCAAAAGATGTAAACTCTTGCATAATACATTGATAACATGTTTTGCCA
ACTTTAAATGCTTAAACATAAGCGAAACCAGTAGCAAGTATGTGGGTCAGCTTAAAAATTTTGATTGTTAATGCC
CTATTTTCTAATTTGGCACCTCTTGATGCCTAAGCAGGTAAGCAGATGCCTAAGCTGTATTTCTCCAAATAAATC
AAGATGAAGTACTGCCCAAGTTAAATATTGATAGCCTAAAGACAAGTTTATGTAGTACTTAATGTACATGATATG
AATGTGAAGCATAAAATTAAATAAAATTTTTCCCCATTAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGGGERYNIPAPQSRNVSKNQQQLNRQKTKEQNSQMKIVHKKKERGHGYNSSAAAWQAMQNGGKNKNFPNNQSWN
SSLSGPRLLFKSQANQNYAGAKFSEPPSPSVLPKPPSHWVPVSFNPSDKEIMTFQLKTLLKVQV

FIGURE 93

GTCTGAGGCTCGGCCGCCTGAGCCGCGGACGGTTTGCTGAGCCCGTTAGTGCGCCCGGCCGAGACACGCCGCCGC
C**ATG**TCCCGCTACCTGCGTCCCCCCAACACGTCTCTGTTCGTCAGGAACGTGGCCGACGACACCAGGTCTGAAGA
CTTGCGGCGTGAATTTGGTCGTTATGGTCCTATAGTTGATGTGTATGTTCCACTTGATTTCTACACTCGCCGTCC
AAGAGGATTTGCTTATGTTCAATTTGAGGATGTTCGTGATGCTGAAGACGCTTTACATAATTTGGACAGAAAGTG
GATTTGTGGACGGCAGATTGAAATACAGTTTGCCCAGGGGGATCGAAAGACACCAAATCAGATGAAAGCCAAGGA
AGGGAGGAATGTGTACAGTTCTTCACGCTATGATGATTATGACAGATACAGACGTTCTAGAAGCCGAAGTTATGA
AAGGAGGAGATCAAGAAGTCGGTCTTTTGATTACAACTATAGAAGATCGTATAGTCCTAGAAACAGTAGACCGAC
TGGAAGACCACGGCGTAGCAGAAGCCATTCCGACAATGATAGACCAAACTGCAGCTGGAATACCCAGTACAGTTC
TGCTTACTACACTTCAAGAAAGATC**TGA**AAGCGGAAAAAGAACCAAAGAAGGGCAGTTCAAGCGACCAAAGGGTG
GGTGGAAGGTGCTGCAGTATGAATACTGTACGAATATTTTGACTCTGGTCTGAAAAGATAAAAGAATGTTATCGA
AAACTACATGGAATAATTGAAGTCCCTTCAAGTTTGAAAGTAAGCATTTTAGGACAAATAAAAGGAAATTCAACT
TTGTACTTGTGGAAACTAATCCCTAAATATGAATAGGTTTATATTGATTCATGGGTAACAGGTCCATAATAAATT
ATTGGAAACTAGGATGTCTGAATATCAAGGAAGACAGCCATAGTCTCTTACAGTGCCTCTGTTGGTCTGTCTCAA
ACTGAATTGGGTGGGAAAAGGTATGGTCCAATATAAAAGTTCCATTTTTGCCATTATTGGCAAATCTTGCCTTTG
TTTATTTTGGTGCCAGTGTTTTCTGCTTAATCATTTGCTTTGTTGGCATCTGTGTTTATTTACTTGTACACCACA
TGCAGTTTACATCTGTCTTAACTACTCCTTCCCAGGTAAATTCCAATTATATTTGACATCCAGCTAAGAGGGCCC
ATCTCTTCTCACCTCTTTCCTAGTCAGTATATTCAGCAAATATTTATTGAGCCCTTACTGTGGGCAAATCATTGT
ACTGGATAATTGAGAAAAATAGATAATTCCCTTATTCAGTAAATGTCTACTGAGCACAATCTAGTGAATCATTAC
AGTATGGCCTCATTGTTTTGTTTGAGGTGTGTTATTCATAACAATATTTTACACCATTCGTATCAATGTAATTAT
AGAACACAATATACGATCAAGGATAAGTAATTGTGTGGTTATCTGCCATTTAAAAGTATCCAGTATTTGATCACA
TTATTATAAATAATGAAAAAATGATTTAATCTGTAATAAACTGGTTTATTGTGCAGTGACTGTAATATACTAGAG
TTATAATAAATTGTTTACTCTGCCTCACCAAACACATGCTAGGATATAACCCCCAAAATAAGTATTTAACTTTGC
ATTAGGTATAAAGGAGACTGGGTGCTATAATTAGATTATTTTGAGGCAGACAGAGAGCTGTTATCCTAACTGATT
TAGTATGTTCTGTAATTGAGAAAATGTTCACCAAATTATACTTTTTAGTGATTTACATGTACATTTTATAGGGGA
CATGTTCTGTGTATAGCGAATAAATAACTTTTATAGTATCAC

FIGURE 94

MSRYLRPPNTSLFVRNVADDTRSEDLRREFGRYGPIVDVYVPLDFYTRRPRGFAYVQFEDVRDAEDALHNLDRKW
ICGRQIEIQFAQGDRKTPNQMKAKEGRNVYSSSRYDDYDRYRRSRSRSYERRRSRSRSFDYNYRRSYSPRNSRPT
GRPRRSRSHSDNDRPNCSWNTQYSSAYYTSRKI

FIGURE 95

GTCTGAGGCTCGGCCGCCTGAGCCGCGGACGGTTTGCTGAGCCCGTTAGTGCGCCCGGCCGAGACACGCCGCCGC
CATGTCCCGCTACCTGCGTCCCCCCAACACGTCTCTGTTCGTCAGGAACGTGGCCGACGACACCAGGTCTGAAGA
CTTGCGGCGTGAATTTGGTCGTTATGGTCCTATAGTTGATGTGTATGTTCCACTTGATTTCTACACTCGCCGTCC
AAGAGGATTTGCTTATGTTCAATTTGAGGATGTTCGTGATGCTGAAGACGCTTTACATAATTTGGACAGAAAGTG
GATTTGTGGACGGCAGATTGAAATACAGTTTGCCCAGGGGGATCGAAAGACACCAAATCAGATGAAAGCCAAGGA
AGGGAGGAATGTGTACAGTTCTTCACGCTATGATGATTATGACAGATACAGACGTTCTAGAAGCCGAAGTTATGA
AAGGAGGAGATCAAGAAGTCGGTCTTTTGATTACAACTATAGAAGATCGTATAGTCCTAGAAACAGTAGACCGAC
TGGAAGACCACGGCGTAGCAGAAGCCATTCCGACAATGATAGATTCAAACACCGAAATCGATCTTTTTCAAGATC
TAAATCCAATTCAAGATCACGGTCCAAGTCCCAGCCCAAGAAAGAAATGAAGGCTAAATCACGTTCTAGGTCTGC
ATCTCACACCAAAACTAGAGGCACCTCTAAAACAGATTCCAAAACACATTATAAGTCTGGCTCAAGATATGAAAA
GGAATCAAGGAAAAAAGAACCACCTAGATCCAAATCTCAGTCAAGATCACAGTCTAGGTCTAGGTCAAAATCTAG
ATCAAGGTCTTGGACTAGTCCTAAGTCCAGTGGCCACTGATAGTATAAACCATGGTCATTTTTAGGCATGTATCA
TTCATTTACTCATAGTTTGGTTTACTTAAATTATCAGGAATACAATGTTGCAATGATGCTTAAAAAACACTTGTT
AGTTTTCCCTGTACCAGGCAATGGTTATAATTAAAATGATATGCTGTTGAGAAGCCACTCTTAAGAGTCCAGTTT
GTTTAATGTTATGGGCAGCTACCAATTTGTGGTGTCTCTGTATATTTTTGTAAAGATTCTCATTTTTTATGCTTG
AAGTATTTGGTGAAAAGATGTTGGTTGACCATAATTTGCAACATTGTCTCATTAAAAATAAACTTTCATATTCAT
ATTTGGTAGAACTGTTAACCTAGAAATGTAGCTTGCTAATAAGATAGAATGATACAAAAGTGAAGTAGTAGCCAC
AGTACAACACTGACTGCTCAGACACATTTAGGTTCAGGGTGGACCTTTATGTCTTGTCAAGATGTCTAGGCCCGG
CTGGGCGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACGAGGTCAGGAGTT
CGAGACCAGCCTGACCAACACGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTATCCGGGCATGGTGGCACA
TGCCTGTAATCTCAGCTACTCAGGAGGCTGAGGCAAGAGAATCGCTTGAACCTGGGAGGTAGAAGTTGCAGTGAG
CCAAAATCACGCCACTGCACTCCAGCCTGGGCAACAGAGTGAGACTCCGTCTCAAAAAAAAAAAAAAACCGGATG
TCTAGGCCAATGATAATTATTTTTGATGCAGTGTGGATTAGTTCTTTTGTTAACCCCACTGTCTTGGGGAATGAT
GCCAGCTGGGAAATTGAGTTTTTGACTGAAACATGGAGCCTTCACTGCTTTTTTTCTGGTTCCTATGAAGATTTG
GAACATAGAAAACACAAAAACTCACCTTAAAATTTGAGCAGGTCGTTGATGGCAAAAATAATTTTAAGGAAAAAG
GAATATTCTTATGTAGTTATTCTAAAGTTTAAGGAGCGTTGTTGACCATAATATTGCTTAGTTTTCTTACTGCTG
TTAAGTAAGTAAATTGTTTCAAAGTAGGTTTTGTGTGTGTGTGCCTAGTGTAAAAGAACTGAAATTTTGATGCTT
ACAGCACTTGGCTCGTGCATTTGTATCAAAATTTGCCTGCCTCTTTATGAGGGAGGCCTGCTTTTCACACCTCAG
TTTATTTAATACGAGGCAAGTTGTAAGACAACACTCATTCTAGGTGATTCTGTGGTGCCATGAAATTTAAGGTAA
TTTGGGGAAAAGGATTAGTCAGTTTTAAGCAAGAGTCACATCTTTTGAGCTTTCGATTATCAGTGTAGTACCTGA
CTAAAAATGAAGTAATACCCTTAAACCATTTATAATTTCTAGTATTTCTCTGAAAGATCGTTTTGGGACAAAAG
TGACTTGACATGTCCAATTTCATTTCAGAATAAAAAGCTAGCATCTTTAAAAATCTCAGATTGCTTGCTTACAGA
TACAAGTACGAATTATGGACAAACGATTCCTTTTAGAGGATTACTTTTTTCAATTTCGGTTTTAGTAATCTAGGC
TTTGCCTGTAAAGAATACAACGATGGATTTTAAATACTGTTTGTGGAATGTGTTTAAAGGATTGATTCTAGAACC
TTTGTATATTTGATAGTATTTCTAACTTTCATTTCTTTACTGTTTGCAGTTAATGTTCATGTTCTGCTATGCAAT
CGTTTATATGCACGTTTCTTTAATTTTTTTAGATTTTCCTGGATGTATAGTTTAAACAACAAAAAGTCTATTTAA
AACTGTAGCAGTAGTTTACAGTTCTAGCAAAGAGGAAAGTTGTGGGGTTAAACTTTGTATTTTCTTTCTTATAGA
GGCTTCTAAAAAGGTATTTTTATATGTTCTTTTTAACAAATATTGTGTACAACCTTTAAAACATCAATGTTTGGA
TCAAAACAAGACCCAGCTTATTTTCTGCTTGCTGTAAATTAAGCAAACATGCTATAATAAAAACAAAATGAAGG

FIGURE 96

MSRYLRPPNTSLFVRNVADDTRSEDLRREFGRYGPIVDVYVPLDFYTRRPRGFAYVQFEDVRDAEDALHNLDRKW
ICGRQIEIQFAQGDRKTPNQMKAKEGRNVYSSSRYDDYDRYRRSRSRSYERRRSRSRSFDYNYRRSYSPRNSRPT
GRPRRSRSHSDNDRFKHRNRSFSRSKSNSRSRSKSQPKKEMKAKSRSRSASHTKTRGTSKTDSKTHYKSGSRYEK
ESRKKEPPRSKSQSRSQSRSRSKSRSRSWTSPKSSGH

FIGURE 97

AGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTGGCTCCAAGGCT
GCATCTCTCCACTGGACTAGCGAGAGGGTTGTCAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAAT
CCTTGCTCTGCGACGGACTATTCCCTGGCTGCAGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTT
ACTGACTATGTTCATGGGGATGCCTCGCAGAAAGCTGCCAAGGCAGGGCTTTTGGCATTTTCAGCTTTAACCTTT
GCTGGGCTTTGCTATTTCAACTATCACGATGTGGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCT
TTTTGACTTCCTACTTTGAAGAATTGATGTATGCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAA
GGAAGAAATAACAGATAAGTCCATTGGTGGACAGCCTTCTTCTCTTAATCACAAGATTATTTCAGAATTTAACT
TTGAGGAAAAGGTTTGAGAGGAATTATATTTAAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTT
GCCTCCCAGCTTCTTATAAGACTCACAGTATAACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATC
TCTTAAAGAGAATC

FIGURE 98

CAGGAACGAGATGGCGGTTCCCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTCTGTTGCTGCG
AACTCCAGTGGTCAGACCTGCTCATATCTCAGCATTTCTTCAGGACCGACCTATCCCAGAATGGTGTGGAGTGCA
GCACATACACTTGTCACCGAGCCACCATTCTGGCTCCAAGGCTGCATCTCTCCACTGGACTAGCGAGAGGGTTGT
CAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAATCCTTGCTCTGCGACGGACTATTCCCTGGCTGC
AGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTTACTGATTATGTTCATGGGGATGCCTCGCAGAA
AGCTGCCAAGGCAGGGCTTTTGGCATTTTCAGCTTTAACCTTTGCTGGGCTTTGCTATTTCAACTATCACGATGT
GGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCTTTTTGACTTCCTACTTTGAAGAATTGATGTAT
GCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAAGGAAGAAATAACAGATAAGCCCATTGGTGGAC
AGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAATCTTTGAGGAAAAGGTTTGAGAGGAATTATATCT
AAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTTGCCTCCCAGCTTCTTATAAGACTCACAATAT
AACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATCTCTTAAAGAGAATCCAGCTTTATTATGATTA
GTACATGATCAAATTTCCATATTTGCCTTGGGAATAATGGACAAAGGGAAATACTCTTAATTCATGAATAAAAAC
TTTGCAGAAAATTAGACAGTGTTTAATTTTCAAAAACTTCCCTCTCTAGTCAGTAGATACCACCTACTGATGGTT
ACATATACTAGGGAAATTTTAAAATTAGGAAATGCTGCTATCTCATATTATAAATTTCTAAATCCTAGGAAGAAA
CGCTTGGAGTGCTTCTGAAGATACAGAAGTTCCATTTAAGGGCAAGTTTCCCCAGAGACATATCAAAATATTATC
CATTGTAAACTGAGATTTAATTCTCAAATGTATTCTACTTGTTCTAAAACAATCTGTCCACAAATATAAAACTAT
AAGTAATAAATTGTTATTTCCGCACAATGGGAATCTCTAATGTGAAAATGTATTCTATGAAAATAATTTTTTTAA
ATAAAATGTTGTATAAAAAAA

FIGURE 99

AGAGAGAAAGGTTGTG**ATG**GCGGCTATAGCTGCATCCGAGGTGCTGGTGGACAGCGCGGAGGAGGGGTCCCTCGC
TGCGGCGGCGGAGCTGGCCGCTCAGAAGCGCGAACAGAGACTGCGCAAATTCCGGGAGCTGCACCTGATGCGGAA
TGAAGCTCGTAAATTAAATCACCAGGAAGTTGTGGAAGAAGATAAAAGACTAAAATTACCTGCAAATTGGGAAGC
CAAAAAAGCTCGTTTGGAGTGGGAACTAAAGGAAGAGGAAAAGAAAAAGGAATGTGCGGCAAGAGGAGAAGACTA
TGAGAAAGTGAAGTTGCTGGAGATCAGTGCAGAAGATGCAGAAAGATGGGAGAGGAAAAAGAAGAGGAAAAACCC
TGATCTGGGATTTTCAGATTATGCTGCTGCCCAGTTACGCCAGTATCATCGGTTGACCAAGCAGATCAAACCTGA
CATGGAAACATATGAGAGACTGAGAGAAAAACATGGAGAAGAGTTTTTCCCAACATCCAATAGTCTTCTTCATGG
AACACATGTGCCTTCCACAGAGGAAATTGACAGGATGGTCATAGATCTGGAAAAACAGATTGAAAAACGAGACAA
ATATAGCCGGAGACGTCCTTATAATGATGATGCAGATATCGACTACATTAATGAAAGGAATGCCAAATTCAACAA
GAAAGCTGAAAGATTCTATGGGAAATACACAGCTGAAATTAAACAGAATTTGGAAAGAGGAACAGCTGTC**TAA**TC
CCTTCAAGAACTGTTTATAGAAGCTTGAGAATGGGGTAAAAATTTCTGCTAGCAAAATCAAGTTCTTTTTGAAAT
TTTATCAGTAATCCAGAATTTAGTAGTCCATGCCTTCTCACTCAGCATTTAGAAATAAAAATGTGGTTTCTTAAA
CGTATATCCTTTCATGTATATTTCCACATTTTTGTGCTTGGATATAAGATGTATTTCTTGTAGTGAAGTTGTTTT
GTAATCTACTTTGTATACATTCTAATTATATTATTTTTCTATGTATTTTAAATGTATATGGCTGTTTAATCTTTG
AAGCATTTTGGGCTTAAGATTGCCAGCAGCACACATCAGATGCAGTCATTGTTGCTATCAGTGTGGAATTTGATA
GAGTCTAGACTCGGGCCACTTGGAGTTGTGTACTCCAAAGCTAAGGACAGTGATGAGGAAGATGGCAGTGGCCAC
CGGAGGACTGGAGCAGTCCCTCCTCATGGCGGCCTGTGACCAAGGTCGGGGAGGAGTGGAGCTATCCTTCCATGA
TCTGATCATGTACAGTTCCCTTTTTAAAAAGCAATAAATGCTTGGGATTAGAATTTCTAAAAAAAAAAA

FIGURE 100

MAAIAASEVLVDSAEEGSLAAAAELAAQKREQRLRKFRELHLMRNEARKLNHQEVVEEDKRLKLPANWEAKKARL
EWELKEEEKKKECAARGEDYEKVKLLEISAEDAERWERKKKRKNPDLGFSDYAAAQLRQYHRLTKQIKPDMETYE
RLREKHGEEFFPTSNSLLHGTHVPSTEEIDRMVIDLEKQIEKRDKYSRRRPYNDDADIDYINERNAKFNKKAERF
YGKYTAEIKQNLERGTAV

FIGURE 101A

GGCGGCCCACTCTGCTCTGTCAGCTTCGGAGCTCCTCCACCCTGGCTGCCGAAAGCCCCTTCCCGCCATCTAATG
ATACACTCTGCATACGCTTCTGTTGAGAATTTGTGGCTAGACATTCCTGTGGGACCGGAATCCAAATTCTTGGT
AGCTAGAGGAAAAAAAAATAAAACAACAGCCAACCAAGTGAATCCCAACCCAACCCCCTGAAGGGCTGAAAATTC
TCGCCTTCTTCAGAGCGGGGCATGGCATCGAACAGCATCTTCGACTCCTTCCCGACCTACTCGCCGACCTTCATC
CGCGACCCAAGCACCAGCCGCCGCTTCACACCTCCCTCCCCGGCCTTCCCCTGCGGCGGCGGCGGCGGCAAGATG
GGCGAGAACAGCGGCGCGCTGAGCGCGCAGGCGGCCGTGGGGCCCGGAGGGCGCGCCCGGCCCGAGGTGCGCTCG
ATGGTGGACGTGCTGGCGGACCACGCAGGCGAGCTCGTGCGCACCGACAGCCCCAACTTCCTCTGCTCCGTGCTG
CCCTCGCACTGGCGCTGCAACAAGACGCTGCCCGTCGCCTTCAAGGTGGTGGCATTGGGGGACGTGCCGGATGGT
ACGGTGGTGACTGTGATGGCAGGCAATGACGAGAACTACTCCGCTGAGCTGCGCAATGCCTCGGCCGTCATGAAG
AACCAGGTGGCCAGGTTCAACGACCTTCGCTTCGTGGGCCGCAGTGGGCGAGGGAAGAGTTTCACCCTGACCATC
ACTGTGTTCACCAACCCCACCCAAGTGGCGACCTACCACCGAGCCATCAAGGTGACCGTGGACGGACCCCGGGAG
CCCAGACGGCACCGGCAGAAGCTGGAGGACCAGACCAAGCCGTTCCCTGACCGCTTTGGGGACCTGGAACGGCTG
CGCATGCGGGTGACACCGAGCACACCCAGCCCCCGAGGCTCACTCAGCACCACAAGCCACTTCAGCAGCCAGCCC
CAGACCCCAATCCAAGGCACCTCGGAACTGAACCCATTCTCCGACCCCCGCCAGTTTGACCGCTCCTTCCCCACG
CTGCCAACCCTCACGGAGAGCCGCTTCCCAGACCCCAGGATGCATTATCCCGGGGCCATGTCAGCTGCCTTCCCC
TACAGCGCCACGCCCTCGGGCACGAGCATCAGCAGCCTCAGCGTGGCGGGCATGCCGGCCACCAGCCGCTTCCAC
CATACCTACCTCCCGCCACCCTACCCGGGGGCCCCGCAGAACCAGAGCGGGCCCTTCCAGGCCAACCCGTCCCCC
TACCACCTCTACTACGGGACATCCTCTGGCTCCTACCAGTTCTCCATGGTGGCCGGCAGCAGCAGTGGGGGCGAC
CGCTCACCTACCCGCATGCTGGCCTCTTGCACCAGCAGCGCTGCCTCTGTCGCCGCCGGCAACCTCATGAACCCC
AGCCTGGGCGGCCAGAGTGATGGCGTGGAGGCCGACGGCAGCCACAGCAACTCACCCACGGCCCTGAGCACGCCA
GGCCGCATGGATGAGGCCGTGTGGCGGCCCTACTGACCGCCCTGGTGGACTCCTCCCGCTGGAGGCGGGGACCCT
AACAACCTTCAAGACCAGTGATGGGCCGGCTCCGAGGCTCCGGGCGGGAATGGGACCTGCGCTCCAGGGTGGTCT
CGGTCCCAGGGTGGTCCCAGCTGGTGGGAGCCTCTGGCTGCATCTGTGCAGCCACATCCTTGTACAGAGGCATAG
GTTACCACCCCCACCCCGGCCCGGGATACTGCCCCCGGCCCAGATCCTGGCCGTCTCATCCCATACTTCTGTGGG
GAATCAGCCTCCTGCCACCCCCCCGGAAGGACCTCACTGTCTCCAGCTATGCCCAGTGCTGCATGGGACCCATGT
CTCCTGGGACAGAGGCCATCTCTCTTCCAGAGAGAGGCAGCATTGGCCCACAGGATAAGCCTCAGGCCCTGGGAA
ACCTCCCGACCCCTGCACCTTCGTTGGAGCCCCTGCATCCCCTGGGTCCAGCCCCCTCTGCATTTACACAGATTT
GAGTCAGAACTGGAAAGTGTCCCCCACCCCCACCACCCTCGAGCGGGGTTCCCCTCATTGTACAGATGGGGCAGG
ACCCAGCACGCTGCTGGCAGAGATGGTTTGAGAACACATCCAAGCCAGTCCCCCCAGCCCAGCTTCCCCTCCGTT
CCTAACTGTTGGCTTTCCCCCAGCCGCACGGGTCCCAGGCCCCAGAGAAGATGAGTCTATGGCATCAGGTTCTTA
AACCCAGGAAAGCACCTACAGACCGGCTCCTCCATGCACTTTACCAGCTCAACGCATCCACTCTCTGTTCTCTTG
GCAGGGCGGGGGAGGGGGGATAGGAGGTCCCCTTTCCCCTAGGTGGTCTCATAATTCCATTTGTGGAGAGAACAG
GAGGGCCAGATAGATAGGTCCTAGCAGAAGGCATTGAGGTGAGGGATCATTTTGGGTCAGACATCAATGTCCCTG
TCCCCCCTGGGTCCAGCCAAGCTGTGCCCCATCCCCCAAGCCTCCTGGGAGGATCCAGCCAAATCTTGCGACTCC
TGGCACACACCTGTCTGTAACCTGTTTTGTGCTCTGAAAGCAAATAGTCCTGAGCAAAAAAAAAAAAAAAAACAAA
AAAACAAAAAAAAAACAAAACAGTTTTTAAAACTGATTTTAGAAAAAGAAGCTTAATCTAACGTTTTCAAACACA
AGGTCTCTTACAGGTATAGTTCCGTGATTATGATAGCTCTGTGATTATAAGCAACATCCCCGCCCCCTCTCCCCC
CCGCGGACCCCCAGCTGCCTCCTGAGGGTGTGGGGTTATTAGGGTCTCAATACTTTCTCAAGGGGCTACACTCCC
CATCAGGCAGCATCCCACCAGCCTGCACCACAGGCTCCCCTGGGAGGACGAGGGAAACGCTGATGAGACGCTGGG
CATCTCTCCTCTGTGGCTCTAGGACATCTGTCCAGGAGGCTGGGCGGAGGTGGGCAGGATGTGAGAGGTGGGGAG
TACTGGCTGTGCGTGGCAGGACAGAAGCACTGTAAAGGGCTCTCCAGCCGCAGCTCAGCTGCACTGCGTTCCGAG
GTGAAGTCTTGCCCCTGAATTTTGCAAAATGGGAAAGTGGGCGCTTGCCCAAGGGCCAGGCTGCATGGATTCTCA
CATCAGAGTTCTCTGGCCCTAGAAAGGCTTAGAAAAGGCGTAAGGGAACTCATAAAGGCTAGCAGCATGCGGTAT
TTTAACTTTCTGCCTCGGCCTCTGTGGATGCAGAAATCTGCCCTACAAAATGCTCTTCATTGGTTGTCTCTGTGA
GAGCACTGTCCCCACCCAACCTGTCACAACGGCCAGAACCATACACCAGAGACACACTGGCAGGTTAGGCAGTCC
TTCTGGTGATCCTATTCCATTCCCTCCTGCTGCGGTTTCTCTTGGCCTGTCCTCACTGGAAAAACAGTCTCCATC
TCCTCAAAATAGTTGCTGACTCCCTGCACCCAAGGGGCCTCTCCATGCCTTCTTAGGAAGCAGCTATGAATCCAT
TGTCCTTGTAGTTTCTTCCCTCCTGTTCTCTGGTTATAGCTGGTCCCAGGTCAGCGTGGGAGGCACCTTTGGGTT

FIGURE 101B

CCCAGTGCCCAGCACTTTGTAGTCTCATCCCAGATTACTAACCCTTCCTGATCCTGGAGAGGCAGGGATAGTAAA
TAAATTGCTCTTCCTACCCCATCCCCCATCCCCTGACAAAAAGTGACGGCAGCCGTACTGAGTCTGTAAGGCCCA
AAGTGGGTACAGACAGCCTGGGCTGGTAAAAGTAGGTCCTTATTTACAAGGCTGCGTTAAAGTTGTACTAGGCAA
ACACACTGATGTAGGAAGCACGAGGAAAGGAAGACGTTTTGATATAGTGTTACTGTGAGCCTGTCAGTAGTGGGT
ACCAATCTTTTGTGACATATTGTCATGCTGAGGTGTGACACCTGCTGCACTCATCTGATGTAAAACCATCCCAGA
GCTGGCGAGAGGATGGAGCTGGGTGGAAACTGCTTTGCACTATCGTTTGCTTGGTGTTTGTTTTTAACGCACAAC
TTGCTTGTACAGTAAACTGTCTTCTGTACTATTTAACTGT

FIGURE 102

CAGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTCTGTTGCTGCG
AACTCCAGTGGTCAGACCTGCTCATATCTCAGCATTTCTTCAGGACCGACCTATCCCAGAATGGTGTGGAGTGCA
GCACATACACTTGTCACCGAGCCACCATTCTGGCTCCAAGGCTGCATCTCTCCACTGGACTAGCGAGAGGGTTGT
CAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAATCCTTGCTCTGCGACGGACTATTCCCTGGCTGC
AGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTTACTGACTATGTTCATGGGGATGCCTCGCAGAA
AGCTGCCAAGGCAGGGCTTTTGGCATTTTCAGCTTTAACCTTTGCTGGGCTTTGCTATTTCAACTATCACGATGT
GGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCTTTTTGACTTCCTACTTTGAAGAATTGATGTAT
GCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAAGGAAGAAATAACAGATAAGTCCATTGGTGGAC
AGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAACTTTGAGGAAAAGGTTTGAGAGGAATTATATTTA
AGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTTGCCTCCCAGCTTCTTATAAGACTCACAGTATA
ACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATCTCTTAAAGAGAATCCAGCTTTAGTATGATTAG
CATATGATCAAACTTCCATATTTGCCTTGGGAATAATGGACTAAGGGAAATACTCTTAATTCATGAATAAAAACT
TTGCAGAAAATTAGACAGTGTTTAATTTTCAAAAACTTCCCTCTCTAGTCGGTAGATACCACCTACCGATGGTTA
CATATACTAGGGAAATTTTAAAATTAGGAAATGCTGATATCTCATATTATAAATTTCTAAATCCTAGGAAGAAAC
GCTTGGAGTGCTTCTGAAGATACAGAAGTTCCATTTAAGGGCAAGTTTCCCCATAGACGTATCAAAATATTACCC
ATTGTAAACTGAGATTTAATTCTCAAATGTATTCTACTTGTTCTAAAACAATCTGTCCACAAATATAAAACTATA
AGTAATAAATTGTTATTTTCGCACAATGGGAATCTCTAATGTGAAAATGTATTCTGTGAAAATAAATTTTTAAAT
AAAATGTTGTATAATAA

FIGURE 103

AGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTGGCTCCAAGGCT
GCATCTCTCCACTGGACTAGCGAGAGGGTTGTCAGTGTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAAT
CCTTGCTCTGCGACGGACTATTCCCTGGCTGCAGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTT
ACTGACTATGTTCATGGGGATGCCTCGCAGAAAGCTGCCAAGGCAGGGCTTTTGGCATTTTCAGCTTTAACCTTT
GCTGGGCTTTGCTATTTCAACTATCACGATGTGGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCT
TTTTGACTTCCTACTTTGAAGAATTGATGTATGCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAA
GGAAGAAATAACAGATAAGTCCATTGGTGGACAGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAACT
TTGAGGAAAAGGTTTGAGAGGAATTATATTTAAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTT
GCCTCCCAGCTTCTTATAAGACTCACAGTATAACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATC
TCTTAAAGAGAATC

FIGURE 104

MAVLRRLSALYGAQGGRALLLRTPVIRPAHISAFLQDRPIPEWCGVQHLHLSPSHHPGSKAASLHWTSERVVSVL
LLGLLPAAYLNPCSAMDYSLAATLTLPGHWGLRQVVTMFMGMPRRKLPRQGFWHFQL

FIGURE 105

AGTGTGGTCAGGCGGCTCGGACTGAGCAGGACTTTCCTTATCCCAGTTGATTGTGCAGAATACACTGCCTATCGC
TTGTCTTCTATTCACCATGGCTTCTTCTGATATCCAGGTGAAAGAACTGGAGAAGCGTGCCTCAGGCCAGGCTTT
TGAGCTGATTCTCAGCCCTCGGTCAAAAGAATCTGTTCCAGAATTCCCCCTTTCCCCTCCAAAGAAGAAGGATCT
TTCCCTGGAGGAAATTCAGAAGAAATTAGAAGCTGCAGAAGAAAGACGCAAGTCCCATGAAGCTGAGGTCTTGAA
GCAGCTGGCTGAGAAACGAGAGCACGAGAAAGAAGTGCTTCAGAAGGCAATAGAAGAGAACAACAACTTCAGTAA
AATGGCAGAAGAGAAACTGACCCACAAAATGGAAGCTAATAAAGAGAACCGAGAGGCACAAATGGCTGCCAAACT
GGAACGTTTGCGAGAGAAGGATAAGCACATTGAAGAAGTGCGGAAGAACAAAGAATCCAAAGACCCTGCTGACGA
GACTGAAGCTGACTAATTTGTTCTGAGAACTGACTTTCTCCCCATCCCCTTCCTAAATATCCAAAGACTGTACTG
GCCAGTGTCATTTTATTTTTTCCCTCCTGACAAATATTTTAGAAGCTAATGTAGGACTGTATAGGTAGATCCAGA
TCCAGACTGTAAGATGTTGTTTTAGGGGCTAAAGGGGAGAAACTGAAAGTGTTTTACTCTTTTTCTAAAGTGTTG
GTCTTTCTAATGTAGCTATTTTTCTTGTTGCATCTTTTCTACTTCAGTACACTTGGTGTACTGGGTTAATGGCTA
GTACTGTATTGGCTCTGTGAAAACATATTTGTGAAAAGAGTATGTAGTGGCTTCTTTTGAACTGTTAGATGCTGA
ATATCTGTTCACTTTTCAATCCCAATTCTGTCCCAATCTTACCAGATGCTACTGGACTTGAATGGTTAATAAAAC
TGCACAGTGCTGTTGGTGGCAGTGACTTCTTTTGAGTTAGGTTAATAAATCAAGCCATAGAGCCCCTCCTGGTTG
ATACTTGTTCCAGATGGGGCCTTTGGGGCTGGTAGAAATACCCAACGCACAAATGACCGCACGTTCTCTGCCCCG
TTTCTTGCCCCAGTGTGGTTTGCATTGTCTCCTTCCACAATGACTGCTTTGTTTGGATGCCTCAGCCCAGGTCAG
CTGTTACTTTCTTTCAGATGTTTATTTGCAAACAACCATTTTTTGTTCTGTGTCCCTTTTAAAAGGCAGATTAAA
AGCACAAGCGTGTTTCTAGAGAACAGTTGAGAGAGAATCTCAAGATTCTACTTGGTGGTTTGCTTGCTCTACGTT
ACAGGTGGGGCATGTCCTCATCCTTTCCTGCCATAAAAGCTATGACACGAGAATCAGAATATTAATAAAACTTTA
TGTACTGCTGT

FIGURE 106

MASSDIQVKELEKRASGQAFELILSPRSKESVPEFPLSPPKKKDLSLEEIQKKLEAAEERRKSHEAEVLKQLAEK
REHEKEVLQKAIEENNNFSKMAEEKLTHKMEANKENREAQMAAKLERLREKDKHIEEVRKNKESKDPADETEAD

FIGURE 107

GTGCAACGGCCGTTAGAGGAGCTGAGGGAGGGAACCACCGCTCACCGCAGACGTAGTGGCTGCAGTCAGTCTTCC
CGAGTGAGGGATTTCGCCGCCCGCTTTCAGGCCCGTTTGGCTTAAATAACTGTGATTG**ATG**GCCATGCAGGAGAA
ATATCCAACTGAGGGGATCTCTCACGTCACTTCACCGAGTTCCGATGTGATTCAGAAGGGCAGTTCCCTGGGGAC
TGAATGGCAGACCCCAGTTATCTCGGAGCCCTTTCGGAGCCGCTTCAGCCGCTGTTCAAGTGTAGCCGACAGTGG
GGACACAGCCATTGGTACATCATGCTCAGATATTGCGGAGGATTTTTGCAGCTCAAGTGGCAGTCCTCCTTTCCA
GCCCATCAAAAGCCACGTAACCATTCCAACAGCCCATGTGATGCCTTCTACTTTAGGGACCTCTCCTGCCAAGCC
AAATTCTACACCTGTTGGACCCTCTTCCTCTAAACTCCCTTTGTCAGGGTTGGCTGAAAGTGTGGGAATGACAAG
AAATGGAGACCTCGGTGCAATGAAACATTCTCCAGGCCTATCTAGAGATCTCATGTATTTCTCTGGTGCTACTGG
AGAAAATGGAATTGAGCAGTCCTGGTTTCCAGCAGTGGGCCATGAAAGACAAGAAGAGGCGAGGAAGTTTGATAT
TCCTAGCATGGAATCTACCCTCAATCAGTCGGCAATGATGGAGACACTTTATTCAGATCCTCACCACCGAGTCCG
CTTCCACAACCCAAGAACCAGCACAAGTAAGGAGTTGTACAGAGTGTTGCCTGAGGCCAAGAAGGCACCGGGCAG
CGGGGCAGTGTTTGAGCGGAATGGACCACATTCTAATAGCAGTGGGGTCCTCCCTTTGGGACTCCAGCCTGCTCC
CGGGCACTCCAGCCAGCCTCTGCCCTCTCAGGTGTGGCAGCCGAGTCCTGACACTTGGCATCCCCGAGAGCAATC
TTGTGAACTCAGCACTTGTCGGCAGCAGCTGGAATTGATTCGTTTACAGATGGAGCAAATGCAGCTTCAGAATGG
AGCCATCTGCCACCATCCTGCTGCTTTTGGTCCTTCACTGCCCATCTTAGAGCCAGCACAGTGGATCAGCATCTT
GAACAGTAATGAACACCTTCTGAAGGAAAAAGAGCTTCTCATTGACAAGCAGAGGAAACACATCTCTCAGCTGGA
GCAGAAAGTGCGAGAGAGCGAACTGCAAGTCCACAGTGCCCTCTTGGGCCGCCCTGCCCCCTTTGGTGATGTCTG
CTTGCTGAGGCTACAGGAATTGCAGCGAGAAAACACTTTCTTACGTGCACAGTTTGCACAGAAGACAGAAGCCTT
GAGCAGAGAAAAGATTGACCTTGAAAAGAAACTCTCTGCTTCTGAAGTTGAAGTCCAGCTCATCAGAGAGTCGCT
CAAAGTGGCGTTGCAGAAGCATTCTGAGGAAGTGAAGAAACAGGAAGAAAGGGTCAAAGGTCGTGATAAACATAT
CAATAATTTGAAAAAGAAATGCCAGAAGGAATCAGAGCAGAACCGGGAGAAGCAGCAGCGTATTGAGACCTTGGA
GCGCTACCTGGCTGACCTGCCCACACTGGAAGACCATCAGAAGCAGAGCCAGCAGCTTAAGGATTCTGAGTTGAA
GAGCACAGAGCTGCAGGAGAAAGTGACTGAGCTGGAGAGTTTGCTGGAGGAGACCCAGGCAATCTGCAGAGAGAA
GGAGATTCAACTGGAAAGCCTGAGGCAGAGAGAAGCAGAATTCTCCTCCGCTGGACATAGCCTGCAAGATAAACA
GTCTGTGGAGGAGACCAGTGGAGAAGGTCCAGAAGTGGAAATGGAGTCCTGGCAGAAGCGATACGATTCGCTCCA
AAAGATTGTGGAGAAGCAGCAGCAGAAGATGGATCAGTTGCGCTCACAAGTACAGAGCCTAGAGCAGGAAGTGGC
TCAAGAAGAAGGAACAAGCCAGGCCCTGAGAGAGGAGGCCCAGCGAAGGGATTCAGCCCTGCAGCAGCTGCGCAC
AGCCGTGAAGGAGCTTTCAGTGCAAAACCAGGACTTGATTGAGAAGAATCTGACACTCCAGGAACACCTGCGCCA
GGCCCAACCAGGGTCTCCACCTTCACCAGACACGGCCCAGCTGGCACTTGAGCTGCACCAGGAGTTGGCCAGTTG
CCTTCAAGATCTGCAGGCTGTCTGTAGCATTGTGACCCAGAGGGCCCAGGGCCATGACCCCAATCTCTCCCTGCT
CCTGGGCATTCACTCACAGCACCCAGAGACTCAGCTAGATTTGCAGAAGCCAGATGTGATCAAGAGGAAACTAGA
AGAGGTTCAACAGCTGCGTCGTGACATTGAGGACTTAAGGACCACCATGTCAGACAGATATGCCCAGGACATGGG
AGAAAACTGTGTCACACAG**TGA**GGAATTCTGGGGGATTCCCCCAGGGAGGAGCTGGGCTGCTGAGAGCCTAGTCC
AGCAGGTTTCTGCCCTGACATTCTCTTGTCTGCTATTCCCAGAGAGGTCTCAGAGGGGAGGGGAGAGCCTGCATC
TGGGGGCCAAGGGCTGATTAGGGAACTGTGTCCTACCCACACTGGCATGTTGGATTACGTTTGTCCTGTTAATTC
ACTCTCGACGGTGAGTTACTAATTAACTTTTGGCAGGTACAACAGATAAGTCCTCACAAACTGTTCCCAGCCCTA
GGCTGACATGAGAGACGAACAGGCTGTCCACCTTTCTTCTCCATCCAATGGGATGGATCCATGTTCATTCCCACT
TCACACCTTGGTCCTGCTGATTAGAGAGCTCATCAGAGGGGCCTGGAAAGGCTGAGCAAGTACCAGTGACAATGG
CCATTTAAGAATTCTCAGGCCCCATGTGCCAGCCTTCTTGGGAACTGAGCTGGCTTTCTGGGTTTTCTCATGCCT
GGTCTTACTGCTTCTTCCTCAGGGCTCTTGTTCTCCCAGAAGCCTCAGGGTAATGTGTTGGTTAGCACGTAACTA
CTAGGATTGGGGCCCTAGGGATTATAGCCAGGACTCTAATCTGCCTACCATGCCATTTAACAAGAGATCCCACTC
TCCAGCTGCCTTGTGTCCCTAGGGTCCTGGCCATGTGTTTAGTGTGCTAAACTTTCTCCTTTGTTCTCAGGCCTT
CCAGGTAGTCCCCTTCCTGGACTTAAGAGTGCAAACTCTTCTCTGTGGTTCTAGCCTTGGGCAGAATTATATCCC
AGAGACCACAGAGCAACTGTCAAGCTGCTTACCCCCTCACCCAGGGCTACAGCCTGTGCCCAGCCCTCTAATTTG
TGCCTCTCTTGTGTTGGGGGTGGTGGGGGTTATTCCTTTCCCTTTCCTGCTCTGGCCTCCTTGAAAGTTCAGAGT
ACCCAGTACAAGTCAGCCACCATGCTGACGGGTATTTTTCCTCATAAAGTTTATAACCAGTTATTTATATGAATC
TTTGTTATGTCCATTTGTTTGTATTGCGTATTTTGATTATAAAATAAAGTATCTTAACAG

FIGURE 108

MAMQEKYPTEGISHVTSPSSDVIQKGSSLGTEWQTPVISEPFRSRFSRCSSVADSGDTAIGTSCSDIAEDFCSSS
GSPPFQPIKSHVTIPTAHVMPSTLGTSPAKPNSTPVGPSSSKLPLSGLAESVGMTRNGDLGAMKHSPGLSRDLMY
FSGATGENGIEQSWFPAVGHERQEEARKFDIPSMESTLNQSAMMETLYSDPHHRVRFHNPRTSTSKELYRVLPEA
KKAPGSGAVFERNGPHSNSSGVLPLGLQPAPGHSSQPLPSQVWQPSPDTWHPREQSCELSTCRQQLELIRLQMEQ
MQLQNGAICHHPAAFGPSLPILEPAQWISILNSNEHLLKEKELLIDKQRKHISQLEQKVRESELQVHSALLGRPA
PFGDVCLLRLQELQRENTFLRAQFAQKTEALSREKIDLEKKLSASEVEVQLIRESLKVALQKHSEEVKKQEERVK
GRDKHINNLKKKCQKESEQNREKQQRIETLERYLADLPTLEDHQKQSQQLKDSELKSTELQEKVTELESLLEETQ
AICREKEIQLESLRQREAEFSSAGHSLQDKQSVEETSGEGPEVEMESWQKRYDSLQKIVEKQQQKMDQLRSQVQS
LEQEVAQEEGTSQALREEAQRRDSALQQLRTAVKELSVQNQDLIEKNLTLQEHLRQAQPGSPPSPDTAQLALELH
QELASCLQDLQAVCSIVTQRAQGHDPNLSLLLGIHSQHPETQLDLQKPDVIKRKLEEVQQLRRDIEDLRTTMSDR
YAQDMGENCVTQ

FIGURE 109

GTAGCAGCTTCTTCTCCGAACCAACCCTTTGCCTTCGGACTTCTCCGGGGCCAGCAGCCGCCCGACCAGGGGCCC
GGGGCCACGGGCTCAGCCGACGACCATGGGCTCCGTGTCCAACCAGCAGTTTGCAGGTGGCTGCGCCAAGGCGGC
AGAAGAGGCGCCCGAGGAGGCGCCGGAGGACGCGGCCCGGGCGGCGGACGAGCCTCAGCTGCTGCACGGTGCGGG
CATCTGTAAGTGGTTCAACGTGCGCATGGGGTTCGGCTTCCTGTCCATGACCGCCCGCGCCGGGGTCGCGCTCGA
CCCCCCAGTGGATGTCTTTGTGCACCAGAGTAAGCTGCACATGGAAGGGTTCCGGAGCTTGAAGGAGGGTGAGGC
AGTGGAGTTCACCTTTAAGAAGTCAGCCAAGGGTCTGGAATCCATCCGTGTCACCGGACCTGGTGGAGTATTCTG
TATTGGGAGTGAGAGGCGGCCAAAAGGAAAGAGCATGCAGAAGCGCAGATCAAAAGGAGACAGGTGCTACAACTG
TGGAGGTCTAGATCATCATGCCAAGGAATGCAAGCTGCCACCCCAGCCCAAGAAGTGCCACTTCTGCCAGAGCAT
CAGCCATATGGTAGCCTCATGTCCGCTGAAGGCCCAGCAGGGCCCTAGTGCACAGGGAAAGCCAACCTACTTTCG
AGAGGAAGAAGAAGAAATCCACAGCCCTACCCTGCTCCCGGAGGCACAGAATTGAGCCACAATGGGTGGGGGCTA
TTCTTTTGCTATCAGGAAGTTTTGAGGAGCAGGCAGAGTGGAGAAAGTGGGAATAGGGTGCATTGGGGCTAGTTG
GCACTGCCATGTATCTCAGGCTTGGGTTCACACCATCACCCTTTCTTCCCTCTAGGTGGGGGGAAAGGGTGAGTC
AAAGGAACTCCAACCATGCTCTGTCCAAATGCAAGTGAGGGTTCTGGGGGCAACCAGGAGGGGGGAATCACCCTA
CAACCTGCATACTTTGAGTCTCCATCCCCAGAATTTCCAGCTTTTGAAAGTGGCCTGGATAGGGAAGTTGTTTTC
CTTTTAAAGAAGGATATATAATAATTCCCATGCCAGAGTGAAATGATTAAGTATAAGACCAGATTCATGGAGCCA
AGCCACTACATTCTGTGGAAGGAGATCTCTCAGGAGTAAGCATTGTTTTTTTTTCACATCTTGTATCCTCATACC
CACTTTTGGGATAGGGTGCTGGCAGCTGTCCCAAGCAATGGGTAATGATGATGGCAAAAAGGGTGTTTGGGGGAA
CAGCTGCAGACCTGCTGCTCTATGCTCACCCCCGCCCCATTCTGGGCCAATGTGATTTTATTTATTTGCTCCCTT
GGATACTGCACCTTGGGTCCCACTTTCTCCAGGATGCCAACTGCACTAGCTGTGTGCGAATGACGTATCTTGTGC
ATTTTAACTTTTTTTCCTTAATATAAATATTCTGGTTTTGTATTTTTGTATATTTTAATCTAAGGCCCCTCATTTC
CTGCACTGTGTTCTCAGGTACATGAGCAATCTCAGGGATAGCCAGCAGCAGCTCCAGGTCTGCGCAGCAGGAATT
ACTTTTTGTTGTTTTTGCCACCGTGGAGAGCAACTATTTGGAGTGCACAGCCTATTGAACTACCTCATTTTTGCC
AATAAGAGCTGGCTTTTCTGCCATAGTGTCCTCTTGAAACCCCCTCTGCCTTGAAAATGTTTTATGGGAGACTAG
GTTTTAACTGGGTGGCCCCATGACTTGATTGCCTTCTACTGGAAGATTGGGAATTAGTCTAAACAGGAAATGGTG
GTACACAGAGGCTAGGAGAGGCTGGGCCCGGTGAAAAGGCCAGAGAGCAAGCCAAGATTAGGTGAGGGTTGTCTA
ATCCTATGGCACAGGACGTGCTTTACATCTCCAGATCTGTTCTTCACCAGATTAGGTTAGGCCTACCATGTGCCA
CAGGGTGTGTGTGTGTTTGTAAAACTAGAGTTGCTAAGGATAAGTTTAAAGACCAATACCCCTGTACTTAATCCT
GTGCTGTCGAGGGATGGATATATGAAGTAAGGTGAGATCCTTAACCTTTCAAAATTTTCGGGTTCCAGGGAGACA
CACAAGCGAGGGTTTTGTGGTGCCTGGAGCCTGTGTCCTGCCCTGCTACAGTAGTGATTAATAGTGTCATGGTAG
CTAAAGGAGAAAAAGGGGGTTTCGTTTACACGCTGTGAGATCACCGCAAACCTACCTTACTGTGTTGAAACGGGA
CAAATGCAATAGAACGCATTGGGTGGTGTGTGTCTGATCCTGGGTTCTTGTCTCCCCTAAATGCTGCCCCCCAAG
TTACTGTATTTGTCTGGGCTTTGTAGGACTTCACTACGTTGATTGCTAGGTGGCCTAGTTTGTGTAAATATAATG
TATTGGTCTTTCTCCGTGTTCTTTGGGGGTTTTGTTTACAAACTTCTTTTTGTATTGAGAGAAAAATAGCCAAAG
CATCTTTGACAGAAGGTTCTGCACCAGGCAAAAAGATCTGAAACATTAGTTTGGGGGGCCCTCTTCTTAAAGTGG
GGATCTTGAACCATCCTTTCTTTTGTATTCCCCTTCCCCTATTACCTATTAGACCAGATCTTCTGTCCTAAAAAC
TTGTCTTCTACCCTGCCCTCTTTTCTGTTCACCCCCAAAAGAAAACTTACACACCCACACACATACACATTTCAT
GCTTGGAGTGTCTCCACAACTCTTAAATGATGTATGCAAAAATACTGAAGCTAGGAAAACCCTCCATCCCTTGTT
CCCAACCTCCTAAGTCAAGACCATTACCATTTCTTTCTTTCTTTTTTTTTTTTTTTTAAAATGGAGTCTCACTGT
GTCACCCAGGCAGAGGTTGCAGTGAGCTGAGATCGCACCACTGCACTCCAGCCTGGTTACAGAGCAAGACTCTGT
CTCAAACAAAACAAAACAAAACAAAAACACACTACTGTATTTTGGATGGATCAAACCTCCTTAATTTTAATTTCT
AATCCTAAAGTAAAGAGATGCAATTGGGGGCCTTCCATGTAGAAAGTGGGGTCAGGAGGCCAAGAAAGGGAATAT
GAATGTATATCCAAGTCACTCAGGAACTTTTATGCAGGTGCTAGAAACTTTATGTCAAAGTGGCCACAAGATTGT
TTAATAGGAGACGAACGAATGTAACTCCATGTTTACTGCTAAAAACCAAAGCTTTGTGTAAAATCTTGAATTTAT
GGGGCGGGAGGGTAGGAAAGCCTGTACCTGTCTGTTTTTTTCCTGATCCTTTTCCCTCATTCCTGAACTGCAGGA
GACTGAGCCCCTTTGGGCTTTGGTGACCCCATCACTGGGGTGTGTTTATTTGATGGTTGATTTTGCTGTACTGGG
TACTTCCTTTCCCATTTTCTAATCATTTTTTAACACAAGCTGACTCTTCCCTTCCCTTCTCCTTTCCCTGGGAAA
ATACAATGAATAAATAAAGACTTATTGGTACGC

FIGURE 110

GAGCAGTGTGAAGAAGAGGCGAGAACGACCCCCGGACCGACCAAAGCCCGCGCGCCGCTGCATCCCGCGTCCAGC
ACCTACGTCCCGCTGCCGTCGCCGCCGCCACC**ATG**CCCAAGAGAAAGGCTGAAGGGGATGCTAAGGGAGATAAAG
CAAAGGTGAAGGACGAACCACAGAGAAGATCCGCGAGGTTGTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCA
AGCCTAAAAAGGCCCCTGCAAAGAAGGGAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGATGCTGGCAAGG
AGGGGAATAACCCTGCAGAAAATGGAGATGCCAAAACAGACCAGGCACAGAAAGCTGAAGGTGCTGGAGATGCCA
AG**TGA**AGTGTGTGCATTTTTGATAACTGTGTACTTCTGGTGACTGTACAGTTTGAAATACTATTTTTTATCAAGT
TTTATAAAAATGCAGAATTTTGTTTTACTTTTTTTTTTTTTTTAAAAGCTATGTTGTTAGCACACAGAACACTTC
ATTGTTGTTTTTGGGGGAAGGGGCATATGTCACTAATAGAATGTCTCCAAAGCTGGATTGATGTGGAGAAAACAC
CTTTCCCTTCTAGTTTTGAGAGACTTCCTCTTGGCTCCCAGGAGGAGGGATTCCCTGACTTTGACACACATGGCC
ACCTTGGCACAAAAGCCTTGTGGTATAGAAAAACAAATTTGTTTTTATGTCCTCTTCTCCCTTTCCATCTTTCAG
CATAGACTTAACTCCCTTAAGCCCAGACATCTGTTGAGACCTGACCCCTAGTCATTGGTTACCAGTGTGTCAGGC
AATCTGGACTTTCCAGTGATGCCACTGAGATGGCACCTGTCAAAAGAGCAGTGGTTCCATTTCTAGATTGTGGAT
CTTCAGATAAATTCTGCCATTTTCATTTCACTTCCTGAAAGTCAGGGTCGGCTTGTGAAAAGTTGTTAAACAACA
TGCTAAATGTGAAATGTCAACCCTCACTCTAAACTTTCCCTGTTCAGAGCATCAGATGAAGACTTCATTGGGTTT
TATAGTGGCTTTCTGATTTTTGGTAGTCCATTGAAGAAGGGAGTTTGAAAGTTGTTGTATACTGTTAACGATTGT
CTGCCCATGTCCTGCCTGAAATACCATGATTGTTTATGGAAAGTATCTTTAATAAAGCTGGATACAGTTTGGC

FIGURE 111

MPKRKAEGDAKGDKAKVKDEPQRRSARLSAKPAPPKPEPKPKKAPAKKGEKVPKGKKGKADAGKEGNNPAENGDA
KTDQAQKAEGAGDAK

FIGURE 112A

GAAAGCGGAGAGTCACAGCGGGGCCAGGCCCTGGGGAGCGGAGCCTCCACCGCCCCCCTCATTCCCAGGCAAGGG
CTTGGGGGGAATGAGCCGGGAGAGCCGGGTCCCGAGCCTACAGAGCCGGGAGCAGCTGAGCCGCCGGCGCCTCGG
CCGCCGCCGCCGCCTCCTCCTCCTCCGCCGCCGCCAGCCCGGAGCCTGAGCCGGCGGGGCGGGGGGGAGAGGAGC
GAGCGCAGCGCAGCAGCGGAGCCCCGCGAGGCCCGCCCGGGCGGGTGGGGAGGGCAGCCCGGGGGACTGGGCCCC
GGGGCGGGGTGGGAGGGGGGGAGAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTCGAGGCGGCGGCTGCGGCAGCGGC
CGAGCGCGGTGGAAATGAAGGCAGCCGCCGGGCAGGAAAGCGAGGGCCCCGCCGTGGGGCCGCCGCATCCGCTGG
GAAAGGAGCTGCTGGACGGGGCCGAGAGCAATGGGGGTGGCGGCGGCGGCGGAGCCGGCAGCGGCGGCGGGCCCG
GCGCGGAGCCGGACCTGAAGAACTCGAACGGGAACGCGGGCCCTAGGCCCGCCCTGAACAATAACCTCACGGAGC
CGCCCGGCGGCGGCGGTGGCGGCAGCAGCGATGGGGTGGGGGCGCCTCCTCACTCAGCCGCGGCCGCCTTGCCGC
CCCCAGCCTACGGCTTCGGGCAACCCTACGGCCGGAGCCCGTCTGCCGTCGCCGCCGCCGCGGCCGCCGTCTTCC
ACCAACAACATGGCGGACAACAAAGCCCTGGCCTGGCAGCGCTGCAGAGCGGCGGCGGCGGGGGCCTGGAGCCCT
ACGCGGGGCCCCAGCAGAACTCTCACGACCACGGCTTCCCCAACCACCAGTACAACTCCTACTACCCCAACCGCA
GCGCCTACCCCCCGCCCGCCCCGGCCTACGCGCTGAGCTCCCCGAGAGGTGGCACTCCGGGCTCCGGCGCGGCGG
CGGCTGCCGGCTCCAAGCCGCCTCCCTCCTCCAGCGCCTCCGCCTCCTCGTCGTCTTCGTCCTTCGCTCAGCAGC
GCTTCGGGGCCATGGGGGGAGGCGGCCCCTCCGCGGCCGGCGGGGGAACTCCCCAGCCCACCGCCACCCCCACCC
TCAACCAACTGCTCACGTCGCCCAGCTCGGCCCGGGGCTACCAGGGCTACCCCGGGGGCGACTACAGTGGCGGGC
CCCAGGACGGGGGCGCCGGCAAGGGCCCGGCGGACATGGCCTCGCAGTGTTGGGGGGCTGCGGCGGCGGCAGCTG
CGGCGGCGGCCGCCTCGGGAGGGGCCCAACAAAGGAGCCACCACGCGCCCATGAGCCCCGGGAGCAGCGGCGGCG
GGGGGCAGCCGCTCGCCCGGACCCCTCAGCCATCCAGTCCAATGGATCAGATGGGCAAGATGAGACCTCAGCCAT
ATGGCGGGACTAACCCATACTCGCAGCAACAGGGACCTCCGTCAGGACCGCAGCAAGGACATGGGTACCCAGGGC
AGCCATACGGGTCCCAGACCCCGCAGCGGTACCCGATGACCATGCAGGGCCGGGCGCAGAGTGCCATGGGCGGCC
TCTCTTATACACAGCAGATTCCTCCTTATGGACAACAAGGCCCCAGCGGGTATGGTCAACAGGGCCAGACTCCAT
ATTACAACCAGCAAAGTCCTCACCCTCAGCAGCAGCAGCCACCCTACTCCCAGCAACCACCGTCCCAGACCCCTC
ATGCCCAACCTTCGTATCAGCAGCAGCCACAGTCTCAACCACCACAGCTCCAGTCCTCTCAGCCTCCATACTCCC
AGCAGCCATCCCAGCCTCCACATCAGCAGTCCCCGGCTCCATACCCCTCCCAGCAGTCGACGACACAGCAGCACC
CCCAGAGCCAGCCCCCCTACTCACAGCCACAGGCTCAGTCTCCTTACCAGCAGCAGCAACCTCAGCAGCCAGCAC
CCTCGACGCTCTCCCAGCAGGCTGCGTATCCTCAGCCCCAGTCTCAGCAGTCCCAGCAAACTGCCTATTCCCAGC
AGCGCTTCCCTCCACCGCAGGAGCTATCTCAAGATTCATTTGGGTCTCAGGCATCCTCAGCCCCCTCAATGACCT
CCAGTAAGGGAGGGCAAGAAGATATGAACCTGAGCCTTCAGTCAAGACCCTCCAGCTTGCCTGATCTATCTGGTT
CAATAGATGACCTCCCCATGGGGACAGAAGGAGCTCTGAGTCCTGGAGTGAGCACATCAGGGATTTCCAGCAGCC
AAGGAGAGCAGAGTAATCCAGCTCAGTCTCCTTTCTCTCCTCATACCTCCCCTCACCTGCCTGGCATCCGAGGCC
CTTCCCCGTCCCCTGTTGGCTCTCCCGCCAGTGTTGCTCAGTCTCGCTCAGGACCACTCTCGCCTGCTGCAGTGC
CAGGCAACCAGATGCCACCTCGGCCACCCAGTGGCCAGTCGGACAGCATCATGCATCCTTCCATGAACCAATCAA
GCATTGCCCAAGATCGAGGTTATATGCAGAGGAACCCCCAGATGCCCCAGTACAGTTCCCCCCAGCCCGGCTCAG
CCTTATCTCCGCGTCAGCCTTCCGGAGGACAGATACACACAGGCATGGGCTCCTACCAGCAGAACTCCATGGGGA
GCTATGGTCCCCAGGGGGGTCAGTATGGCCCACAAGGTGGCTACCCCAGGCAGCCAAACTATAATGCCTTGCCCA
ATGCCAACTACCCCAGTGCAGGCATGGCTGGAGGCATAAACCCCATGGGTGCCGGAGGTCAAATGCATGGACAGC
CTGGCATCCCACCTTATGGCACACTCCCTCCAGGGAGGATGAGTCACGCCTCCATGGGCAACCGGCCTTATGGCC
CTAACATGGCCAATATGCCACCTCAGGTTGGGTCAGGGATGTGTCCCCCACCAGGGGGCATGAACCGGAAAACCC
AAGAAACTGCTGTCGCCATGCATGTTGCTGCCAACTCTATCCAAAACAGGCCGCCAGGCTACCCCAATATGAATC
AAGGGGGCATGATGGGAACTGGACCTCCTTATGGACAAGGGATTAATAGTATGGCTGGCATGATCAACCCTCAGG
GACCCCCATATTCCATGGGTGGAACCATGGCCAACAATTCTGCAGGGATGGCAGCCAGCCCAGAGATGATGGGCC
TTGGGGATGTAAAGTTAACTCCAGCCACCAAAATGAACAACAAGGCAGATGGGACACCCAAGACAGAATCCAAAT
CCAAGAAATCCAGTTCTTCTACTACAACCAATGAGAAGATCACCAAGTTGTATGAGCTGGGTGGTGAGCCTGAGA
GGAAGATGTGGGTGGACCGTTATCTGGCCTTCACTGAGGAGAAGGCCATGGGCATGACAAATCTGCCTGCTGTGG
GTAGGAAACCTCTGGACCTCTATCGCCTCTATGTGTCTGTGAAGGAGATTGGTGGATTGACTCAGGTCAACAAGA
ACAAAAAATGGCGGGAACTTGCAACCAACCTCAATGTGGGCACATCAAGCAGTGCTGCCAGCTCCTTGAAAAAGC

FIGURE 112B

AGTATATCCAGTGTCTCTATGCCTTTGAATGCAAGATTGAACGGGGAGAAGACCCTCCCCCAGACATCTTTGCAG
CTGCTGATTCCAAGAAGTCCCAGCCCAAGATCCAGCCTCCCTCTCCTGCGGGATCAGGATCTATGCAGGGGCCCC
AGACTCCCCAGTCAACCAGCAGTTCCATGGCAGAAGGAGGAGACTTAAAGCCACCAACTCCAGCATCCACACCAC
ACAGTCAGATCCCCCCATTGCCAGGCATGAGCAGGAGCAATTCAGTTGGGATCCAGGATGCCTTTAATGATGGAA
GTGACTCCACATTCCAGAAGCGGAATTCCATGACTCCAAACCCTGGGTATCAGCCCAGTATGAATACCTCTGACA
TGATGGGGCGCATGTCCTATGAGCCAAATAAGGATCCTTATGGCAGCATGAGGAAAGCTCCAGGGAGTGATCCCT
TCATGTCCTCAGGGCAGGGCCCCAACGGCGGGATGGGTGACCCCTACAGTCGTGCTGCCGGCCCTGGGCTAGGAA
ATGTGGCGATGGGACCACGACAGCACTATCCCTATGGAGGTCCTTATGACAGAGTGAGGACGGAGCCTGGAATAG
GGCCTGAGGGAAACATGAGCACTGGGGCCCCACAGCCGAATCTCATGCCTTCCAACCCAGACTCGGGGATGTATT
CTCCTAGCCGCTACCCCCCGCAGCAGCAGCAGCAGCAGCAGCAACGACATGATTCCTATGGCAATCAGTTCTCCA
CCCAAGGCACCCCTTCTGGCAGCCCCTTCCCCAGCCAGCAGACTACAATGTATCAACAGCAACAGCAGAATTACA
AGCGGCCAATGGATGGCACATATGGCCCTCCTGCCAAGCGGCACGAAGGGGAGATGTACAGCGTGCCATACAGCA
CTGGGCAGGGGCAGCCTCAGCAGCAGCAGTTGCCCCCAGCCCAGCCCCAGCCTGCCAGCCAGCAACAAGCTGCCC
AGCCTTCCCCTCAGCAAGATGTATACAACCAGTATGGCAATGCCTATCCTGCCACTGCCACAGCTGCTACTGAGC
GCCGACCAGCAGGCGGCCCCCAGAACCAATTTCCATTCCAGTTTGGCCGAGACCGTGTCTCTGCACCCCCTGGCA
CCAATGCCCAGCAAAACATGCCACCACAAATGATGGGCGGCCCCATACAGGCATCAGCTGAGGTTGCTCAGCAAG
GCACCATGTGGCAGGGGCGTAATGACATGACCTATAATTATGCCAACAGGCAGAGCACGGGCTCTGCCCCCCAGG
GCCCCGCCTATCATGGCGTGAACCGAACAGATGAAATGCTGCACACAGATCAGAGGGCCAACCACGAAGGCTCGT
GGCCTTCCCATGGCACACGCCAGCCCCCATATGGTCCCTCTGCCCCTGTGCCCCCCATGACAAGGCCCCCTCCAT
CTAACTACCAGCCCCCACCAAGCATGCAGAATCACATTCCTCAGGTATCCAGCCCTGCTCCCCTGCCCCGGCCAA
TGGAGAACCGCACCTCTCCTAGCAAGTCTCCATTCCTGCACTCTGGGATGAAAATGCAGAAGGCAGGTCCCCCAG
TACCTGCCTCGCACATAGCACCTGCCCCTGTGCAGCCCCCCATGATTCGGCGGGATATCACCTTCCCACCTGGCT
CTGTTGAAGCCACACAGCCTGTGTTGAAGCAGAGGAGGCGGCTCACAATGAAAGACATTGGAACCCCGGAGGCAT
GGCGGGTAATGATGTCCCTCAAGTCTGGTCTCCTGGCAGAGAGCACATGGGCATTAGATACCATCAACATCCTGC
TGTATGATGACAACAGCATCATGACCTTCAACCTCAGTCAGCTCCCAGGGTTGCTAGAGCTCCTTGTAGAATATT
TCCGACGATGCCTGATTGAGATCTTTGGCATTTTAAAGGAGTATGAGGTGGGTGACCCAGGACAGAGAACGCTAC
TGGATCCTGGGAGGTTCAGCAAGGTGTCTAGTCCAGCTCCCATGGAGGGTGGGGAAGAAGAAGAAGAACTTCTAG
GTCCTAAACTAGAAGAGGAAGAAGAAGAGGAAGTAGTTGAAAATGATGAGGAGATAGCCTTTTCAGGCAAGGACA
AGCCAGCTTCAGAGAATAGTGAGGAGAAGCTGATCAGTAAGTTTGACAAGCTTCCAGTAAAGATCGTACAGAAGA
ATGATCCATTTGTGGTGGACTGCTCAGATAAGCTTGGGCGTGTGCAGGAGTTTGACAGTGGCCTGCTGCACTGGC
GGATTGGTGGGGGGGACACCACTGAGCATATCCAGACCCACTTCGAGAGCAAGACAGAGCTGCTGCCTTCCCGGC
CTCACGCACCCTGCCCACCAGCCCCTCGGAAGCATGTGACAACAGCAGAGGGTACACCAGGGACAACAGACCAGG
AGGGGCCCCCACCTGATGGACCTCCAGAAAAACGGATCACAGCCACTATGGATGACATGTTGTCTACTCGGTCTA
GCACCTTGACCGAGGATGGAGCTAAGAGTTCAGAGGCCATCAAGGAGAGCAGCAAGTTTCCATTTGGCATTAGCC
CAGCACAGAGCCACCGGAACATCAAGATCCTAGAGGACGAACCCCACAGTAAGGATGAGACCCCACTGTGTACCC
TTCTGGACTGGCAGGATTCTCTTGCCAAGCGCTGCGTCTGTGTGTCCAATACCATTCGAAGCCTGTCATTTGTGC
CAGGCAATGACTTTGAGATGTCCAAACACCCAGGGCTGCTGCTCATCCTGGGCAAGCTGATCCTGCTGCACCACA
AGCACCCAGAACGGAAGCAGGCACCACTAACTTATGAAAAGGAGGAGGAACAGGACCAAGGGGTGAGCTGCAACA
AAGTGGAGTGGTGGTGGGACTGCTTGGAGATGCTCCGGGAAAACACCTTGGTTACACTCGCCAACATCTCGGGGC
AGTTGGACCTATCTCCATACCCCGAGAGCATTTGCCTGCCTGTCCTGGACGGACTCCTACACTGGGCAGTTTGCC
CTTCAGCTGAAGCCCAGGACCCCTTTTCCACCCTGGGCCCCAATGCCGTCCTTTCCCCGCAGAGACTGGTCTTGG
AAACCCTCAGCAAACTCAGCATCCAGGACAACAATGTGGACCTGATTCTGGCCACACCCCCCTTCAGCCGCCTGG
AGAAGTTGTATAGCACTATGGTGCGCTTCCTCAGTGACCGAAAGAACCCGGTGTGCCGGGAGATGGCTGTGGTAC
TGCTGGCCAACCTGGCTCAGGGGGACAGCCTGGCAGCTCGTGCCATTGCAGTGCAGAAGGGCAGTATCGGCAACC
TCCTGGGCTTCCTAGAGGACAGCCTTGCCGCCACACAGTTCCAGCAGAGCCAGGCCAGCCTCCTCCACATGCAGA
ACCCACCCTTTGAGCCAACTAGTGTGGACATGATGCGGCGGGCTGCCCGCGCGCTGCTTGCCTTGGCCAAGGTGG
ACGAGAACCACTCAGAGTTTACTCTGTACGAATCACGGCTGTTGGACATCTCGGTATCACCGTTGATGAACTCAT
TGGTTTCACAAGTCATTTGTGATGTACTGTTTTTGATTGGCCAGTCATGACAGCCGTGGGACACCTCCCCCCCCC

FIGURE 112C

GTGTGTGTGTGCGTGTGTGGAGAACTTAGAAACTGACTGTTGCCCTTTATTTATGCAAAACCACCTCAGAATCCA
GTTTACCCTGTGCTGTCCAGCTTCTCCCTTGGGAAAAAGTCTCTCCTGTTTCTCTCTCCTCCTTCCACCTCCCCT
CCCTCCATCACCTCACGCCTTTCTGTTCCTTGTCCTCACCTTACTCCCCTCAGGACCCTACCCCACCCTCTTTGA
AAAGACAAAGCTCTGCCTACATAGAAGACTTTTTTTATTTTAACCAAAGTTACTGTTGTTTACAGTGAGTTTGGG
GAAAAAAAATAAAATAAAAATGGCTTTCCCAGTCCTTGCATCAACGGGATGCCACATTTCATAACTGTTTTTAAT
GGTAAAAAAAAAAAAAA

FIGURE 113

CAACAATGTGGACCTGATTCTGGCCACACCCCCCTTCAGCCGCCTGGAGAAGTTGTATAGCACTATGGTGCGCTT
CCTCAGTGACCGAAAGAACCCGGTGTGCCGGGAGATGGCTGTGGTACTGCTGGCCAACCTGGCTCAGGGGGACAG
CCTGGCAGCTCGTGCCATTGCAGTGCAGAAGGGCAGTATCGGCAACCTCCTGGGCTTCCTAGAGGACAGCCTTGC
CGCCACACAGTTCCAGCAGAGCCAGGCCAGCCTCCTCCACATGCAGAACCCACCCTTTGAGCCAACTAGTGTGGA
CATGATGCGGCGGGCTGCCCGCGCGCTGCTTGCCTTGGCCAAGGTGGACGAGAACCACTCAGAGTTTACTCTGTA
CGAATCACGGCTGTTGGACATCTCGGTATCACCGTTGATGAACTCATTGGTTTCACAAGTCATTTGTGATGTACT
GTTTTTGATTGGCCAGTCATGACAGCCGTGGGACACCTCCCCCCCCCGTGTGTGTGTGCGTGTGTGGAGAACTTA
GAAACTGACTGTTGCCCTTTATTTATGCAAAACCACCTCAGAATCCAGTTTACCCTGTGCTGTCCAGCTTCTCCC
TTGGGAAAAAGTCTCTCCTGTTTCTCTCTCCTCCTTCCACCTCCCCTCCCTCCATCACCTCACGCCTTTCTGTTC
CTTGTCCTCACCTTACTCCCCTCAGGACCCTACCCCACCCTCTTTGAAAAGACAAAGCTCTGCCTACATAGAAGA
CTTTTTTTATTTTAACCAAAGTTACTGTTGTTTACAGTGAGTTTGGGGAAAAAAAATAAAATAAAAATGGCTTTC
CCAGTCCTTGCATCAACGGGATGCCACATTTCATAACTGTTTTTAATGGTAAAAAAAAAAAAAAAAAATACAAAA
AAAAATTCTGAAGGACAAAAAAGGTGACTGCTGAACTGTGTGTGGTTTATTGTTGTACATTCACAATCTTGCAGG
AGCCAAGAAGTTCGCAGTTGTGAACAGACCCTGTTCACTGGAGAGGCCTGTGCAGTAGAGTGTAGACCCTTTCAT
GTACTGTACTGTACACCTGATACTGTAAACATACTGTAATAATAATGTCTCACATGGAAACAGAAAACGCTGGGT
CAGCAGCAAGCTGTAGTTTTTAAAAATGTTTTTAGTTAAACGTTGAGGAGAAAAAAAAAAAAAGGCTTTTCCCCCA
AAGTATCATGTGTGAACCTACAACACCCTGACCTCTTTCTCTCCTCCTTGATTGTATGAATAACCCTGAGATCAC
CTCTTAGAACTGGTTTTAACCTTTAGCTGCAGCGGCTACGCTGCCACGTGTGTATATATATGACGTTGTACATTG
CACATACCCTTGGATCCCCACAGTTTGGTCCTCCTCCCAGCTACCCCTTTATAGTATGACGAGTTAACAAGTTGG
TGACCTGCACAAAGCGAGACACAGCTATTTAATCTCTTGCCAGATATCGCCCCTCTTGGTGCGATGCTGTACAGG
TCTCTGTAAAAAGTCCTTGCTGTCTCAGCAGCCAATCAACTTATAGTTTATTTTTTTCTGGGTTTTTGTTTTGTT
TTGTTTTCTTTCTAATCGAGGTGTGAAAAAGTTCTAGGTTCAGTTGAAGTTCTGATGAAGAAACACAATTGAGAT
TTTTTCAGTGATAAAATCTGCATATTTGTATTTCAACAATGTAGCTAAAACTTGATGTAAATTCCTCCTTTTTTT
CCTTTTTTGGCTTAATGAATATCATTTATTCAGTATGAAATCTTTATACTATATGTTCCACGTGTTAAGAATAAA
TGTACATTAAATCTTGGT

FIGURE 114

ATTGGTCCCAGGCAGCAGTTAGCCCGCCGCCCGCCTGTGTGTCCCCAGAGCCATGGAGAGAGCCAGTCTGATCCA
GAAGGCCAAGCTGGCAGAGCAGGCCGAACGCTATGAGGACATGGCAGCCTTCATGAAAGGCGCCGTGGAGAAGGG
CGAGGAGCTCTCCTGCGAAGAGCGAAACCTGCTCTCAGTAGCCTATAAGAACGTGGTGGGCGGCCAGAGGGCTGC
CTGGAGGGTGCTGTCCAGTATTGAGCAGAAAAGCAACGAGGAGGGCTCGGAGGAGAAGGGGCCCGAGGTGCGTGA
GTACCGGGTCTTCTACCTGAAGATGAAGGGTGACTACTACCGCTACCTGGCCGAGGTGGCCACCGGTGACGACAA
GAAGCGCATCATTGACTCAGCCCGGTCAGCCTACCAGGAGGCCATGGACATCAGCAAGAAGGAGATGCCGCCCAC
CAACCCCATCCGCCTGGGCCTGGCCCTGAACTTTTCCGTCTTCCACTACGAGATCGCCAACAGCCCCGAGGAGGC
CATCTCTCTGGCCAAGACCACTTTCGACGAGGCCATGGCTGATCTGCACACCCTCAGCGAGGACTCCTACAAAGA
CAGCACCCTCATCATGCAGCTGCTGCGAGACAACCTGACACTGTGGACGGCCGACAACGCCGGGGAAGAGGGGGG
CGAGGCTCCCCAGGAGCCCCAGAGCTGAGTGTTGCCCGCCACCGCCCCGCCCTGCCCCCTCCAGTCCCCCACCCT
GCCGAGAGGACTAGTATGGGGTGGAGGCCCCACCCTTCTCCCCTAGGCGCTGTTCTTGCTCCAAAGGGCTCCGT
GGAGAGGGACTGGCAGAGCTGAGGCCACCTGGGGCTGGGGATCCCACTCTTCTTGCAGCTGTTGAGCGCACCTAA
CCACTGGTCATGCCCCCACCCCTGCTCTCCGCACCCGCTTCCTCCCGACCCCAGGACCAGGCTACTTCTCCCCTC
CTCTTGCCTCCCTCCTGCCCCTGCTGCCTCTGATCGTAGGAATTGAGGAGTGTCCCGCCTTGTGGCTGAGAACTG
GACAGTGGCAGGGGCTGGAGATGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCGCGCGCGCCAGTGCA
AGACCGAGATTGAGGGAAAGCATGTCTGCTGGGTGTGACCATGTTTCCTCTCAATAAAGTTCCCCTGTGACACTC

FIGURE 115

MERASLIQKAKLAEQAERYEDMAAFMKGAVEKGEELSCEERNLLSVAYKNVVGGQRAAWRVLSSIEQKSNEEGSE
EKGPEVREYREKVETELQGVCDTVLGLLDSHLIKEAGDAESRVFYLKMKGDYYRYLAEVATGDDKKRIIDSARSA
YQEAMDISKKEMPPTNPIRLGLALNFSVFHYEIANSPEEAISLAKTTFDEAMADLHTLSEDSYKDSTLIMQLLRD
NLTLWTADNAGEEGGEAPQEPQS

FIGURE 116

CCGGAAGTCGAGTTAGTCTAGTTAGTATCGGCCTGTTATCTCCTTTTGCGCGACACGGTCTCAGCTGTTCCGCCT
GAGGCGAGTGACGCTGGCCGCCAACGAGGTATACGTACTGGGACCCTCGCCCTCAGTCTCGTCTCCGGCGCGGCT
ACCTGCCCCGTTTTCCCTGTGAGTTGACCTGCTCCGGGCCGCGGGCCGCCA**ATG**GCAGGGGCCGCTCCGACCACG
GCCTTCGGGCAGGCGGTGACCGGCCCGCCGGGCTCAGGGAAGACCACGTACTGCCTGGGCATGAGTGAGTTCCTG
CGCGCGCTGGGCCGGCGCGTGGCGGTGGTGAACCTGGACCCGGCCAACGAGGGGCTGCCGTACGAGTGTGCCGTG
GACGTGGGCGAGCTGGTGGGGCTGGGCGACGTGATGGACGCGCTGCGCCTGGGGCCCAACGGCGGCCTGCTCTAC
TGCATGGAGTACCTGGAAGCCAACCTGGACTGGCTGCGTGCCAAGCTCGACCCCCTCCGCGGCCACTACTTCCTC
TTCGACTGCCCAGGCCAGGTGGAGCTCTGCACGCATCACGGCGCCTTGCGCAGCATCTTCTCCCAAATGGCGCAG
TGGGACCTCAGGCTGACTGCCGTCCACCTCGTGGATTCTCACTACTGCACAGACCCTGCCAAGTTCATTTCAGTA
CTGTGTACCTCCCTGGCCACCATGCTGCACGTGGAACTGCCCCACATCAACCTCCTTTCCAAGATGGACCTCATT
GAGCATTATGGGAAGCTGGCCTTCAACCTGGACTACTACACAGAGGTTCTGGACCTCTCCTACCTGCTTGACCAC
CTGGCTTCTGACCCTTTCTTCCGCCACTACCGCCAGCTCAATGAGAAGCTAGTGCAGCTCATCGAAGACTATAGC
CTTGTCTCCTTTATCCCTCTCAACATCCAGGACAAGGAGAGCATCCAGCGAGTCCTGCAGGCTGTGGATAAAGCC
AATGGATACTGTTTCAGAGCCCAAGAGCAGCGAAGCTTGGAAGCCATGATGTCTGCCGCAATGGGAGCCGACTTC
CATTTCTCTTCCACACTGGGCATCCAGGAGAAGTACCTGGCACCCTCGAACCAGTCAGTGGAGCAGGAAGCCATG
CAGCTG**TAG**CAACAAGGTGGACCCTGGAGAGCAGGATGCATAATCCAGCACTGGGGAAAGTGGAGGCTCCTGATG
CAGGCTGCAGACCCAAGAGCAAGTCCTCCCAGCCAGAGCTGGCGGGCTGGCAAGGGGATATTCAGCTCTGCAAAG
GACTTCTGGCCAAAAAGCCAGACATGGTGCCAAGCAGAACACCCCCCATACTGTCAGTGGTGTCCGTGAGCTCTG
GGCCCTGCCACCAGAAAGTCGAGCACTGGTCCTAGTCAGGCTGTGATGAAATGTGCTACAATACAAGAGTTTATT
TTCT

FIGURE 117

MAGAAPTTAFGQAVTGPPGSGKTTYCLGMSEFLRALGRRVAVVNLDPANEGLPYECAVDVGELVGLGDVMDALRL
GPNGGLLYCMEYLEANLDWLRAKLDPLRGHYFLFDCPGQVELCTHHGALRSIFSQMAQWDLRLTAVHLVDSHYCT
DPAKFISVLCTSLATMLHVELPHINLLSKMDLIEHYGKLAFNLDYYTEVLDLSYLLDHLASDPFFRHYRQLNEKL
VQLIEDYSLVSFIPLNIQDKESIQRVLQAVDKANGYCFRAQEQRSLEAMMSAAMGADFHFSSTLGIQEKYLAPSN
QSVEQEAMQL

FIGURE 118

TAGAGTCGTTGGGCCCGGCGCGACCCGCAGGAGCGTAGAGAGCGCGGGACTAGAGTGCAGAGCTCCGGGACGTGG
ATCGGAGCCGGCGCG**ATG**GGCGGAGAGCAGGAGGAGGAGCGGTTCGACGGCATGTTGCTGGCCATGGCTCAGCAG
CACGAGGGCGGCGTGCAGGAGCTTGTGAACACCTTCTTCAGCTTCCTTCGACGCAAAACAGACTTTTTCATTGGA
GGAGAAGAAGGGATGGCAGAGAAGCTTATCACACAGACTTTCAGCCACCACAATCAGCTGGCACAGAAGACCCGG
CGGGAGAAGAGAGCCCGGCAGGAGGCCGAGCGGCGGGAGAAGGCGGAGCGGGCGGCCAGACTGGCCAAGGAAGCC
AAGTCAGAGACCTCAGGGCCCCAGATCAAGGAGCTAACTGATGAAGAGGCAGAGAGGCTGCAGCTAGAGATTGAC
CAGAAAAAGGATGCAGAGAATCATGAGGCCCAGCTCAAGAACGGCAGCCTTGACTCCCCAGGGAAGCAGGATACT
GAGGAAGATGAGGAGGAAGATGAGAAGGACAAAGGAAAACTGAAGCCCAACCTAGGCAACGGGGCAGACCTGCCC
AATTACCGCTGGACCCAGACCCTGTCGGAGCTGGACCTGGCGGTCCCTTTCTGTGTGAACTTCCGGCTGAAAGGG
AAGGACATGGTGGTGGACATCCAGCGGCGGCACCTCCGGGTGGGGCTCAAGGGGCAGCCAGCGATCATTGATGGG
GAGCTCTACAATGAAGTGAAGGTGGAGGAGAGCTCGTGGCTCATTGAGGACGGCAAGGTGGTGACTGTGCATCTG
GAGAAGATCAATAAGATGGAGTGGTGGAGCCGCTTGGTGTCCAGTGACCCTGAGATCAACACCAAGAAGATTAAC
CCTGAGAATTCCAAGCTGTCAGACCTGGACAGTGAGACTCGCAGCATGGTGGAAAAGATGATGTATGACCAGCGA
CAGAAGTCCATGGGGCTGCCAACTTCAGACGAACAGAAGAAACAGGAGATTCTGAAGAAGTTCATGGATCAACAT
CCGGAGATGGATTTTTCCAAGGCTAAATTCAAC**TAG**CCCCTGTTTTTTCCTCCCTGAACTCTTGGGGCTGAGCTG
CAACCACCCAACTTTCTTTCCCACTCTTCTCTGGGACTTGTGGGCCTCAGGGCTTGGGGCAGGCATGGGACTGGC
CCAGGCACACAGGTCCCGGGGCATCAGGAGAAAGGCTGGGTCTTGGGACCTTGTCCTCCCCAGTTGGCCTACTGT
TACACATTAAAACGATTTGCCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 119

MGGEQEEERFDGMLLAMAQQHEGGVQELVNTFFSFLRRKTDFFIGGEEGMAEKLITQTFSHHNQLAQKTRREKRA
RQEAERREKAERAARLAKEAKSETSGPQIKELTDEEAERLQLEIDQKKDAENHEAQLKNGSLDSPGKQDTEEDEE
EDEKDKGKLKPNLGNGADLPNYRWTQTLSELDLAVPFCVNFRLKGKDMVVDIQRRHLRVGLKGQPAIIDGELYNE
VKVEESSWLIEDGKVVTVHLEKINKMEWWSRLVSSDPEINTKKINPENSKLSDLDSETRSMVEKMMYDQRQKSMG
LPTSDEQKKQEILKKFMDQHPEMDFSKAKFN

FIGURE 120

CCTGGTATGATTCCATCCTGAGCGGCTGTTCTCTTGAGCAGCGTTCATTTATCTCCGTCTGCCTTCTGTCCCACC
TAAGTGTGTGCCGCCACCCAATAGAAGATTCG**ATG**GACATGGACATGAGCCCCCTGAGGCCCCAGAACTATCTTT
TCGGTTGTGAACTAAAGGCTGACAAAGATGATCACTTTAAGGTGGATAATGATGAAAATGAGCACCAGTTATCTT
TAAGAACGGTCAGTTTAGGGGCTGGTACAAAGGATGAATTGCACATTGTTGAAGCAGAGGCAATGAATTACAAAG
GCAGTCCAATTAAAGTAACACTGGCAACTTTGAAAATGTCTGCACAGCCAACAGTTTCCCTTGGGGGCTTTGAAA
TAACACCACCAGTGGTCTTAAGATTTAAGTGTGGTTCAGGGCCAGTGCATATTAGTGGACAGCACTTAGTAGCTG
TGGAGGAAGATGCAGAGTCAGAAGATGAAGAGGAGGAGGATGTGAAACTCTTAAGTATATCTGGAAAGCGGTCTG
CCCCTGGAGGTGGTAGCAAGGTTCCACAGAAAAAAGTAAAACTTGCTGTTGATGAAGATGATGATGATGATGATG
ATGATGATGATGATGATTTTGATGATGAGGAAGCTGAAGAAAAAGTGCCAGTGAAGAAAGGACAAGAATCCTTCA
AAACACAGGAAAAAACTCCTAAAACACCAAAAGGATCTAGTTCTGTAGAAGACATTAAAGCAAAAATGCAAGCAA
GTATAGAAAAAGGGGGTTCTCTTCCCAAAGTGGAAGCCGAGTTCATCAATTTTGTGAAGAATTGCTTCTGGATGA
CTGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCCT**TAA**GAAAATAGTTTCAACAATTTGTTAA
AAATTTTCCATCATATTTCATTTCTGTAACAGTTGATATCTGGCTGTCCTTTTTATAATGCAGAGTGAGAACTTT
CCCTACCGTGTTTGATAAATGTTGTCCAGGTTCCATTGCCAAGAATGTGTTGTCCAAAATGCCTGTTTAGTTTTT
AAAGATGGAACTCACCCTTTGCTTGGTTTTAAATATGTATGGAATGTTATGATAGGACATAGTAGTAGCGGTGGT
CAGACATGGAAATTGTGGGAAGACAAAAATATGCCTGTGAAATAAAACTCAATATTTTAATAAAGTAAAAAAAAA
AAAAAA

FIGURE 121

MDMDMSPLRPQNYLFGCELKADKDDHFKVDNDENEHQLSLRTVSLGAGTKDELHIVEAEAMNYKGSPIKVTLATL
KMSAQPTVSLGGFEITPPVVLRFKCGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGKRSAPGGGSKVPQK
KVKLAVDEDDDDDDDDDDDDDFDDEEAEEKVPVKKGQESFKTQEKTPKTPKGSSSVEDIKAKMQASIEKGGSLPKV
EAEFINFVKNCFWMTDQEAIQDLWQWRKSP

FIGURE 122

AGCTGCTGGCTGGGCTGCCTGTTGAGTCAGCCTTCTTCCCTCACGGCTCTTCTCCCGGTCCCTGAAACTCGGCTG
CCAGGGGAGCTGGAGCCACCTGCGAAGGTGTCCTCCCATACTGGACCCCTACAGGAAGCTCCGTGTGCCCAGCTG
GGGCACAGCCCCAGCTG**ATG**CCCCAGAGGGGCCACCCATCGCAAGAGGGGCTTTGGGCTCTGCCCTCCCTCCCCA
TGGCGCATGGGCCAAAGCCTGAGACTGAAGGACTGTTGGACCTCAGCTTCCTGACAGAGGAGGAGCAGGAGGCCA
TTGCTGGCGTCCTCCAACGAGATGCCCGCCTGCGCCAGCTGGAGGAGGGGCGGGTCAGCAAGCTCCGGGCCTCAG
TGGCAGACCCTGGGCAGCTGAAGATCCTGACAGGGGACTGGTTCCAGGAAGCACGCTCCCAGCGGCACCACAATG
CCCACTTCGGCTCTGACCTTGTCCGAGCGTCTATGCGCAGGAAGAAGAGCACCAGGGGAGACCAGGCTCCAGGCC
ACGACAGGGAGGCTGAGGCTGCTGTGAAAGAGAAGGAAGAGGGGCCAGAGCCCAGGCTCACCATTGATGAGGCCC
CTCAGGAGAGGCTCAGGGAGACTGAGGCTTCAGATCCTGAGGAGGCGTCCCAGGCCCAGGAAGATCCTGGCCAAG
GAGACCAACAGGTCTGTGCCGAGGAGGCTGACCCGGAGCTGGAGCCCGCGTCGGGGGGAGAGCAGGAGCCGCGGC
CCCAGCAAGCCCAGACCAAGGCCGCGTCCCAGATCCTGGAGAATGGGGAGGAGGCCCCGGGGCCCGACCCCTCTC
TCGACCGCATGCTCAGCAGCAGCTCCTCGGTGTCCAGCCTTAACTCCTCCACGCTGAGCGGCAGCCAGATGAGCC
TGTCAGGCGACGCGGAGGCGGTGCAGGTCCGCGGCTCCGTGCACTTCGCGCTGCACTACGAGCCGGGCGCCGCCG
AGCTGCGCGTGCACGTGATCCAGTGCCAGGGCCTGGCCGCCGCCCGGCGCCGCCGCTCGGACCCCTACGTCAAAA
GCTACCTCCTCCCGGATAAGCAGAGCAAGCGCAAGACGGCGGTGAAGAAACGGAATCTGAATCCGGTTTTCAACG
AGACTCTCCGGTACTCCGTCCCGCAGGCCGAGCTTCAGGGCCGCGTGCTGAGCCTGTCTGTGTGGCACCGCGAAA
GCCTGGGTCGCAACATCTTTCTGGGCGAAGTTGAAGTGCCCCTGGACACGTGGGACTGGGGCTCTGAGCCCACCT
GGCTCCCCCTGCAGCCCCGGGTCCCACCCTCTCCCGACGACCTTCCGAGCCGCGGGTTACTCGCCCTGTCCCTCA
AGTACGTCCCCGCCGGCTCCGAGGGCGCAGGACTGCCCCCGAGCGGGGAGCTGCACTTCTGGGTGAAGGAGGCTC
GGGACCTCCTGCCGCTGCGGGCAGGATCCCTGGACACTTACGTACAATGCTTCGTGCTGCCTGATGACAGCCAGG
CCAGCCGCCAGCGTACAAGGGTTGTGCGACGCAGCCTCAGCCCTGTGTTCAATCACACCATGGTGTACGATGGCT
TTGGGCCTGCTGACCTGCGCCAGGCTTGTGCCGAGCTCTCCCTCTGGGACCATGGGGCCCTGGCCAACCGCCAGC
TGGGGGGCACACGCCTCAGCCTGGGCACCGGCAGCAGCTATGGGCTGCAGGTGCCCTGGATGGATTCCACACCTG
AGGAGAAGCAGCTGTGGCAAGCCCTCCTGGAGCAGCCGTGCGAATGGGTGGATGGCCTTCTACCCCTCAGAACCA
ACCTGGCCCCCAGGACG**TAG**CCCCACCAAGCCTCTCTCTCTGGACCCCCATCTCAGGGCCTGCCCTTGGCTAAAG
TCAATAAAGTCTATTCTAAGAGC

FIGURE 123

MPQRGHPSQEGLWALPSLPMAHGPKPETEGLLDLSFLTEEEQEAIAGVLQRDARLRQLEEGRVSKLRASVADPGQ
LKILTGDWFQEARSQRHHNAHFGSDLVRASMRRKKSTRGDQAPGHDREAEAAVKEKEEGPEPRLTIDEAPQERLR
ETEASDPEEASQAQEDPGQGDQQVCAEEADPELEPASGGEQEPRPQQAQTKAASQILENGEEAPGPDPSLDRMLS
SSSSVSSLNSSTLSGSQMSLSGDAEAVQVRGSVHFALHYEPGAAELRVHVIQCQGLAAARRRRSDPYVKSYLLPD
KQSKRKTAVKKRNLNPVFNETLRYSVPQAELQGRVLSLSVWHRESLGRNIFLGEVEVPLDTWDWGSEPTWLPLQP
RVPPSPDDLPSRGLLALSLKYVPAGSEGAGLPPSGELHFWVKEARDLLPLRAGSLDTYVQCFVLPDDSQASRQRT
RVVRRSLSPVFNHTMVYDGFGPADLRQACAELSLWDHGALANRQLGGTRLSLGTGSSYGLQVPWMDSTPEEKQLW
QALLEQPCEWVDGLLPLRTNLAPRT

FIGURE 124

ATGCCGTTAGTAACGAGGAACATCGAGCCAAGGCACCTGTGCCGTCAGACGTTGCCTAGCGTTAGAAGCGAGCTG
GAATGCGTGACCAACATCACCCTGGCAAATGTCATCCGACAGCTGGGCAGCCTGAGTAAATATGCAGAGGACATT
TTTGGAGAGCTCTTTACTCAGGCAAATACCTTTGCCTCTCGGGTAAGCTCCCTTGCTGAGAGGGTCGACCGACTA
CAGGTTAAAGTCACTCAGCTGGATCCCAAGGAAGAAGAAGTGTCACTGCAAGGAATCAACACCCGAAAAGCCTTC
AGAAGTTCCACCATTCAAGACCAGAAGCTTTTTGACAGAAACTCTCTCCCAGTGCCTGTCTTAGAAACATACAAT
ACCTGTGATACTCCTCCCCCTCTCAACAATCTTACCCCTTACAGGGACGATGGAAAAGAGGCACTCAAATTCTAC
ACAGACCCTTCATACTTCTTTGATCTTTGGAAGGAGAAGATGCTGCAGGACACCAAGGATATCATGAAAGAGAAG
AGAAAGCACAGGAAAGAAAAGAAAGATAATCCAAATCGAGGGAATGTAAACCCACGTAAAATCAAGACACGTAAG
GAAGAGTGGGAGAAAATGAAGATGGGGCAAGAATTTGTGGAGTCCAAAGAAAAGCTGGGGACTTCTGGGTATCCA
CCCACTTTGGTGTACCAGAATGGCAGCATTGGCTGTGTTGAAAACGTGGATGCAAGTAGCTATCCGCCACCACCA
CAGTCAGACTCTGCTTCTTCACCTTCTCCTTCCTTCTCCGAGGACAACTTGCCTCCTCCACCAGCAGAATTCAGT
TACCCAGTGGACAACCAAAGAGGATCTGGTTTGGCTGGACCCAAAAGATCCAGTGTGGTCAGCCCAAGCCATCCA
CCACCAGCTCCTCCTCTAGGCTCTCCACCAGGCCCTAAACCCGGGTTTGCTCCACCACCTGCCCCTCCGCCACCT
CCGCCTCCAATGATAGGCATCCCACCTCCACCACCGCCTGTAGGATTTGGGTCTCCAGGGACGCCTCCACCACCC
TCACCCCCATCTTTCCCACCTCACCCTGATTTTGCTGCCCCTCCACCTCCTCCTCCACCACCAGCAGCTGACTAC
CCAACTCTGCCACCACCTCCCTTGTCCCAGCCAACAGGAGGAGCACCTCCTCCTCCCCCTCCTCCTCCTCCTCCG
GGGCCCCCTCCTCCCCCTTTCACTGGTGCAGATGGCCAGCCTGCTATACCACCACCGCTTTCTGATACCACCAAG
CCCAAGTCCTCCTTGCCTGCCGTGAGCGATGCCCGTAGCGACCTGCTTTCAGCCATCCGTCAAGGTTTTCAGCTG
CGCAGGGTTGAGGAGCAGCGGGAACAAGAGAAGCGGGATGTTGTGGGCAATGACGTGGCCACCATCTTGTCTCGT
CGCATTGCTGTTGAGTACAGTGACTCAGAAGATGACTCCTCTGAATTTGATGAGGACGACTGGTCCGAT**TAA**

FIGURE 125

MPLVTRNIEPRHLCRQTLPSVRSELECVTNITLANVIRQLGSLSKYAEDIFGELFTQANTFASRVSSLAERVDRL
QVKVTQLDPKEEEVSLQGINTRKAFRSSTIQDQKLFDRNSLPVPVLETYNTCDTPPPLNNLTPYRDDGKEALKFY
TDPSYFFDLWKEKMLQDTKDIMKEKRKHRKEKKDNPNRGNVNPRKIKTRKEEWEKMKMGQEFVESKEKLGTSGYP
PTLVYQNGSIGCVENVDASSYPPPPQSDSASSPSPSFSEDNLPPPPAEFSYPVDNQRGSGLAGPKRSSVVSPSHP
PPAPPLGSPPGPKPGFAPPPAPPPPPPPMIGIPPPPPPPVGFGSPGTPPPPSPPSFPPHPDFAAPPPPPPPPPAADY
PTLPPPPLSQPTGGAPPPPPPPPPPGPPPPPFTGADGQPAIPPPLSDTTKPKSSLPAVSDARSDLLSAIRQGFQL
RRVEEQREQEKRDVVGNDVATILSRRIAVEYSDSEDDSSEFDEDDWSD

FIGURE 126

GCAGCACCCCAGTTCTCCCCGCACGCCGGCACTCGCGGCTGCTGGAGCCCCGGCTGGCTCACCCCGGGGCCGGGC
AGAATTGGGCTCCAGGTCTCTGACCCCTCCCAAGGATCATGCCGCAGCCCCACTGACCCAGGAGTAGGGGCCTAA
GGGCAGGGAACCTGGAATGGGCTGTGTGTTCTGCAAGAAATTGGAGCCGGTGGCCACGGCCAAGGAGGATGCTGG
CCTGGAAGGGGACTTCAGAAGCTACGGGGCAGCAGACCACTATGGGCCTGACCCCACTAAGGCCCGGCCTGCATC
CTCATTTGCCCACATCCCCAACTACAGCAACTTCTCCTCTCAGGCCATCAACCCTGGCTTCCTTGATAGTGGCAC
CATCAGGGGTGTGTCAGGGATTGGGGTGACCCTGTTCATTGCCCTGTATGACTATGAGGCTCGAACTGAGGATGA
CCTCACCTTCACCAAGGGCGAGAAGTTCCACATCCTGAACAATACTGAAGGTGACTGGTGGGAGGCTCGGTCTCT
CAGCTCCGGAAAAACTGGCTGCATTCCCAGCAACTACGTGGCCCCTGTTGACTCAATCCAAGCTGAAGAGTGGTA
CTTTGGAAAGATTGGGAGAAAGGATGCAGAGAGGCAGCTGCTTTCACCAGGCAACCCCCAGGGGGCCTTTCTCAT
TCGGGAAAGCGAGACCACCAAAGGTGCCTACTCCCTGTCCATCCGGGACTGGGATCAGACCAGAGGCGATCATGT
GAAGCATTACAAGATCCGCAAACTGGACATGGGCGGCTACTACATCACCACACGGGTTCAGTTCAACTCGGTGCA
GGAGCTGGTGCAGCACTACATGGAGGTGAATGACGGGCTGTGCAACCTGCTCATCGCGCCCTGCACCATCATGAA
GCCGCAGACGCTGGGCCTGGCCAAGGACGCCTGGGAGATCAGCCGCAGCTCCATCACGCTGGAGCGCCGGCTGGG
CACCGGCTGCTTCGGGGATGTGTGGCTGGGCACGTGGAACGGCAGCACTAAGGTGGCGGTGAAGACGCTGAAGCC
GGGCACCATGTCCCCGAAGGCCTTCCTGGAGGAGGCGCAGGTCATGAAGCTGCTGCGGCACGACAAGCTGGTGCA
GCTGTACGCCGTGGTGTCGGAGGAGCCCATCTACATCGTGACCGAGTTCATGTGTCACGGCAGCTTGCTGGATTT
TCTCAAGAACCCAGAGGGCCAGGATTTGAGGCTGCCCCAATTGGTGGACATGGCAGCCCAGGTAGCTGAGGGCAT
GGCCTACATGGAACGCATGAACTACATTCACCGCGACCTGAGGGCAGCCAACATCCTGGTTGGGGAGCGGCTGGC
GTGCAAGATCGCAGACTTTGGCTTGGCGCGTCTCATCAAGGACGATGAGTACAACCCCTGCCAAGGTTCCAAGTT
CCCCATCAAGTGGACAGCCCCAGAAGCTGCCCTCTTTGGCAGATTCACCATCAAGTCAGACGTGTGGTCCTTTGG
GATCCTGCTCACTGAGCTCATCACCAAGGGCCGAATCCCCTACCCAGGCATGAATAAACGGGAAGTGTTGGAACA
GGTGGAGCAGGGCTACCACATGCCGTGCCCTCCAGGCTGCCCAGCATCCCTGTACGAGGCCATGGAACAGACCTG
GCGTCTGGACCCGGAGGAGAGGCCTACCTTCGAGTACCTGCAGTCCTTCCTGGAGGACTACTTCACCTCCGCTGA
ACCACAGTACCAGCCCGGGGATCAGACATAGCCTGTCCGGGCATCAACCCTCTCTGGCGGTGGCCACCAGTCCTT
GCCAATCCCCAGAGCTGTTCTTCCAAAGCCCCCAGGCTGGCTTAGAACCCCATAGAGTCCTAGCATCACCGAGGA
CGTGGCTGCTCTGACACCACCTAGGGCAACCTACTTGTTTTACAGATGGGGCAAAAGGAGGCCCAGAGCTGATCT
CTCATCCGCTCTGGCCCCAAGCACTATTTCTTCCTTTTCCACTTAGGCCCCTACATGCCTGTAGCCTTTCTCACT
CCATCCCCACCCAAAGTGCTCAGACCTTGTCTAGTTATTTATAAAACTGTATGTACCTCCCTCACTTCTCTCCTA
TCACTGCTTTCCTACTCTCCTTTTATCTCACTCTAGTCCAGGTGCCAAGAATTTCCCTTCTACCCTCTATTCTCT
TGTGTCTGTAAGTTACAAAGTCAGGAAAAGTCTTGGCTGGACCCCTTTCCTGCTGGGTGGATGCAGTGGTCCAGG
ACTGGGGTCTGGGCCCAGGTTTGAGGGAGAAGGTTGCAGAGCACTTCCCACCTCTCTGAATAGTGTGTATGTGTT
GGTTTATTGATTCTGTAAATAAGTAAAATGACAATATGAATCCTC

FIGURE 127

GGCACGAGGCTTCGTAAAGATGGCCGCGGAGGCTTTTGGAGCCAACTGGGAGCGCAGTACGCGTTTTCTGGAGCA
TGGGCAGAGGAGACAGGAACAAGCGTAGCATCCGTGAGCACCGATTGGCTGAAGCGAGCACCCCGGGAGCTGACT
GGCTCCGCCATTCGCGGGAAGGCGTTTGTGGTGCCAGAGAAAAGTAGCCAGAGCGGCGCAGTGGCGGCCGCGTTC
TGTGGTTTTCCGCTATTCCCCCAGACCCGCACCTTCTCGGCCTCTTTGCGGAGAATCGTGACCAAG**ATG**TGGAAC
AGTGGATTCGAAAGCTATGGCAGCTCCTCATACGGGGGAGCCGGCGGCTACACGCAGTCCCCGGGGGGCTTTGGA
TCGCCCGCACCTTCTCAAGCCGAAAAGAAATCAAGAGCCCGAGCCCAGCACATTGTGCCCTGTACTATATCTCAG
CTGCTTTCTGCCACTTTGGTTGATGAAGTGTTCAGAATTGGGAATGTTGAGATTTCACAGGTCACTATTGTGGGG
ATCATCAGACATGCAGAGAAGGCTCCAACCAACATTGTTTACAAAATAGATGACATGACAGCTGCACCCATGGAC
GTTCGCCAGTGGGTTGACACAGATGACACCAGCAGTGAAAACACTGTGGTTCCTCCAGAAACATATGTGAAAGTG
GCAGGCCACCTGAGATCTTTTCAGAACAAAAAGAGCCTGGTAGCCTTTAAGATCATGCCCCTGGAGGATATGAAT
GAGTTCACCACACATATTCTGGAAGTGATCAATGCACACATGGTACTAAGCAAAGCCAACAGCCAGCCCTCAGCA
GGGAGAGCACCTATCAGCAATCCAGGAATGAGTGAAGCAGGGAACTTTGGTGGGAATAGCTTCATGCCAGCAAAT
GGCCTCACTGTGGCCCAAAACCAGGTGTTGAATTTGATTAAGGCTTGTCCAAGACCTGAAGGGTTGAACTTTCAG
GATCTCAAGAACCAGCTGAAACACATGTCTGTATCCTCAATCAAGCAAGCTGTGGATTTTCTGAGCAATGAGGGG
CACATCTATTCTACTGTGGATGATGACCATTTTAAATCCACAGATGCAGAA**TAA**CTGGATCTAACTGGGTACCTG
AGATATTTTACAGCTGGACCTAGTTTCACAATCTGTTGTCTCCAGCTCTGCATATGTCTGGCCAGGGGGCTTCTA
GGAAGTAGGTTTCATCTATCAAATGTCTCCTCTGACTTCCTTTTGAAACTTACTGCTCTTCTGTTTTATTTTGTT
TTGTTTGAAGCTCAGAGGGAGATGGGCAATTGACAGGGATGCAATCCAGGGTGGGATTTCTTGAGGAAGTTACAA
ATAAGCTTGTTACAACATCAAGATAGATGGAATTGGAAGGATGCTACCAGGAGAGTACTTACATAGTGCTCAGGA
GTTTCTCTTCTTAAAATGTTTACTGCTGAAAGATGAGCAGGACCAGGGCGTTATAGGCAGAGCCCTAGCCGAGAA
ACCTGCTGGCCTCTGCCTGTTTTCATTTCCCACTTTGGTTGTGTGGCATTACTTTCAGAATTGCACTTTCCTGCT
TGTCATGACTTTTTGACACACTTGCCATGACGTGTGTTTCTGTGAACATGAAGTTCTGCGGTAGTGCCTCCAGGG
GCAGAGGAAAAGAAGAAGTGTTACTGCGTTTTGTACAAAATAAATACAGTCATATGTTTAATAAAACAGTTCTAT
TGTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 128

MWNSGFESYGSSSYGGAGGYTQSPGGFGSPAPSQAEKKSRARAQHIVPCTISQLLSATLVDEVFRIGNVEISQVT
IVGIIRHAEKAPTNIVYKIDDMTAAPMDVRQWVDTDDTSSENTVVPPETYVKVAGHLRSFQNKKSLVAFKIMPLE
DMNEFTTHILEVINAHMVLSKANSQPSAGRAPISNPGMSEAGNFGGNSFMPANGLTVAQNQVLNLIKACPRPEGL
NFQDLKNQLKHMSVSSIKQAVDFLSNEGHIYSTVDDDHFKSTDAE

FIGURE 129

GGAGGGAGACGCAGAGGCGGACAAGATGGCGGCGGCAGCTGTACAGGGCGAGAGAAGCGGTGGTAGCGGAGGCTG
TAGTGGGGCTGGTGGTGCTTCCAACTGCGGGACAGGGAGTGGCCGTAGCGGCTTGTTGGATAAGTGGAAGATAGA
TGATAAGCCTGTAAAAATTGACAAGTGGGATGGATCAGCTGTGAAAAACTCTTTGGATGATTCTGCCAAAAAGGA
GAAGAGCATCTTTCTCGTGGCCCACAGGAAAGATCCTACAGGAATGGATCCTGATGATATTTGGCAGCTGTCCTC
CAGTCTTAAAGGGTTTGATGACAAATACACCTTGAAGCTGACCTTCATCAGTGGGAGAACAAAGCAGCAGCGGGA
AGCCGAGTTCACAAAGTCCATTGCTAAGTTTTTTGACCACAGTGGGACACTGGTCATGGATGCATATGAGCCTGA
AATATCCAGGCTCCATGACAGTCTTGCCATAGAAAGAAAAATAAAGTAGCCAATTCTAAAAGTAGCCCTCTTTCT
CCTGGATCTTGCTGAATTAGTGGCTTGGGGGGTGGGGGAGATAAAAAGAACTTAAAATGGGTAAAGTAAGAAATG
TTAAAAAG

FIGURE 130

CTGGGCCGGGGAAATGGCGGCTTCAGGAGAGAGCGGGACTTCAGGCGGCGGAGGCAGCACCGAGGAAGCATTTAT
GACCTTCTACAGTGAGGTGAAACAAATAGAGAAGAGAGACTCGGTTCTAACTTCGAAAAATCAGATTGAAAGACT
GACCCGTCCTGGTTCCTCTTACTTCAATTTGAACCCATTTGAGGTTCTTCAGATAGATCCTGAAGTTACAGATGA
AGAAATAAAAAAGAGGTTTCGGCAGTTATCCATCTTGGTGCATCCTGACAAAAATCAAGATGATGCTGACAGAGC
ACAAAAGGCTTTTGAAGCTGTGGACAAAGCTTACAAGTTGCTACTGGATCAGGAGCAAAAGAAGAGGGCCCTGGA
TGTAATTCAGGCAGGAAAAGAATACGTGGAACACACTGTGAAAGAGCGAAAAAAACAATTAAAGAAGGAAGGAAA
ACCTACAATTGTAGAGGAGGATGATCCTGAGCTGGAAACGACAAAGGGAAGAAGAGATTGAAGCTCAAGAAAAAG
CCAAACGGGAAAGAGAGTGGCAGAAAAACTTTGAGG

FIGURE 131

TCCAGCACCAAAGCGGCCGTTCTCGGATTCCGGAGCGTTCTGGAGCCCCGAGAGACGCCCCGGGGTTCTAGAAGC
TCCCCGGCGGCGCCCAGTCCCGGCTTCATTCGGGCGTCCCTCCGAAACCCACTCGGGTGCACGGGTCGTCGGCGA
GCCGCGACCGGGTCCTGGCGCGCACCATGATCGTGGCGGACTCCGAGTGCCGCGCAGAGCTCAAGGACTACCTGC
GGTTCGCCCCGGGCGGCGTCGGCGACTCGGGCCCCGGAGAGGAGCAGAGGGAGAGCCGGGCTCGGCGAGGCCCTC
GAGGGCCCAGCGCCTTCATCCCCGTGGAGGAGGTCCTTCGGGAGGGGGCTGAGAGCCTCGAGCAGCACCTGGGGC
TGGAGGCACTGATGTCCTCTGGGCGAGTAGACAACCTGGCAGTGGTGATGGGCCTGCACCCTGACTACTTTACCA
GCTTCTGGCGCCTGCACTACCTGCTGCTGCACACGGATGGTCCCTTGGCCAGCTCCTGGCGCCACTACATTGCCA
TCATGGCTGCCGCCCGCCATCAGTGTTCTTACCTGGTAGGCTCCCACATGGCCGAGTTTCTGCAGACTGGTGGTG
ACCCTGAGTGGCTGCTGGGCCTCCACCGGGCCCCCGAGAAGCTGCGCAAACTCAGCGAGATCAACAAGTTGCTGG
CGCATCGGCCATGGCTCATCACCAAGGAACACATCCAGGCCTTGCTGAAGACCGGCGAGCACACTTGGTCCCTGG
CCGAGCTCATTCAGGCTCTGGTCCTGCTCACCCACTGCCACTCGCTCTCCTCCTTCGTGTTTGGCTGTGGCATCC
TCCCTGAGGGGGATGCAGATGGCAGCCCTGCCCCCCAGGCACCTACACCCCCTAGTGAACAGAGCAGCCCCCCAA
GCAGGGACCCGTTGAACAACTCTGGGGGCTTTGAGTCTGCCCGCGACGTGGAGGCGCTGATGGAGCGCATGCAGC
AGCTGCAGGAGAGCCTGCTGCGGGATGAGGGGACGTCCCAGGAGGAGATGGAGAGCCGCTTTGAGCTGGAGAAGT
CAGAGAGCCTGCTGGTGACCCCCTCAGCTGACATCCTGGAGCCCTCTCCACACCCAGACATGCTGTGCTTTGTGG
AAGACCCTACTTTCGGATATGAGGACTTCACTCGGAGAGGGGCTCAGGCACCCCCTACCTTCCGGGCCCAGGATT
ATACCTGGGAAGACCATGGCTACTCGCTGATCCAGCGGCTTTACCCTGAGGGTGGGCAGCTGCTGGATGAGAAGT
TCCAGGCAGCCTATAGCCTCACCTACAATACCATCGCCATGCACAGTGGTGTGGACACCTCCGTGCTCCGCAGGG
CCATCTGGAACTATATCCACTGCGTCTTTGGCATCAGATATGATGACTATGATTATGGGGAGGTGAACCAGCTCC
TGGAGCGGAACCTCAAGGTCTATATCAAGACAGTGGCCTGCTACCCAGAGAAGACCACCCGAAGAATGTACAACC
TCTTCTGGAGGCACTTCCGCCACTCAGAGAAGGTCCACGTGAACTTGCTGCTCCTGGAGGCGCGCATGCAAGCCG
CTCTGCTGTACGCCCTCCGTGCCATCACCCGCTACATGACCTGACTCCTGAGCAGGACCTGGGCCCGGTTCAGCT
CCCCACAAGGACTTCTCTGTCTGGAGACAGCCCCAGACCCTTTTGTGTCCCATGCCCACCCTCCCCACGCTGCAG
TGGGCTTGTGTGTGATGTGCAGTCCCGAAGCCACACCCTCCCTTTTCCTCACTGGAATGGACAGTTCATTGCACT
GACTCTGGGATCTCAGCCCTGCTCCTGGGAGCTGGAAGAGCACTTGGAGATCCTAAGGGACCACACCCTTCCTCC
TTCCCCTGCCCACAGAGGCAGAGGGCACAGGAAAGAAGCCGGGCCAAGCTCGGAATTAATGTGCCACAAGTGTTG
TGGCCTTCCTGAACTGGGAAGTCCCTGGCTGGCCCCCGGGGGAGAGGGGCAAATGCCTCCGGGACTGACACTCCA
GGCAGCTTTGCCTTCTCTCCCCTGTCATTTCCAGATTTCATTACCTCCTACTTGCCATTCACCCATCAATGTGAA
AGTCAGGGTCACAGCTGGTCTGTGTGTCCAGTTCCCTAAAAGCCTGTTCTGTTGGGCAGCCTGAGGCTGTTGCCC
GAATCCTAGTTCAGTTTTTTGACTTCCTTTGCCCTTTTTCCCTTTTCTCCATGCTTAATGGTGTGAGGCGTCAGG
AGAGAGGCCAAGTACATAAAAAAAAAAAAAAAGCAGATTATCTCTAGAGAGTTTGAGCCTTTGCTGGTCACATTGC
CTTCTGAAGAGGAGGGAGTATTAGATTATAAATCCTCTTTATTTTGGTCCTTTATGCTTGAGGTTCCAACCTGGA
GCCACAGTGTGTGAGAGGAGGAGGAGAGGGAGAATTCTGTTCTCCCAGAGCTGCACCTGCCTCGCAGAGGCCAGC
ACCCCACTCTCCTGCCTCCAGTGGCCCTGCCGCAGATGTCTCCCAAAAAGTTGAGCCTTTCTAGATGGCTTAGGT
GGCACCATGGCTCAGCAGGAGGGGCGGGAGGCACCAGGGTTCTTGTTTGGACCCTGCCCCTGGGCCATGGCCAGG
TGACCATGGCTACATTGCCAAACCTCTGACTGCCACAGCTGCAGACTGAGAGGGTGGGTCTGAGTCCCCACAATG
TCTGAAGCTGCCCCTGGGATTCTCAGGCCAACCTGCCAACAGCAAGCGGATTTTCTTGCAAGATCAGGGACCCCA
TTTCTGCAGCCAGTGTCTCCTGGGTGCCTTCTGAGGACTCCCACCCCCATCCCAGTATCTCATCTGTCCCCTCTC
CTGGGGCTTAAGTGGGTTGCTTCCAGGCAGAAGCAGCCAAGGACCGATTCCAGGCACTTTCTGTAGCAAATGACT
GTGAATTACGACTTCTCTTGCCCTTCTTCTAGCAGTCTGTGCCTCCTCTCTGACCAGTTTGGAGGGCACTGAAGA
AAGGCAAGGGCCGTGCTGCTGCTGGGCGGGGCAGGAGAGGAGCCTGGCCAGTGTGCCACATTAAATACCCGTGCA
GGCGCGGAGAAGCAACCGGCACCCCCTTCCGGCCTGAAAGCCCTCCCTGCAAGAAGGTGTGCAGGAGAGAAGAGG
CCCCGGCATGGGGATCTGGGTTCTAGAGGGCATGTGATGACTGTAAATGTTCACTGGGTGGGTAGGGAGTGGTAT
CCAGTGTTCAAGTGCAGAAATCTTTGGCTTTGCTACCAGTTCCATATGATGAGAAATAAACGTTCGCTGAGGTTT
TGTTTCATAAAAAAAAAAAAAAAAAAA

FIGURE 132

MIVADSECRAELKDYLRFAPGGVGDSGPGEEQRESRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGR
VDNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAAARHQCSYLVGSHMAEFLQTGGDPEWLLGLH
RAPEKLRKLSEINKLLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLSSFVFGCGILPEGDADGS
PAPQAPTPPSEQSSPPSRDPLNNSGGFESARDVEALMERMQQLQESLLRDEGTSQEEMESRFELEKSESLLVTPS
ADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQDYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTY
NTIAMHSGVDTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTVACYPEKTTRRMYNLFWRHFRHS
EKVHVNLLLLEARMQAALLYALRAITRYMT

FIGURE 133

GAGACGTCGGCTTCCGACCGGAAGTGAGAAGAGGAGGAAGTTGGCTGGTTGCACCGATCTGGGGGCTTCCCGGGC
TCGGGTAACCGGAGTGCTGGTATCTAATCGTCGCTCAAAAGCTCCTAGGTATATCCCGTGCCTTACCTGACTGGG
GGCTCTGAGTCCAGTTGTGTTGTCTTCAACTTAGACACCATGGAGGCACCTCCAGTCACCATGATGCCTGTCACT
GGGGGCACCATTAACATGATGGAGTACCTGTTGCAGGGAAGTGTTTTAGATCACAGTTTGGAAAGCCTCATCCAC
CGCCTTCGTGGTTTGTGTGACAACATGGAACCTGAGACTTTCCTTGACCATGAGATGGTATTCCTCCTTAAGGGC
CAGCAAGCCAGCCCATTTGTTCTCAGGGCCCGACGCTCTATGGACAGGGCAGGGGCACCCTGGCATCTGCGCTAC
CTGGGACAGCCAGAAATGGGAGACAAGAACCGCCATGCCCTGGTGCGAAACTGCGTGGACATTGCCACATCTGAG
AACCTCACCGACTTCTTGATGGAAATGGGCTTCCGCATGGACCATGAGTTTGTTGCTAAGGGACATTTGTTCCGT
AAGGGCATCATGAAGATTATGGTGTACAAGATTTTCCGCATCCTGGTGCCAGGGAACACAGACAGCACTGAGGCC
TTGTCACTCTCCTATCTCGTGGAATTAAGTGTGGTAGCACCCGCTGGGCAGGACATGGTCTCTGATGACATGAAG
AACTTCGCAGAACAGCTAAAACCTCTGGTTCACCTAGAGAAAATAGACCCCAAGAGGCTCATGTGACTAAGAGGA
TCTGTCCACATTTGGGGCCTATCCTTACTTGTTTGAAAAAATATGTTTGCTTTTTTTGGTTTTTGTTTTGTTTTG
TTTTTGAGACAGAGTCTCGCTTTGTTTCCCAGGCTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAACCTCTGC
CTCCTGGGTTCAAGCAATTCTCCCACCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACATGCCACCATGCTCAG
CTAATTTTTGTATTTTTAGTAGAAATGGGGATTCACCATGTTGGTCAGGCTATTCTCGAACTCCTGACCTCGTGA
TCCACCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACGCCTGGCCAAAAAAATATGTTTT
AAATGTCCCATTTCACCATTGCCAGGCAGGCATTCTTCCTTCAGGGAGAGGATGGTGAGAATTAATTGGTTCTTT
GCACTGTTCTCCTCATGTGGCGATTTCACTTTCATGACAGCCTTTCTATATTAAAGGCTCAGGATGTCACGGAGA
ATCTATCTAATCCCACTGTATTAAGAGGGGAAACCGGGCCAAGCGCAGTGGCTCACACCTCTAATCCCAGCACTT
TGGGAGGCTGAGGTAGGTGGATCACCCAAGGTCAGGAGTTTGAGACCAGCCTGGCCAAATGGTGAAACCCCATCT
CTACGAAAAATACAAAATTTAGCCGGGCATGGTAGCAGGCGCTTGTAATCCCAGCTACTTGGGAGGCTGAGGCTG
GAGAATCGCTTGAACCCAGGAGGTGAAGGTTGCAGTGACCAGAGATGACGCCATTGCACTCCAGCCTGGGTGAGA
AGAGCGAAACTCCGTCTCAAAAAAAAATAAAAATGAAGAGGGGAAACCAGAATAAATTATCTTTTGGAAAGGACA
ATTTCTTGTTTGGCCATTTGTGTATAAGGTTGGTAACATTAGAGGCTGTGAGCTTGTGTTACATGGTAATAAAGC
CAATGAAGAG

FIGURE 134

GGCCGGCCTCTCCCTTCCCGGGGTTCTTCGCGCCGGGCCCCTTCCGCGTGGGTGAGTGAATGTGAGAGTCAGCGC
TCGCGCCGCGCGCGCCGCCCGCCTCCGCTGTTCGGCGCTCTGCTTTAGGCGGTGGGGGCGGGCGCGCGCGTAAA
AGCATAGAGACGGGCATTGAGCTCTTGGGCTAGAGCGTCGCCGAGTCGGAGCCGGAGCCTGAGCCGCGCGCTGTG
TCTCCGCTGCGTCCGCCGAGGCCCCCGAGTGTCAGGGACAAAAGCCTCCGCCTGCTCCCGCAGACGGGGCTCATC
TGCCGCCGCCGCCGCGCTGAGGAGAGTTCGCCGCCGTCGCCGCCCGTGAGGATCTGAGAGCCATGTCGGCCAGCA
GCCTCTTGGAGCAGAGACCAAAAGGTCAAGGAAACAAAGTACAAAATGGATCTGTACATCAAAAGGATGGATTAA
ACGATGATGATTTTGAACCTTACTTGAGTCCACAGGCAAGGCCCAATAATGCATATACTGCCATGTCAGATTCCT
ACTTACCCAGTTACTACAGTCCCTCCATTGGCTTCTCCTATTCTTTGGGTGAAGCTGCTTGGTCTACGGGGGGTG
ACACAGCCATGCCCTACTTAACTTCTTATGGACAGCTGAGCAACGGAGAGCCCCACTTCCTACCAGATGCAATGT
TTGGGCAACCAGGAGCCCTAGGTAGCACTCCATTTCTTGGTCAGCATGGTTTTAATTTCTTTCCCAGTGGGATTG
ACTTCTCAGCATGGGGAAATAACAGTTCTCAGGGACAGTCTACTCAGAGCTCTGGATATAGTAGCAATTATGCTT
ATGCACCTAGCTCCTTAGGTGGAGCCATGATTGATGGACAGTCAGCTTTTGCCAATGAGACCCTCAATAAGGCTC
CTGGCATGAATACTATAGACCAAGGGATGGCAGCACTGAAGTTGGGTAGCACAGAAGTTGCAAGCAATGTTCCAA
AAGTTGTAGGTTCTGCTGTTGGTAGCGGGTCCATTACTAGTAACATCGTGGCTTCCAATAGTTTGCCTCCAGCCA
CCATTGCTCCTCCAAAACCAGCATCTTGGGCTGATATTGCTAGCAAGCCTGCAAAACAGCAACCTAAACTGAAGA
CCAAGAATGGCATTGCAGGGTCAAGTCTTCCGCCACCCCCGATAAAGCATAACATGGATATTGGAACTTGGGATA
ACAAGGGTCCCGTTGCAAAAGCCCCCTCACAGGCTTTGGTTCAGAATATAGGTCAGCCAACCCAGGGGTCTCCTC
AGCCTGTAGGTCAGCAGGCTAACAATAGCCCACCAGTGGCTCAGGCATCAGTAGGGCAACAGACACAGCCATTGC
CTCCACCTCCACCACAGCCTGCCCAGCTTTCAGTCCAGCAACAGGCAGCTCAGCCAACCCGCTGGGTAGCACCTC
GGAACCGTGGCAGTGGGTTCGGTCATAATGGGGTGGATGGTAATGGAGTAGGACAGTCTCAGGCTGGTTCTGGAT
CTACTCCTTCAGAACCCCACCCAGTGTTGGAGAAGCTTCGGTCCATTAATAACTATAACCCCAAAGATTTTGACT
GGAATCTGAAACATGGCCGGGTTTTCATCATTAAGAGCTACTCTGAGGACGATATTCACCGTTCCATTAAGTATA
ATATTTGGTGCAGCACAGAGCATGGTAACAAGAGACTGGATGCTGCTTATCGTTCCATGAACGGGAAAGGCCCCG
TTTACTTACTTTTCAGTGTCAACGGCAGTGGACACTTCTGTGGCGTGGCAGAAATGAAATCTGCTGTGGACTACA
ACACATGTGCAGGTGTGTGGTCCCAGGACAAATGGAAGGGTCGTTTTGATGTCAGGTGGATTTTTGTGAAGGACG
TTCCCAATAGCCAACTGCGACACATTCGCCTAGAGAACAACGAGAATAAACCAGTGACCAACTCTAGGGACACTC
AGGAAGTGCCTCTGGAAAAGGCTAAGCAGGTGTTGAAAATTATAGCCAGCTACAAGCACACCACTTCCATTTTTG
ATGACTTCTCACACTATGAGAAACGCCAAGAGGAAGAAGAAAGTGTTAAAAAGGAACGTCAAGGTCGTGGGAAAT
AAAAGGCAGTTCTACACAGACTGCAGCAACGGTTGCATCTGCATATCCTAAGAGGAAAAAATGACCTTCAAGAGA
ATTAGGACTTTTTTCTTAATTTCACTGACTTCAGAGACGATTGCAGACTTGCAGTTTAAGTATTGGAATTTCACA
AAAGACATAGGACTTAACTGGAAAATGAAAAAAAAAAGAAAAAGAAAAAACTAAACAAAAAATCCCTCTAGGTAG
TTTAGGTGAAAAATGTCCCTTTTATTTTGGCTTTGGTTGTGATTTCAGAGCATAATGCTATGTTTTTTTGTCTTT
TTACTATGTTTTTCGGATTTTTAAGTCCGTAAGTGCATACAGTTTTCTCTAATTTTTAAACCCTTTCCTCCTCCC
ATTTTGACATTTGCACTTGGAGAACACTTGAGTTGTGAAGGTTTTGGGCATCCACCCCAGAAAGTGGGAATTTGA
TTTTATCCTTCCGAACTGGAAGAACATTTTTATGAAGAATTTTTGTCTAGGAGAATATAACAGTGTTACCCAAGG
TTGTGTCTTTAAGGGTGGTTCATTTTCTCTGACCTTTTGTTACTCAAAGTAAAGTACTAGGAGTCCTAAGAAATG
TTCTGTTCTTGTACATTATACTGATTAAGTCAGGATTAATTTGATTTCAAAGCTGAGAACAGTGGTAAAAACTCG
TTTACAGAAATGCATTTTGGAAGAGAAAAATACTGTAAAACGTGTCGTGAATGTTTCTTCAGTTTCTTGTTCAGC
CAATGAGGAAAGGGCATTGCCTTTCTTTTTACCATTAATCACTTCTCAATAAACGTGAGATCCTGTTGAGCATC

FIGURE 135

GTACGTCGCCGGGGTTCGGCTGCGTCCGTCCCGCCGCCCGCCCGTTGCCGCCGCCGCCGCTGCCGCCGTGCTCTC
GCTTTGCCCGCCGCCGCCTAAGGGGGGCTGGGGCCGGGGCCAGCCATCACTGCCGTTGCCGGGATGCCGCGGGTG
TACATCGGCCGCCTGAGCTACCAGGCCCGGGAGCGCGATGTGGAGCGCTTCTTTAAGGGCTACGGGAAGATCCTG
GAGGTGGATCTGAAGAACGGATATGGTTTTGTGGAGTTTGATGATCTGCGTGATGCAGATGATGCTGTTTATGAA
CTGAATGGCAAAGACCTTTGTGGTGAGCGAGTAATTGTTGAGCATGCCCGCGGCCCACGGCGAGATGGCAGTTAC
GGTTCTGGACGCAGTGGATATGGTTATAGAAGAAGTGGCCGAGATAAATATGGCCCTCCTACTCGCACAGAGTAC
AGACTTATTGTGGAGAATTTGTCAAGTCGGTGCAGCTGGCAAGACCTAAAGGATTATATGCGTCAGGCAGGAGAA
GTGACTTATGCAGATGCTCACAAGGGACGCAAAAATGAAGGGGTGATTGAATTTGTATCTTATTCTGATATGAAA
AGAGCTTTGGAAAAGTTGGATGGAACTGAAGTCAATGGGAGAAAAATCAGATTAGTTGAAGACAAGCCAGGTTCC
AGACGACGCCGGTCCTACTCCAGAAGCCGGAGTCATTCAAGGTCTCGCTCTCGAAGCAGACATTCCCGTAAGAGC
AGAAGCCGAAGTGGCAGCAGCAAAAGCAGTCATTCTAAGAGTAGATCTCGGTCCAGGTCGGGCTCCCGCTCCCGG
AGCAAGAGCCGGAGCCGGAGCCAGAGTCGGAGCCGGAGCAAGAAAGAGAAAAGCAGGAGCCCCAGCAAGGAAAAG
AGCCGCAGCCGCAGCCATAGCGCTGGCAAGAGCCGCAGCAAGAGCAAAGACCAAGCTGAAGAGAAGATCCAAAAC
AATGACAATGTCGGGAAACCCAAGAGCCGGAGTCCTAGCAGGCATAAAAGTAAGAGCAAAAGTCGGAGCAGGAGT
CAGGAGAGGAGAGTGGAGGAGGAGAAGCGAGGGAGTGTGAGCAGGGGCAGGAGCCAGGAGAAGAGCCTCCGCCAG
AGTCGGAGCCGGAGCAGGAGCAAAGGGGGCAGCAGGAGCCGGAGCAGGAGCCGCAGCAAGAGCAAGGACAAGAGG
AAGGGCAGGAAGAGAAGCAGAGAGGAGAGCCGCAGTCGCAGTCGCAGCCGCAGCAAGAGTGAGAGGAGCAGAAAG
CGAGGCAGCAAGCGAGACAGCAAGGCGGGCAGCAGCAAGAAGAAGAAGAAGGAAGACACTGACCGCTCCCAGTCC
AGATCTCCATCCCGCTCCGTGTCAAAGGAGCGGGAACATGCCAAGTCTGAATCCAGCCAGAGGGAAGGTCGAGGA
GAGAGTGAGAATGCTGGCACCAATCAGGAGACCCGGTCCAGGTCGAGATCCAATTCCAAATCGAAACCAAACCTT
CCATCAGAATCACGCTCCAGATCAAAGTCAGCTTCAAAAACCCGATCTCGGTCCAAGTCTAGATCCAGGTCTGCT
TCCAGATCGCCCTCCCGATCTAGATCTAGGTCCCACTCAAGGTCCTAACTGGCTATGGCCACAGCTGGAACTACC
CGAGAAGTCTTTTGTACATGTTTGGTAGCCGTAGCACAAGTGATTGGAGTAGAACATGTCACTGCTGTACATTTT
TAACTCCCCTAATGGTGTGTCTATAATTGTTAAATCTAAGTGCTTCCTCTCAGTAAAGCCTCCTGGCACCAGGCC
TTCCTGCTCGACTGAAAAAAATTTTCTCTTTGAAAATCCCCTTTTACTCATGGCCCACAGTAGAATATCCAAAAC
GCCTTGGCTTTCAGGCCTGGCCTTTCCTACAGGGAGCTCAGTAACCTGGACGGCTCTAAGGCTGGAATGACCACA
TAGGTAGGTATGGTGAGTTCAACCATTTTTGCTCTTGAATTGATGCCCTTCGATGTATGCCATTTAGTGAAAGTG
CTAAGTCTTAAGTTTCCTACCACTTTGGTTTCATATTTTTGGACTTAACAAAGTTGTGAATAGCACAGTCGAGGA
AAATTGATACCTGCAGTAACCCATAGGAAATAAACTGTAGAGTTCCATATTCTGGTATTGTGATTATATTGTTTT
ATATT

FIGURE 136

AGGGTTCTCTCCCCTTGCCACCATGAGCGAGTCATTTGACTGTGCAAAATGCAACGAGTCCCTGTATGGACGCAA
GTACATCCAGACAGACAGCGGCCCCTACTGTGTGCCCTGCTATGACAATACCTTTGCCAACACCTGTGCTGAGTG
CCAGCAGCTTATCGGGCATGACTCGAGGGAGCTGTTCTATGAAGACCGCCATTTCCACGAGGGCTGCTTCCGCTG
CTGCCGCTGCCAGCGCTCACTAGCCGATGAACCCTTCACCTGCCAGGACAGTGAGCTGCTCTGCAATGACTGCTA
CTGCAGTGCGTTTTCCTCGCAGTGCTCCGCTTGTGGGGAGACTGTCATGCCTGGGTCCCGGAAGCTGGAATATGG
AGGCCAGACATGGCATGAGCACTGCTTCCTGTGCAGTGGCTGTGAACAGCCACTGGGCTCCCGTTCTTTTGTGCC
CGACAAGGGTGCTCACTACTGCGTGCCCTGCTATGAGAACAAGTTTGCTCCTCGCTGCGCCCGCTGCAGCAAGAC
GCTGACACAGGGTGGAGTGACATACCGTGATCAGCCGTGGCATCGAGAATGTCTGGTCTGTACCGGATGCCAGAC
GCCCCTGGCAGGGCAGCAGTTCACCTCCCGGGATGAAGATCCCTACTGTGTGGCCTGTTTTGGAGAACTCTTTGC
ACCTAAGTGCAGCAGCTGCAAGCGCCCCATCGTAGGACTCGGTGGAGGCAAGTATGTGTCCTTTGAAGACCGACA
CTGGCACCACAACTGCTTCTCCTGCGCCCGCTGCTCTACCTCCCTGGTGGGCCAGGGCTTCGTACCGGATGGAGA
CCAAGTGCTCTGCCAGGGCTGTAGCCAGGCAGGGCCCTAAGCCAGGGCTCCTGGACCCAGGCTTTCCCATACCAC
GGGCCCAGGACTGTGGCTCCTTTTCTAAACCACCTCTGGGACTCAGCTCCCCCCGCCAAAAAAAATGGGTCTCCT
TCTGGGCTCCAGGATTGTCTCCCCACTCCAGCATCCCCAAACTGGTACTCCCTGACCCAGGGCCCCAAACCTGGG
CTCTTACAGAGCCTCCATGAGTCAAGCCCCCTCCCCACACCTGGACTCCAGAATTCACCCTCTCCCCTGCAGTCT
GGGTTCCCAGACTGAGTCCTCTCCCCAAATCAGGGCTCTAGACCCGAGCCCTCCAAACCTGGACTCTGGGACTTA
GGCCCCCTTAAATCTAGACTTCTCTTTATAGGTTTCAGGTCTCCTATGGGTGCCTGGGAAGTCCTTGAAAGTGGA
CTGTTCTCAGGCTTGACCTGCCCCACCCCATCCCCGCGGTTGAGGCTGTGGGGGCAGCAGATCAGGAGCCCACTG
ATAAGGGGCCCTAGGGTACAGGGTGCTGCCCAGCAGGTCGCCACCGAGTGTCTTCTCATTTTATTTCAGCTCCAT
TTTGCCCATAGATGGGCAGAGGGGTGAGATTGGCTCATCCCCCTTCCAGATTCTGCAATAAAGCGGTGTGAGG

FIGURE 137

CTACAGATACTGCCGTGTGAGAGTACCTGAGGGGCTCCTGAAAGACCTACTGCCAGGACCAGTGACCCTGGTGAT
GGAACGCTCGGAGGAGCTCAACAAGGACCTAAACCCTTTTACGCCTCTTGTAGGCATTCGGATTCCTGATCATGC
TTTTATGCAAGACTTGGCTCAGATGTTTGAGGGTCCGCTTGCTCTCACTAGTGCCAACCTCAGCTCCCAGGCCAG
TTCTCTGAATGTCGAGGAGTTCCAGGATCTCTGGCCTCAGTTGTCCTTGGTTATTGATGGGGGACAAATTGGGGA
TGGCCAGAGCCCCGAGTGTCGCCTTGGCTCAACTGTGGTTGATTTGTCTGTGCCCGGAAAGTTTGGCATCATTCG
TCCAGGCTGTGCCCTGGAAAGTACTACAGCCATCCTCCAACAGAAGTACGGACTGCTCCCCTCACATGCGTCCTA
CCTGTGAAACTCTGGGAAGCAGGAAGGCCCAAGACCTGGTGCTGGATACTATGTGTCTGTCCACTGACGACTGTC
AAGGCCTCATTTGCAGAGGCCACCGGAGCTAGGGCACTAGCCTGACTTTTAAGGCAGTGTGTCTTTCTGAGCACT
GTAGACCAAGCCCTTGGAGCTGCTGGTTTAGCCTTGCACCTGGGGAAAGGATGTATTTATTTGTATTTTCATATA
TCAGCCAAAAGCTGAATGGAAAAGTTAAGAACATTCCTAGGTGGCCTTATTCTAATAAGTTTCTTCTGTCTGTTT
TGTTTTTCAATTGAAAAGTAATTAAATAACAGATTTAGAATCTAGTGAGAGCCTCCTCTCTGGTGGGTGGTGGCA
TTTAAGGTTCAAACCAGCCAGAAGTGCTGGTGCTGTTTAAAAAGTCTCAGGTGGCTGCGTGTGGTGGCTCATGCC
TGTAATCCCAACATTCTGGGAGGCCCAGGCGGGAGAACTGCTTGAGCCCAGGAGTTCAGAATCAGCCTGGGCAAC
ATAGCAATACTCCGTCTCATAAAAATTAATAAATAAAAAGTCTCAGGTGACCAAAGGCTCCTGAAGCTAGAACCA
GGTTTGGATAAAGATTGAAGAGCCACAGGCCACTCTTCCCTCTGAGCCATTGGGCCTAGTGGTGTCATGTATTGT
AATTGCTCGCAGGGAGAGCAGTCTTTTTGGTGTAATAGTGGGATGTCTGCTTAGTTGGCAGGGGTTCAGTCCAAA
TGGAAGAATATTGGGAAATAAACCTCCACTATCCTTTATAGCCAGGGACTTTTTTCTTATTTATTCATAAAATAA
ATTATAGTTAATTATACCCATAACACCTTTATTTAAATCCAGTGTTCTCCGCAGCCTTTTGTCTATTTATATGTG
TACCAAGTGTTAAACATAATTATTATTGGCATTTGAACTTTGTTTTTCTTTAAAGAAATGCTGCTATTAAACAT
ATTTGTAAATGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 138

MERSEELNKDLNPFTPLVGIRIPDHAFMQDLAQMFEGPLALTSANLSSQASSLNVEEFQDLWPQLSLVIDGGQIG
DGQSPECRLGSTVVDLSVPGKFGIIRPGCALESTTAILQQKYGLLPSHASYL

FIGURE 139A

AGGCCCAGCGCTGGCGCAGTGAGAACTTCGAGAGACCCGTGGACCTGGAGGGCTCTGGGGATGATGACTCCTTTC
CCGATGATGAACTGGATGACCTCTACTCGGGGTCGGGCTCGGGCTGTAAGTACCCCCCTCCCTACCTCTGCCTGG
GGGCAGTGACCAGTCTGTATCCAGCCTCAACTCTGAGAAGCCCACGGGGGGCTTGCTTCAGTGAGGCAGGGGGCA
TTCACTGCCTGGGTCAGGCAAGTTCTTCTTGCTCTGGATCCCCAGAACAAGAAGGGCAGAACATCCTTCTGGGGA
TAGAACAAGACCTGGGAGGACCTCAGGGCCCAGAATGTCCAGGTCTCCAGGGTCCCACGTCTGCATCTTTGTGTG
TGCTATGTGGCTTTCTCTGCAGACCTTGCTTGGTTCCGGTGGTCCCGTCAGGTGCAATAAGCTGTGGCCAATGGT
GGGGTTAGGGCAGTGATGACACAGGGCAGGTGCTTCAAGTGGTGCCTGGGATGGCCCCGCCCTGGGGAAGGGGAG
CCAGGTCAGCTGGGTCTAGCAGAATCTCGGGAGAGAAGGGCACCGCGAACCCCACTCTGCCATGTAGCAACTGTG
TGCCCCTCGGTGCTCCCCCTCCCTGAATCCCTGTATTTTCACCTGTGGATGGTGAGAAATACGACTTCTTCTCAG
TGCCTCTAGGAGGGTTTGGGATAGGAAGCTGGGGTCTGGCACAGAGGAGGAGCTCTCAAAATGGTAGCAAAAAGA
AGGCAGCTGAGACTGGGCCCAGTGAGGGCACGGGCTGGCATCTGAGGAGATGGTACGGGGTCTGCACGCCACAGA
GCTGGCTCCCCACAGCCCTCGCCTCTGGTCTCCCCTCCTTAGCCAAGTCCTTTGAGCCTCTTTCAAATTAATCTT
TGTAAAACCCGTTTATATTGGGTCACATCTCTATTCGCAAAGTTCCCTGGCTCCCCTCCCTCCTGCCTGGTTCCG
AGCCCAGGAGCTGGCTGTGGCTTCTCCCTCCCCCATCCCCTACTCCCCATCTCATTTCCTCCCAAGTTCCTTCAC
TGTCCCGGCTTTGCGTCAGCCAGATTGCTCAAGCAGTTCCCCTGCCTCAAGGGCTTCTTTTCCCTTTTACCCTCC
GCCTCTGCCTCTGGGGGAAGCCCTTAGTGTACCACCCCTGCCTTGAGCTTGTGGTAGGGGTGCCTTTGGGGTCTG
ACTCTTCCCAGAATGCCACTCCTGTGTTCCCCTGCAAGCCCCAGCAAGTTTTGCAGCCAGTAGCGCCTCAGTTGC
TGCTGCCTGGATTCAACCTCATAGAAACTGTAGGCTGGGTGGGCAGGAATAGTCAAGGAAGGCTTCCCGGGAGAG
GCGGCCCCCAGAATTTTTGACTTGGCAGAGAGAAGTTGGGGAACATCAGCAACTGACCACCTTTAGCTGGGCTGT
GCCTTCCTCCTTTCTCTCATCTTTTCTGGGAAAATTGGGTAAAGAGAGGGGGTTGGGAGACCTAATCTTGATGGC
CATTGCTTACCTGGGATCCTCATGCCCCTCACAACCACCCAGCTCCCTAGCTCTCTCCCTCTCCCCCACCCCCTC
AGACTTCGAGCAGGAGTCGGGCATTGAGACAGCCATGCGCTTCAGCCCAGATGTAGCCCTGGCGGTGTCCACCAC
ACCTGCGGTGCTGCCCACCACGAACATCCAGCCTGTGGGCACACCATTTGAAGAGCTCCCCTCTGAGCGCCCCAC
CCTGGAGCCAGCCACCAGCCCCCTGGTGGTGACAGAAGTCCCGGAAGAGCCCAGCCAGAGAGCCACCACCGTCTC
CACTACCATGGCTACCACTGCTGCCACAAGCACAGGGGACCCGACTGTGGCCACAGTGCCTGCCACAGTGGCCAC
CGCCACCCCCAGCACCCCTGCAGCACCCCCTTTTACGGCCACCACTGCTGTTATAAGGACCACTGGCGTACGGAG
GCTTCTGCCTCTCCCACTGACCACAGTGGCTACGGCACGGGCCACTACCCCCGAGGCGCCCTCCCCGCCCACCAC
GGCGGCTGTCTTGGACACCGAGGCCCCAACACCCAGGCTGGTCAGCACAGCTACCTCCCGGCCAAGAGCCCTTCC
CAGGCCGGCCACCACCCAGGAGCCTGACATCCCTGAGAGGAGCACCCTGCCCCTGGGGACCACTGCCCCTGGACC
CACAGAGGTGGCTCAGACCCCAACTCCAGAGACCTTCCTGACCACAATCCGGGATGAGCCAGAGGTTCCGGTGAG
TGGGGGGCCCAGTGGAGACTTCGAGCTGCCAGAAGAAGAGACCACACAACCAGACACAGCCAATGAGGTGGTAGC
TGTGGGAGGGGCTGCGGCCAAGGCATCATCTCCACCTGGGACACTGCCCAAGGGTGCCCGCCCGGGCCCTGGCCT
CCTGGACAATGCCATCGACTCGGGCAGCTCAGCTGCTCAGCTGCCTCAGAAGAGTATCCTGGAGCGGAAGGAGGT
GCTCGTAGCTGTGATTGTGGGCGGGGTGGTGGGCGCCCTCTTTGCTGCCTTCTTGGTCACACTGCTCATCTATCG
TATGAAGAAAAAGGATGAGGGCAGCTACACGCTGGAGGAACCCAAGCAGGCGAGCGTCACATACCAGAAGCCTGA
CAAGCAGGAGGAGTTCTATGCCTAGTGGAGCCACAGTGCCTCCCTGCAGCCTCAACACCACCCTGCTGTCCAGTC
CCCAGCCTGGCCCCACCAGCCCAAGCCTGGGACTGGGCCTGGAACCTGGCCCCAGTTCTTCTCTGCCCTCTCTCC
CAAGGTCTGCCCAGGCTGCCAGCCTCACACAGATCTTCCCCGAGGAAGAGGGGCTGCTGCCATCTGCCCCAGACT
GTGCCCTTACGAGCTCATCTCTTGTTCCCCTCATCCCTGCCACCAGTCTGGGGCTTCAGGACCTCATGTCAGATG
GATGGGAGGAAGAAAGCTCCTGATTGGCTGGTGGTGGAAGAAAGGGTGGGGCTTGAGATGAGCCTGAGCCCTGAC
TTGGCACCCACAGTGCTCACTGAGATCTCCTTTTTGGGGCAGAGAGGCACTCAGGCTGGTTTCCAGGACAAACAT
TTGGTAAACACAGCCCTTGAAATCATCTAGACACTGCAACCTCTTGCTCGTATCCCAGGGCCTCTCTCTAGCTGG
GTGAGAGGGTGTCCCTTGTCACCAGCCTGTTTTGTCCTGGTCTCTCTGGGGTTGTTGAATCTCTCCTCTTGCCTG
CCAAGTACACATGTACCCAGACTTCATTTCTTTCTGCATCTTCCCCCAAGAAACAGCTTCCTGAGGGTGCTGGGG
CAGCCACTGGTGAGGAGGGGCTGCTCTGATGTCCCTCCTATGAGGGGACTCTGCACAGACACCATTGCCCACACT
ATCACCATATTTTCACTCAGTCACACACAAGACAAAAGCATGCAATGACAAAACCATACGCAATCCTGACCGCCC
AGCCAATCAAGACATATCACAGAACACACGCGTCCTTCCAAGAATGTTTATCCTCATGCATCACTTACACACCCC
CAGACACGTACTGCAATGCAAGTCACTAGTCATGGTCACATGACAGTGACAGTGTGGCCTCCTCCTACCCCAAAT

FIGURE 139B

ACACCCACACTCTGGCACCACACACATTGTCTCCAGCTTTCAGGCTTACTGGGGAGGGTGGAATCGAGCCAGAAC
AATCAGCCCATATTGGGTCCCCCTAAGTTGCCCCGTCATACTCAGTCCCATGCCATGGTGCCCACACCAACCATG
CAGCCGCCAACCCCAGCCAGTGTCAGACACAATCCCATGTGGATGCACAGTCTCACTCCACATGACCTGCTCTCA
ATGCTGGAGGGAAACAGGCAGGCCCTTGCCTTTCTCGGAAAAAGTGTGGGGCCACAGCCCTTTTAGGGCATTGCA
TGCAGGTGGGCCTGGCTTCACCCCTACCTGCTTCCTCCCCACCGCAGCTGGCAGAGGGGGAGGTTTGGGGCCAGA
CCCCCACTAGCTGGGAGCCTGGGGGCTCCTCTAAGGCTGAGGAAGGAAATTTGGCCCCAGGTTGTTGGGGGGTCT
TGGGTCTCCCAGGACGGAAGGCCCAGGGCAGGGAGGGGGCATGTGGTTGGGCTCCTTTATCTCCCTGTGTCCCCT
TCCTGCTTTGAGCTAGGGGGCTGACTCTGCCTCCCAGGACACAAGTCTCCAAAGTGCCTGTGAGGGCGGGCCCTC
CGCACCCTCTGCCCTCTGCCTGGCAGGCCAACCTCAGCCCACCTGCCCAGAGGCCCTCCCTGTGGACACCCCCTC
ACCTATTTGGCCAAACAATTCTGGCTGCAGCTTCAGGGGCCATGGCTGGAAGCAGCCCCTGCAGATCCCTCAGGC
CCCGAGGTCAGGGTTTGAGGGATGAGACCAGGTGATAGTGGGGGAGGGGTTACTTCCTTTGTTACCTAGCAAGTA
GGGCTATTTCCATCGGTATTTTAAATGTGGGGTCACAGATCTTTTGGGGAGGGTGTGCTTGGCAGGGGGCCTCTT
GGAGCCAAAGGGATGTGGTGTGAGTTGCGATTGGCTGGCACTCACACCCCCACCCCTCACCCACATCCCAGATTC
AAGTCAGGAAGGCAGGTTTTATTTCAGGGCCCTTTTCAAGATGCCCTGGCAGCAGATTTCTGCAGGATGAGGGGT
AGCGGTGTGTAGGCAGTGAGGGGGAGGTTCCAGGGGCTGTCCCACAGCCTGTCTTTTCCAGGCTGGGCTCCATCT
TCCAGTCCCAAAACCCTCCTTCACAGGGCCCAGAGGCTTGTGAGGAAGCCAGGTGGACCCAGCCTTAGAAGAGTG
GGCATGGGGGGCCCCTGATATCTGGAGGGGGGCGGGTTGGCCTCAGTCATCTTTGGAGCAGAAGGGCTGGGTCCTG
GGGCCACAGACCACAAGGCTCAGCCTCCCTACCCTGCTCCCTGGGGTGCTGCTGTCTTGGAGAGCACAGCTCTGG
TGAGACGGCCTGGGCAGGCCGAGGCTGAGAAACCAGGGAGGATAGAGGAGAAAAGGGCTTGGGCCCCCAGCCCCA
GAAGATGCTGGACCCCAGGTGGGAGACCCAACAGTGGGTGCAGTTTCTCAGTAGGGCTGGAGCCAATGGTGGGGG
TGGCCCCGGCAGGCCTGGCTCCTCACATCCCAGGGGTTGGCTTCTGATTTGGGGCTTGGGCTCCAGGCACTGGCT
TCTCTTCTCTGTGTCCTTAGCATTTGAGAGAAGAGGCCAGGGGCCTTGTTCATGGATCCCTGGACCCAAGGCAGA
TGTCCAGGCTTTATCCTCCTGAGGATGAGGAGTCTGACCAGCCCAAATCTGCCCTGGCCGGCCTGACCGGGGCAA
GGCAGTCCAAGAGAGTTCAGTGAGGACCAGCTAGGCTCTCCCAGGTGCAATGTGGGTGCAGGGCCCTCATGTCCC
CCTACCCCTGCCTGTGATGGAGTGTTCTGAGGGGCTTTGGCATTTGCTGGAAGCACAGGGAGTTCCAAATGAGAG
GGAGCTTCTGTGGCTTGAGAGCCTCTGGGGCCTTGGCTGCCAGAGCACGAGGCAGGCCAGGACCTGGAGAGCCCA
GACCCTGTCTCCAGGAGGCCAGGAGGCCAGATGGGGGCCTTGCCTGAAAGACTGGTCCCCTTGATCGCTGGAGGC
ATGTGGGTGGCAACCAGGGCTGGGCAGGGCTTAGGGTGTGTGGGCCAAACCCCCCTGGGGTTGGCAAAGCCGCCT
GTCAGGCCTCCTGGTGGGGGCCCCTGGACACAGGGAGCAGACCCTCTGCCTCATGGGGTAGGAGTGGCTGCCTCC
TGTGTTCTCTGGATTTCTTCTCCCAACAACTACAACCCTGGACTTGCCTCCCCAGGCCTCTTGCCTGTAAATAGA
AGCCCGCAAACTGTACAGATTTACAGAGGCATCGAGACTGGGCCCTGGGAGTTGCCATCTGAGAGCCGATGGCCC
CAGCATCCCCCAGGTGCCTGCCTGGCACCACAGTGACCCTGGCCTCAGCGTGGCAAATGCATGTAAATATTTTTC
GTAGGCAGCGTGGCTCCAGAGAGCCCCCTGAAGACAGTGTCCCTCCCTCCTGTGAGTCCTTTCTCCTGTACAGAA
CCTGCCTGGGGTGGGTGGGGGTCTGCCATTCCCTCCCCCAGGCCTTCCCTGCCCCTTCTCTCCCCTGTAACCTGT
TTATTAACCATACCTGTCCTGAGTTCATGGCCAAAACCTTAAATAAGAAAAACAAAAGAAAAAGACAGTGGAAAA
AAGAGACCAAGGCGCCTGCCCCACTGCGGGTACTCTCCTGTTCCAGCCTTGTGAAGGAACTGGTTTTGTTTTTGT
TTTTTTTTTTTTTTTTTTTTTTTGTTTGTTTGTTTTTTTAACACTTCCTGTGCTGTGCCCATTTATAAGAGGAA
ATAAAATTAAGCTGAAATG

FIGURE 140

AGCCATGCCTTTCTTGGACATCCAGAAAAGGTTCGGCCTTAACATAGATCGATGGTTGACAATCCAGAGTGGTGA
ACAGCCCTACAAGATGGCTGGTCGATGCCATGCTTTTGAAAAAGAATGGATAGAATGTGCACATGGAATCGGTTA
TACTCGGGCAGAGAAAGAGTGCAAGATAGAATATGATGATTTCGTAGAGTGTTTGCTTCGGCAGAAAACGATGAG
ACGTGCAGGTACCATCAGGAAGCAGCGGGATAAGCTGATAAAGGAAGGAAAGTACACCCCTCCACCTCACCACAT
TGGCAAGGGGGAGCCTCGGCCCTGAACAGAGCAGCTGCTGATGTCTGGAGGCTGATTTTCCTGTTCTCTGTTCTC
CACTGGAAAGGTTGTTTACGACAAACCTCCTTGTCAAAGTGTGTAAAAATAAAGGATTGCTCCATCCT

FIGURE 141

GCTGAGCGGGCTTTGGACACCATGAACTTTGATGTGATTAAGGGAAAGCCAATCCGCATCATGTGGTCTCAGAGG
GATCCCTCTTTGAGAAAATCTGGTGTGGGAAACGTCTTCATCAAGAACCTGGACAAATCTATAGATAACAAGGCA
CTTTATGATACTTTTTCTGCTTTTGGAAACATACTGTCCTGCAAGGTGGTGTGTGATGAGAACGGCTCTAAGGGT
TATGCCTTTGTCCACTTCGAGACCCAAGAGGCTGCCGACAAGGCCATCGAGAAGATGAATGGCATGCTCCTCAAT
GACCGCAAAGTATTTGTGGGCAGATTCAAGTCTCGCAAAGAGCGGGAAGCTGAGCTTGGAGCCAAAGCCAAGGAA
TTCACCAATGTTTATATCAAAAACTTTGGGGAAGAGGTGGATGATGAGAGTCTGAAAGAGCTATTCAGTCAGTTT
GGTAAGACCCTAAGTGTCAAGGTGATGAGAGATCCCAATGGGAAATCCAAAGGCTTTGGCTTTGTGAGTTACGAA
AAACACGAGGATGCCAATAAGGCTGTGGAAGAGATGAATGGAAAAGAAATAAGTGGTAAAATCATATTTGTAGGC
CGTGCACAAAAGAAAGTAGAACGGCAGGCAGAGTTAAAACGGAAATTTGAACAGTTGAAACAGGAGAGAATTAGT
CGATATCAGGGGGTGAATCTCTACATTAAGAACTTGGATGACACTATTGATGATGAGAAATTAAGGAAAGAATTT
TCTCCTTTTGGATCAATTACCAGTGCTAAGGTAATGCTGGAGGATGGAAGAAGCAAAGGGTTTGGCTTCGTCTGC
TTCTCATCTCCTGAAGAAGCAACCAAAGCAGTCACTGAGATGAATGGACGCATTGTGGGCTCCAAGCCACTATAT
GTTGCCCTGGCCCAGAGGAAGGAAGAGAGAAAGGCTCACCTGACCAACCAGTATATGCAACGAGTGGCTGGAATG
AGAGCACTTCCTGCCAATGCCATCTTAAATCAGTTCCAGCCTGCAGCGGGTGGCTACTTTGTGCCAGCAGTCCCA
CAGGCTCAGGGAAGGCCTCCATATTATACACCTAACCAGTTAGCACAGATGAGGCCTAATCCACGCTGGCAGCAA
GGTGGGAGACCTCAAGGCTTCCAAGGAATGCCAAGTGCTATACGCCAGTCTGGGCCTCGTCCAACTCTTCGCCAT
CTGGCTCCAACTGGTAATGCTCCGGCCTCTCGTGGCCTCCCTACTACCACTCAGAGAGTCGGGTCTGAGTGCCCG
GACCGCTTGGCTATGGACTTTGGTGGGGCTGGTGCCGCCCAGCAAGGGCTGACTGACAGCTGCCAGTCTGGAGGC
GTTCCCACAGCTGTGCAGAACTTAGCGCCACGCGCTGCTGTTGCTGCTGCTGCTCCCCGGGCTGTTGCCCCCTAC
AAATACGCCTCCAGTGTCCGCAGCCCTCATCCTGCCATACAGCCTCTGCAGGCACCCCAGCCTGCGGTCCATGTG
CAGGGGCAGGAGCCACTGACTGCCTCCATGCTGGCTGCAGCACCCCCCCAGGAACAGAAGCAGATGCTGGGAGAA
CGCTTGTTCCCACTCATCCAAACAATGCATTCAAATCTGGCTGGGAAGATCACGGGAATGCTGCTGGAGATAGAC
AACTCTGAGCTGCTGCACATGTTAGAGTCCCCCGAGTCTCTCCGCTCCAAGGTGGATGAAGCTGTAGCAGTTCTA
CAGGCTCATCATGCCAAGAAAGAAGCTGCCCAGAAGGATTCAAAAGCCAAATAACCCCTTATGGAATTCAACTCA
AGGTTTGAAGACTTCCTAGCTTGTCCTATGGACCTCAACACCAAGGATTACAAATTGCAAATTTAATAGGTCATT
TTGTATCAAAAGGTCAATTATGAAGCACCTAGAATTTTTCAATTATACGAATATGTTCTTTGGGTTCTGCTGTGG
CCCAGACAGTGTTAACTTTTTTTTTATTGTGGGTTTTGATTTTTTCCCCCAGAAATTGGTTTTATTTGATGTACC
CAAGTCTTACGTTTCCCAATAAAGAAAAAAAATCTCCAT

FIGURE 142

ACCAGGCAGCCTGCGTTCGCC**ATG**AAGCGACCCAAGGAGCCGAGCGGCTCCGACGGGGAGTCCGACGGACCCATC
GACGTGGGCCAAGAGGGCCAGCTGAGCCAGATGGCCAGGCCGCTGTCCACCCCCAGCTCTTCGCAGATGCAAGCC
AGGAAGAAACGCAGAGGGATCATAGAGAAACGGCGTCGAGACCGCATCAACAGTAGCCTTTCTGAATTGCGACGC
TTGGTCCCCACTGCCTTTGAGAAACAGGGCTCTTCCAAGCTGGAGAAAGCCGAGGTCTTGCAGATGACGGTGGAT
CACTTGAAAATGCTCCATGCCACTGGTGGGACAGGATTCTTTGATGCCCGAGCCCTGGCAGTTGACTTCCGGAGC
ATTGGTTTTCGGGAGTGCCTCACTGAGGTCATCAGGTACCTGGGGGTCCTTGAAGGGCCCAGCAGCCGTGCAGAC
CCCGTCCGGATTCGCCTTCTCTCCCACCTCAACAGCTACGCAGCCGAGATGGAGCCTTCGCCCACGCCCACTGGC
CCTTTGGCCTTCCCTGCCTGGCCCTGGTCTTTCTTCCATAGCTGTCCAGGGCTGCCAGCCCTGAGCAACCAGCTC
GCCATCCTGGGAAGAGTGCCCAGCCCTGTCCTCCCCGGTGTCTCCTCTCCTGCTTACCCCATCCCAGCCCTCCGA
ACCGCTCCCCTTCGCAGAGCCACAGGCATCATCCTGCCAGCCCGGAGGAATGTGCTGCCCAGTCGAGGGGCATCT
TCCACCCGGAGGGCCCGCCCCCTAGAGAGGCCAGCGACCCCTGTGCCTGTCGCCCCCAGCAGCAGGGCTGCCAGG
AGCAGCCACATCGCTCCCCTCCTGCAGTCTTCCTCCCCAACACCCCCTGGTCCTACAGGGTCGGCTGCTTACGTG
GCTGTTCCCACCCCCAACTCATCCTCCCCAGGGCCAGCTGGGAGGCCAGCGGGAGCCATGCTCTACCACTCCTGG
GTCTCTGAAATCACTGAAATCGGGGCTTTC**TGA**GCTGCCCCTTCACCACCCCGCCCCAAGGAATAAGGAAGGTTC
TTTTACCAGGAGCCCAAAAAAGGGCACTGCCTTTTCTGCTTTGCTTCGTGGACTGGCTCATATGTGAAGGCACGT
TCTCCAGCCATCAGAGGCCCCCTCCTCCTCCAACCCATCTCTCCTTCTCACTGTTATCCCAGCTTATCCACCCAG
CTCTCCTGGAGCTGTTCTGGTCTCAGAGGCTTGGTTCCATTTCTCACCTGAACAGATGAGTCCTGGGAGAGACCC
TCAGAGATCCGCCCAGACCCCTCTCCTGCCCTCTGCACACCAGCAGCAGGCATGAACCTTGGGTCTGGGAAAAAG
CTTTAACCTGCAGGGCACCAGGACCCAAGGCAGGCTGTTCCTTGGGGCGGTCAGACCCCAGTCAGGAGCAATGAC
TGACTGGCTGCAGCCTTCCCACGCCAAGAGGCTGGAACATAGTGTCTGCCTCGCTTCCTGGAGATAGTAACTGAG
CAGGGGCTACAAAGAGGTCTCCTGGGAACCCTGTCTGCCCCTTCCCACCTGTCCTTGGGCCACACCATCACACTG
AACCACAGGACAGACCCTTTCTCCACCACAGCCAAGGCCTGGAGACTGGGGGCCCAGCAGAGCCTGCTCCCACCC
TCCTCCCAGCAGCAGACACCCACCCTCTCACTGACTAACAGGTCCCTGCACACAGCTGGCCTGGTAAACCCAGCT
GGGAGGTTTCTAGGCAGCAGCAAAACTCTGTGACAGGGTGTCCTCACACCAGGCCTTGGACAGCTCTCCCAGACA
GGAGCCAGGGTTGAGCAATGGAGAGCCCAGCCCCCACGTCTTACAGTCGCCATCCTCCAGGCGTGTGGTCCCTCC
CCATTGGGTGCACAGTGCAGAGGGGCCGTGGCCCCATGTGATGGTGCGCAGAGAGGAACCTCTTGGGATTCAGCA
CCAGACGTCTGTGCTGCCTGGTTTGCATCCGGCTCACAGAGCCCAGACTGCTGGAACAGCCAAGGACTGTCAGGC
TGGACAAAAATAACTGCAAGGAGGGGCAAGAGAAAGGATGATTCGAGGCACCTTGGCCCTTCAAGGTCATGCAGT
GGGTCGAGCGCCTGAGATCCTGTTCACCAGGACTCCACAGAGCTGGCTCTGCTCAGAAGCCATTTCATTCCCCGG
CTCCACCCTAGGCCACTTTTTCTAACAGAGGAAACAAATGGTCCAGCAGTCGTTCCCAGCAGAACAGCGGAGCCT
GGACTGACACCCAGTGGGACCAGTGTTGCCACACCAGTTGATAAAATGCAGAAACCCTTCTGTACTCGTTGGTAA
ATATCTACTCCCCCAAGTGACTCCAGGTGCCCCCCACCGCCTGGCACTTCCCCCAGGACTCCTACGATCTGGTTA
CTGCCTGGCCGATCCAAGGCTGTGGAGTCCCAGAGCCAGCAGTTCACTGGTGCTCATTCCACACTGGTTAGATAC
TTCAGTTGTCACCCCTGGGAAGATTCTCCCACCTCCTCCCTTTGATGGAACCACCCTCCCCAGAGGCTGCATTGA
GGAGACTCCACAGACTGAAAAGTGAGTTTGCAGAAACCTTGGGGAAAAGGGCCCTTTCAAAGAAGTGGATAAGAG
GGAGGAGATCATTGAGTGACCCAGAAAGCTCTTTTGAAAAGACAGACTCCTCAAGGAGAGATAAAGAGGAAAGCA
CCTCTTTCATTTTTTAGTGTGAGCTAATTCCATCAGACTGCTGTCCTCCTGGACCCATCTGAGATGTGCAGTAGC
AAGGAGAGGGGGGATCATTTTAGAGAGTGGGTCATTGGCAGGGAGTGCTCCGGAGGGAGGCAGAGGGGAGACTGT
GGTAGAAGGAAGACAGAACTCACACATGCTCCCAGGATTGGGGACAGGGACAGAGGAGGTAACAGAAGGCAAAGG
CCAGTTTCCCCGTTATCATGAAGGGGCCCACTCAGGACAGGAACAAGGACAACTCCTCCTCCTCCTCCTCCTCTC
CTGCTGCTCCTGGGATACCAGGTCAGTGATGTAGTCTTGCAGTTTGGCAACTTCCTAGCCTGAGAATCCCTAGTG
GGGCTGTGGGAAACACATTTCCACGTTGCAAGCATGCAACTCCAAAGAATCTGTGATGCCACTGAAATGAGATGG
GAATGATCCAGCTCTTTCAGCATCTTGGTTGAACTTGCTTTCATTGTCCCTGGGATATTGTGGAAGGAAAGGTGA
CTGTGTGATCTGATTCTGTGGTCAAGGACTTGCATCTTGTGTTTCTATCCCCAAGCCTTCCTGGTGTCTCCAACT
CCTACCCCATTGCATGGGTTGTTGCGGACATCCAATAAAGATTTTTTTAGTGCTTCTGGAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACC

FIGURE 143

MKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQMQARKKRRGIIEKRRRDRINSSLSELRRLVPTAFE
KQGSSKLEKAEVLQMTVDHLKMLHATGGTGFFDARALAVDFRSIGFRECLTEVIRYLGVLEGPSSRADPVRIRLL
SHLNSYAAEMEPSPTPTGPLAFPAWPWSFFHSCPGLPALSNQLAILGRVPSPVLPGVSSPAYPIPALRTAPLRRA
TGIILPARRNVLPSRGASSTRRARPLERPATPVPVAPSSRAARSSHIAPLLQSSSPTPPGPTGSAAYVAVPTPNS
SSPGPAGRPAGAMLYHSWVSEITEIGAF

FIGURE 144

GATCCTAAATTGCAGCAAGGCTACAATGCTATGGGATTCTCCCAGGGAGGCCAATTTCTGAGGGCAGTGGCTCAG
AGATGCCCTTCACCTCCCATGATCAATCTGATCTCGGTTGGGGGACAACATCAAGGTGTTTTTGGACTCCCTCGA
TGCCCAGGAGAGAGCTCTCACATCTGTGACTTCATCCGAAAAACACTGAATGCTGGGGCGTACTCCAAAGTTGTT
CAGGAACGCCTCGTGCAAGCCGAATACTGGCATGACCCCATAAAGGAGGATGTGTATCGCAACCACAGCATCTTC
TTGGCAGATATAAATCAGGAGCGGGGTATCAATGAGTCCTACAAGAAAAACCTGATGGCCCTGAAGAAGTTTGTG
ATGGTGAAATTCCTCAATGATTCCATTGTGGACCCTGTAGATTCGGAGTGGTTTGGATTTTACAGAAGTGGCCAA
GCCAAGGAAACCATTCCCTTACAGGAGACCTCCCTGTACACACAGGACCGCCTGGGGCTAAAGGAAATGGACAAT
GCAGGACAGCTAGTGTTTCTGGCTACAGAAGGGGACCATCTTCAGTTGTCTGAAGAATGGTTTTATGCCCACATC
ATACCATTCCTTGGATGAAACCCGTATAGTTCACAATAGAGCTCAGGGAGCCCCTAACTCTTCCAAACCACATGG
GAGACAGTTTCCTTCATGCCCAAGCCTGAGCTCAGATCCAGCTTGCAACTAATCCTTCTATCATCTAACATGCCC
TACTTGGAAAGATCTAAGATCTGAATCTTATCCTTTGCCATCTTCTGTTACCATATGGTGTTGAATGCAAGTTTA
ATTACCATGGAGATTGTTTTACAAACTTTTGATGTGGTCAAGTTCAGTTTTAGAAAAGGGAGTCTGTTCCAGATC
AGTGCCAGAACTGTGCCCAGGCCCAAAGGAGACAACTAACTAAAGTAGTGAGATAGATTCTAAGGGCAAACATTT
TTCCAAGTCTTGCCATATTTCAAGCAAAGAGGTGCCCAGGCCTGAGGTACTCACATAAATGCTTTGTTTTGCTGG
TGATTTAACCAGTGCTTGGAAAAATCTTGCTTGGCTATTTCTGCATCATTTCTTAAGGCTGCCTTCCTCTCTCAG
TACGTTGCCCTCTGTGCTATCATCTTATCATCAATTATTAGACAAATCCCACTGGCCTACAGTCTTGCTTCTGCA
GCACCCACTTTGTCTCCTCAGGTAGTGATGAATTAGTTGCTGTCACAAAAGGAGGGAAGTAGCACCCAAATTAAG
TTGCTTAAGAGAGGAAATGTACATCTTGTATAACTTAGGGAGCGAAGAAAATGTAGGCGCGAAAGTGAAAAGTGA
GGCAGCTAGTTCTTCCTATTCCATTCTCGACCAACCTGCCCTTTCTTAATATGACTAGTGGTCTTGATGCTAGAG
TCAACTTACTCTGTTGCTGGCTTTAGCAGAGAATAGGAGGAACCATATGAAAAAGATCAGGCTTTCTGACTTCCA
TCCCCAAAACACATTTACCAGCATACTCCAAACTGTTTCTGATGTGTTCCATGAGAAAAGGATTGTTTGCTCAAA
AAGCTTGGAAAATACTACACACTCCCTTTCTCCTTCTGGAGATCAACCCACATTAGAGTGTCTAAGGACTCCTGA
GAATTCCTGTTACAGTAAACAAAACTAACGTAATCTACCATTTCCTACACTATTTGAGCATGGAAATCATAGTCC
CCACTCTGTGAAAACTTAACGCTTTTTGGAAGACATTTCTGTAGCATGTCAGTTTGGAGAAATGATGAGCTACGC
CTTGATGAAAGAACCGTGTTGGTGCTGCTAAGTTTAGCCATTATGGTTTTTCCTTTCTCTCTCTTAAGCCTTATT
CTTCAACTAAAAGATGAGGATTAAGAGCAAGAAGTTGGGGGGGATGTGAAAATAATTTTATGAGGTTGTCTAAAA
T

FIGURE 145

GGGTCGCGCGGAGATTGCTGGGCGGTTCTTGCCGGAAGCGGAGAGCGGCTGATCGCAGTCCGGAGGTGAGGCGGA
ACTCTGAGGCAGATATCCTCCCTTTCCTCCTCGGCTGCTGCTCTTACTTTGACAAGCCAGGCTAACATTGAAGGT
GGTCCATTATGGCTGACATGCAAAATCTGGTAGAAAGATTGGAGAGGGCAGTGGGCCGCCTGGAGGCAGTATCTC
ATACCTCTGACATGCACCGTGGGTATGCAGACAGTCCTTCAAAAGCAGGAGCAGCTCCATATGTGCAGGCATTTG
ACTCGCTGCTTGCTGGTCCTGTGGCAGAGTACTTGAAGATCAGTAAAGAGATTGGGGGAGACGTGCAGAAACATG
CGGAGATGGTCCACACAGGTTTGAAGTTGGAGCGAGCTCTGTTGGTTACAGCTTCTCAGTGTCAACAGCCAGCAG
AAAATAAGCTTTCCGATTTGTTGGCACCCATCTCAGAGCAGATCAAAGAAGTGATAACCTTTCGGGAGAAGAACC
GAGGCAGCAAGTTGTTTAATCACCTGTCAGCTGTCAGCGAAAGTATCCAGGCCCTGGGCTGGGTGGCTATGGCTC
CCAAGCCTGGCCCTTATGTGAAAGAAATGAATGATGCCGCCATGTTTTATACAAACCGAGTCCTCAAAGAGTACA
AAGATGTGGATAAGAAGCATGTAGACTGGGTCAAAGCTTATTTAAGTATATGGACAGAGCTGCAGGCTTACATTA
AGGAGTTCCATACCACCGGACTGGCCTGGAGCAAAACGGGGCCTGTGGCAAAAGAACTGAGCGGACTGCCATCTG
GACCCTCTGCCGGATCAGGTCCTCCTCCCCCTCCACCATGCCCCCCTCCTCCCCCAGTCTCTACCAGTTCATGCT
CATATGAGTCTGCTTCCCGCTCAGCACTGTTCGCGCAGATTAATCAGGGGGAGAGCATTACACATGCCCTGAAAC
ATGTATCTGATGACATGAAGACTCACAAGAACCCTGCCCTGAAGGCTCAGAGTGGTCCAGTACGCAGTGGCCCCA
AACCATTCTCTGCACCTAAACCCCAAACCAGCCCATCCCCCAAACGAGCCACAAAGAAGGAGCCAGCTGTACTTG
AACTGGAGGGCAAGAAGTGGAGAGTGGAAAATCAGGAAAATGTTTCCAACCTGGTGATTGAGGACACAGAGCTGA
AACAGGTGGCTTACATATACAAGTGTGTCAACACGACATTGCAAATCAAGGGCAAAATTAACTCCATTACAGTAG
ATAACTGTAAGAAACTTGGCCTGGTATTCGATGACGTGGTGGGCATTGTGGAGATAATCAACAGTAAGGATGTCA
AAGTTCAGGTAATGGGTAAAGTGCCAACCATATCCATCAACAAAACAGATGGCTGCCATGCTTACCTGAGCAAGA
ATTCCCTGGATTGTGAAATAGTCAGTGCCAAATCTTCCGAGATGAATGTCCTCATTCCTACAGAAGGCGGTGACT
TTAATGAATTCCCAGTTCCTGAGCAGTTCAAGACCCTATGGAACGGGCAGAAGTTGGTCACCACAGTGACAGAAA
TTGCTGGATAAGCGAAGTGCCACTGGGTTCTTTGCCCTCCCTTCACACCATGGGATAAATCTGTATCAAGACGGT
TCTTTTCTAGATTTCCTCTACCTTTTTGCTCTTAAAACTGCTTCTCTGCTCTGAGAAGCACAGCTACCTGCCTTC
ACTGAAATATACCTCAGGCTGAAATTTGGGGTGGGATAGCAGGTCAGTTGATCTTCTGCAGGAAGGTGCAGCTTT
TCCATATCAGCTCAACCACGCCGCCAGTCCATTCTTAAGGAACTGCCGACTAGGACTGATGATGCATTTTAGCTT
TGAGCTTTTGGGGGTTATTCTACCAACAAACAGTCCATTGGAAAGAAAACAGTCCCTGGAATTAACAGATCAGAA
TGTTCACACTGGTTAATCTTTTTTTAACAATGAGCATGAAGGTAGCAGAAGCTGGTGTGTTTCCAGATGGTTCTT
CTAACCAAACTAATTTTTCACTGTTGACAAGCGAGGCAAGGGTTGCACTGGACCAAAGGCTGAGGCTTGGCCATC
TAGCATTCCATACAAAATTGTTTCCTATAAGCATTCCTTTTATTCTCTATTCTATCCTGGGTCTGCCTCAACCGT
GAGATAGGAGAGTCTCTGGTACTAGCTGCTGTAGCAGTGCCCTTCATCCAGGGCAGTTAATGGAGTCTTGGACCC
TTTCTTTCTCTGGGATCCCTGCCCAGCACCTTCCTATAGAGATGACTTTAAAAGGAAAAAAAAAAAAAAAAAAAC
CCACATGATTTCAAGGAGTCTGGCATTCCTGAATCCTTCTTCCCTGCCAGGTGCCTGTCACCTGTCTTCACTGCC
TCCTTTTCCCTGTCATGCTCATCAGCTTATGGCTTCTGTCTAAGCACCTGAACAGAGGACTGAAACCTCCACTGC
AGGCTGGTTTTAGGTCTTGAATTATGTAAGAATCTTGCACAGCACTGCTAATGTAAATTTCAGTTGTTTTTCCCT
CTAGGACAAACACTTACCAAAATATGCAACTTTTTTTTGGTGGGAAGAGAGATTGTCCTGTGATTTCTACCCATT
TCCTGAGGCCTGTGGAAATAAACCTTTATGTACTTAAAGTTATACAGAAAATAGAATAAAGTTAATACCAAACTT
G

FIGURE 146

GGCTTCGGTCGCTACCGCTCCCGCTCTGCCACCCCCGCCAACCGCCGCTCGGGCCTCCGTCGCTGCCGCGTCGCT
TTCTCGCTCCTTGGATCGCACATCCTCCCAG**ATG**CAGCGCCGGGACGACCCCGCCGCGCGCATGAGCCGGTCTTC
GGGCCGTAGCGGCTCCATGGACCCCTCCGGTGCCCACCCCTCGGTGCGTCAGACGCCGTCTCGGCAGCCGCCGCT
GCCTCACCGGTCCCGGGGAGGCGGAGGGGGATCCCGCGGGGGCGCCCGGGCCTCGCCCGCCACGCAGCCGCCACC
GCTGCTGCCGCCCTCGGCCACGGGTCCCGACGCGACAGTGGGCGGGCCAGCGCCGACCCCGCTGCTGCCCCCCTC
GGCCACAGCCTCGGTCAAGATGGAGCCAGAGAACAAGTACCTGCCCGAACTCATGGCCGAGAAGGACTCGCTCGA
CCCGTCCTTCACTCACGCCATGCAGCTGCTGACGGCAGAAATTGAGAAGATTCAGAAAGGAGACTCAAAAAAGGA
TGATGAGGAGAATTACTTGGATTTATTTTCTCATAAGAACATGAAACTGAAAGAGCGAGTGCTGATACCTGTCAA
GCAGTATCCCAAGTTCAATTTTGTGGGGAAGATTCTTGGACCACAAGGGAATACAATCAAAAGACTGCAGGAAGA
GACTGGTGCAAAGATCTCTGTATTGGGAAAGGGCTCAATGAGAGACAAAGCCAAGGAGGAAGAGCTGCGCAAAGG
TGGAGACCCCAAATATGCCCACTTGAATATGGATCTGCATGTCTTCATTGAAGTCTTTGGACCCCCATGTGAGGC
TTATGCTCTTATGGCCCATGCCATGGAGGAAGTCAAGAAATTTCTAGTACCGGATATGATGGATGATATCTGTCA
GGAGCAATTTCTAGAGCTGTCCTACTTGAATGGAGTACCTGAACCCTCTCGTGGACGTGGGGTGCCAGTGAGAGG
CCGGGGAGCTGCACCTCCTCCACCACCTGTTCCCAGGGGCCGTGGTGTTGGACCACCTCGGGGGGCTTTGGTACG
TGGTACACCAGTAAGGGGAGCCATCACCAGAGGTGCCACTGTGACTCGAGGCGTGCCACCCCCACCTACTGTGAG
GGGTGCTCCAGCACCAAGAGCACGGACAGCGGGCATCCAGAGGATACCTTTGCCTCCACCTCCTGCACCAGAAAC
ATATGAAGAATATGGATATGATGATACATACGCAGAACAAAGTTACGAAGGCTACGAAGGCTATTACAGCCAGAG
TCAAGGGGACTCAGAATATTATGACTATGGACATGGGGAGGTTCAAGATTCTTATGAAGCTTATGGCCAGGACGA
CTGGAATGGGACCAGGCCGTCGCTGAAGGCCCCTCCTGCTAGGCCAGTGAAGGGAGCATACAGAGAGCACCCATA
TGGACGTTAT**TAA**AAACAAACATGAGGGGAAAATATCAGTTATGAGCAAAGTTGTTACTGATTTCTTGTATCTCC
CAGGATTCCTGTTGCTTTACCCACAACAGACAAGTAATTGTCTAAGTGTTTTTCTTCGTGGTCCCCTTCTTCTCC
CCACCTTATTCCATTCTTAACTCTGCATTCTGGCTTCTGTATGTAGTATTTTAAAATGAGTTAAAATAGATTTAG
GAATATTGAATTAATTTTTAAGTGTGTAGATGCTTTTTTCTTTGTTGTTTAAATATAAACAGAAGTGTACCTTT
TATAATAAAAAAAAGAAGTTGAGTAAAAAAAAAAAACACACAAACCTGTTAGTTTCAAAAATGACATTGCTTGCT
TAAAGGTTCTGAAGTAAAGGCTTGTTAAGTTTCTCTTAGTTTTGATTTGAGGCATCCCGTAAAGTTGTAGTTGCA
GAATCCCAAACTAGGCTACATTTCAAAATTCAGGGCTGTTTAAGATTTAAAATCACAAACATTAACGGCAGTAGG
CACCACCATGTAAAAGTGAGCTCAGACGTCTCTAAAAAATGTTTCCTTTATAAAAGCACATGGCGGTTGAATCTT
AAGGTTAAATTTTAATATGAAAGATCCTCATGAATTAAATAGTTGATGCAATTTTTAACGTTAATTGATATAAAA
AAAAAAACAACAAAATTAGGCTTGTAAAACTGACTTTTTCATTACGTGGGTTTTGAAATCTAGCCCCAGACATAC
TGTGTTGAGAGATACTTAGAGGGAGGGAGTAGGTTTTGAAGAGGTTGATGGTGGTGGGGAGGGAAGGCCTCCTGA
ATTGAGTTTGATGCAGAGCTTTTTAGCCATGAAGAATCTTTCAGTCATAGTACTAATAATTAAATTTTCAGTATT
TAAAAAGACAAAGTATTTTGTCCATTTGAGATTCTGCACTCCATGAAAAGTTCACTTGGACGCTGGGGCCAAAAG
CTGTTGATTTTCTTAAGTTGACGGTTGTCAATATATCGAACTGTTCCCAAGTTAGTCAAGTATGTCTCAACACTA
GCATGATATAAAAAGGGACACTGCAGCTGAATGAAAAAGGAATCAAAATCCACTTTGTACATAAGTTAAAGTCCT
AATTGGATTTGTACCGTCCTCCCATTTTGTTCTCGGAAGATTAAATGCTACATGTGTAAGTCTGCCTAAATAGGT
AGCTTAAACTTATGTCAAAATGTCTGCAGCAGTTTGTCAATAAAGTTTAGTCCTTTTTTA

FIGURE 147

MQRRDDPAARMSRSSGRSGSMDPSGAHPSVRQTPSRQPPLPHRSRGGGGGSRGGARASPATQPPPLLPPSATGPD
ATVGGPAPTPLLPPSATASVKMEPENKYLPELMAEKDSLDPSFTHAMQLLTAEIEKIQKGDSKKDDEENYLDLFS
HKNMKLKERVLIPVKQYPKFNFVGKILGPQGNTIKRLQEETGAKISVLGKGSMRDKAKEEELRKGGDPKYAHLNM
DLHVFIEVFGPPCEAYALMAHAMEEVKKFLVPDMMDDICQEQFLELSYLNGVPEPSRGRGVPVRGRGAAPPPPPV
PRGRGVGPPRGALVRGTPVRGAITRGATVTRGVPPPPTVRGAPAPRARTAGIQRIPLPPPPAPETYEEYGYDDTY
AEQSYEGYEGYYSQSQGDSEYYDYGHGEVQDSYEAYGQDDWNGTRPSLKAPPARPVKGAYREHPYGRY

FIGURE 148

CTCGCGTCACAGCCGGG**ATG**AAGCCGATCCTACTGCAGGGCCATGAGCGGTCCATTACGCAGATTAAGTATAACC
GCGAAGGAGACCTCCTCTTTACTGTGGCCAAGGACCCTATCGTCAATGTATGGTACTCTGTGAATGGTGAGAGGC
TGGGCACCTACATGGGCCATACCGGAGCTGTGTGGTGTGTGGACGCTGACTGGGACACCAAGCATGTCCTCACTG
GCTCAGCTGACAACAGCTGTCGTCTCTGGGACTGTGAAACAGGAAAGCAGCTGGCCCTTCTCAAGACCAATTCGG
CTGTCCGGACCTGCGGTTTTGACTTTGGGGGCAACATCATCATGTTCTCCACGGACAAGCAGATGGGCTACCAGT
GCTTTGTGAGCTTTTTTGACCTGCGGGATCCGAGCCAGATTGACAACAATGAGCCCTACATGAAGATCCCTTGCA
ATGACTCTAAAATCACCAGTGCTGTTTGGGGACCCCTGGGGGAGTGCATCATCGCTGGCCATGAGAGTGGAGAGC
TCAACCAGTATAGTGCCAAGTCTGGAGAGGTGTTGGTGAATGTTAAGGAGCACTCCCGGCAGATCAACGACATCC
AGTTATCCAGGGACATGACCATGTTTGTGACCGCGTCCAAGGACAACACAGCCAAGCTTTTTGACTCCACAACTC
TTGAACATCAGAAGACTTTCCGGACAGAACGTCCTGTCAACTCAGCTGCCCTCTCCCCCAACTATGACCATGTGG
TCCTGGGCGGTGGTCAGGAAGCCATGGATGTAACCACAACCTCCACCAGGATTGGCAAGTTTGAGGCCAGGTTCT
TCCATTTGGCCTTTGAAGAAGAGTTTGGAAGAGTCAAGGGTCACTTTGGACCTATCAACAGTGTTGCCTTCCATC
CTGATGGCAAGAGCTACAGCAGCGGCGGCGAAGATGGTTACGTCCGTATCCATTACTTCGACCCACAGTACTTTG
AATTTGAGTTTGAGGCT**TAA**GAAGCTGGATCTCCTGCCGGGCGTGGTTGGCTCATGCCTGTAATCCCACCACTTT
TTTTTTAAGGCAGGCGGATCACCTGAGGTCAGGAGTTTAAGACCAGCCTGACCAACATGGAGAAACCTCGTCTCT
ACTAAAAATACAAAAATTAGCCAGGCATGGTGGCACACGCCTATAGTCCCAGCTACTCAGGAGGCTGAGGCAGGA
GAATCACTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCACGTCATTGCACTCCATCCTGAGCCACAAG
AGCAAAACTCCGTCTCAAAAAAAAAAAAGAAGAAGGTGGATCTCCAACCAGGCCAGAGAAGATTCTCACAGAAGG
TTTTGAACTCTAAGAAATAAATTGGTTTGGTAATAAATGGCTTCTGGTCAGA

FIGURE 149

MKPILLQGHERSITQIKYNREGDLLFTVAKDPIVNVWYSVNGERLGTYMGHTGAVWCVDADWDTKHVLTGSADNS
CRLWDCETGKQLALLKTNSAVRTCGFDFGGNIIMFSTDKQMGYQCFVSFFDLRDPSQIDNNEPYMKIPCNDSKIT
SAVWGPLGECIIAGHESGELNQYSAKSGEVLVNVKEHSRQINDIQLSRDMTMFVTASKDNTAKLFDSTTLEHQKT
FRTERPVNSAALSPNYDHVVLGGGQEAMDVTTTSTRIGKFEARFFHLAFEEEFGRVKGHFGPINSVAFHPDGKSY
SSGGEDGYVRIHYFDPQYFEFEFEA

FIGURE 150

GAGCGGAGCCGCGGGCGGGAGGGCGGACGGACCGACTGACGGTAGGGACGGGAGGCGAGCAAG**ATG**GCGCAGACG
CAGGGCACCCGGAGGAAAGTCTGTTACTACTACGACGGGGATGTTGGAAATTACTATTATGGACAAGGCCACCCA
ATGAAGCCTCACCGAATCCGCATGACTCATAATTTGCTGCTCAACTATGGTCTCTACCGAAAAATGGAAATCTAT
CGCCCTCACAAAGCCAATGCTGAGGAGATGACCAAGTACCACAGCGATGACTACATTAAATTCTTGCGCTCCATC
CGTCCAGATAACATGTCGGAGTACAGCAAGCAGATGCAGAGATTCAACGTTGGTGAGGACTGTCCAGTATTCGAT
GGCCTGTTTGAGTTCTGTCAGTTGTCTACTGGTGGTTCTGTGGCAAGTGCTGTGAAACTTAATAAGCAGCAGACG
GACATCGCTGTGAATTGGGCTGGGGGCCTGCACCATGCAAAGAAGTCCGAGGCATCTGGCTTCTGTTACGTCAAT
GATATCGTCTTGGCCATCCTGGAACTGCTAAAGTATCACCAGAGGGTGCTGTACATTGACATTGATATTCACCAT
GGTGACGGCGTGGAAGAGGCCTTCTACACCACGGACCGGGTCATGACTGTGTCCTTTCATAAGTATGGAGAGTAC
TTCCCAGGAACTGGGGACCTACGGGATATCGGGGCTGGCAAAGGCAAGTATTATGCTGTTAACTACCCGCTCCGA
GACGGGATTGATGACGAGTCCTATGAGGCCATTTTCAAGCCGGTCATGTCCAAAGTAATGGAGATGTTCCAGCCT
AGTGCGGTGGTCTTACAGTGTGGCTCAGACTCCCTATCTGGGGATCGGTTAGGTTGCTTCAATCTAACTATCAAA
GGACACGCCAAGTGTGTGGAATTTGTCAAGAGCTTTAACCTGCCTATGCTGATGCTGGGAGGCGGTGGTTACACC
ATTCGTAACGTTGCCCGGTGCTGGACATATGAGACAGCTGTGGCCCTGGATACGGAGATCCCTAATGAGCTTCCA
TACAATGACTACTTTGAATACTTTGGACCAGATTTCAAGCTCCACATCAGTCCTTCCAATATGACTAACCAGAAC
ACGAATGAGTACCTGGAGAAGATCAAACAGCGACTGTTTGAGAACCTTAGAATGCTGCCGCACGCACCTGGGGTC
CAAATGCAGGCGATTCCTGAGGACGCCATCCCTGAGGAGAGTGGCGATGAGGACGAAGACGACCCTGACAAGCGC
ATCTCGATCTGCTCCTCTGACAAACGAATTGCCTGTGAGGAAGAGTTCTCCGATTCTGAAGAGGAGGGAGAGGGG
GGCCGCAAGAACTCTTCCAACTTCAAAAAAGCCAAGAGAGTCAAAACAGAGGATGAAAAAGAGAAAGACCCAGAG
GAGAAGAAAGAAGTCACCGAAGAGGAGAAAACCAAGGAGGAGAAGCCAGAAGCCAAAGGGGTCAAGGAGGAGGTC
AAGTTGGCC**TGA**ATGGACCTCTCCAGCTCTGGCTTCCTGCTGAGTCCCTCACGTTTCTTCCCCAACCCCTCAGAT
TTTATATTTCTATTTCTCTGTGTATTTATATAAAAATTTATTAAATATAAATATCCCCAGGGACAGAAACCAAG
GCCCCGAGCTCAGGGCAGCTGTGCTGGGTGAGCTCTTCCAGGAGCCACCTTGCCACCCATTCTTCCCGTTCTTAA
CTTTGAACCATAAAGGGTGCCAGGTCTGGGTGAAAGGATACTTTTATGCAACCATAAGACAAACTCCTGAAATG
CCAAGTGCCTGCTTAGTAGCTTTGGAAAGGTGCCCTTATTGAACATTCTAGAAGGGGTGGCTGGGTCTTCAAGGA
TCTCCTGTTTTTTTCAGGCTCCTAAAGTAACATCAGCCATTTTTAGATTGGTTCTGTTTTCGTACCTTCCCACTG
GCCTCAAGTGAGCCAAGAAACACTGCCTGCCCTCTGTCTGTCTTCTCCTAATTCTGCAGGTGGAGGTTGCTAGTC
TAGTTTCCTTTTTGAGATACTATTTTCATTTTTGTGAGCCTCTTTGTAATAAAATGGTACATTTCT

FIGURE 151

MAQTQGTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMTKYHSDDYIKF
LRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLNKQQTDIAVNWAGGLHHAKKSEASGF
CYVNDIVLAILELLKYHQRVLYIDIDIHHGDGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVN
YPLRDGIDDESYEAIFKPVMSKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGG
GGYTIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIKQRLFENLRMLPH
APGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEFSDSEEEGEGGRKNSSNFKKAKRVKTEDEKE
KDPEEKKEVTEEEKTKEEKPEAKGVKEEVKLA

FIGURE 152

GGCACGAGGGCGCGGAGCGGAGCGGCGGCGGGCGCAGCTAGCGGGTCGGCCGCGGAGCGGAGGTGCAGCTCGGCT
TCCCCCGGCACCCCTCCCCCTCGGGCGCCAGCCCCACCCCTCCGCCGGCCGGGCCGACCCCGCCGTACTATCCCC
TGCGGCGCGAGCCCGGGGCGGCTCCAAGCGCCCCCCAGCAGACCCCCATC<u>ATG</u>GGCAGCCAGAGCTCCAAGGCTC
CCCGGGGCGACGTGACCGCCGAGGAGGCAGCAGGCGCTTCCCCCGCGAAGGCCAACGGCCAGGAGAATGGCCACG
TGAAAAGCAATGGAGACTTATCCCCCAAGGGTGAAGGGGAGTCGCCCCCTGTGAACGGAACAGATGAGGCAGCCG
GGGCCACTGGCGATGCCATCGAGCCAGCACCCCCTAGCCAGGGTGCTGAGGCCAAGGGGGAGGTCCCCCCCAAGG
AGACCCCCAAGAAGAAGAAGAAATTCTCTTTCAAGAAGCCTTTCAAATTGAGCGGCCTGTCCTTCAAGAGAAATC
GGAAGGAGGGTGGGGGTGATTCTTCTGCCTCCTCACCCACAGAGGAAGAGCAGGAGCAGGGGGAGATCGGTGCCT
GCAGCGACGAGGGCACTGCTCAGGAAGGGAAGGCCGCAGCCACCCCTGAGAGCCAGGAACCCCAGGCCAAGGGGG
CAGAGGCTAGTGCAGCCTCAGAAGAAGAGGCAGGGCCCCAGGCTACAGAGCCATCCACTCCCTCGGGGCCGGAGA
GTGGCCCTACACCAGCCAGCGCTGAGCAGAATGAG<u>TAG</u>CTAGGTAGGGGCAGGTGGGTGATCTCTAAGCTGCAAA
AACTGTGCTGTCCTTGTGAGGTCACTGCCTGGACCTGGTGCCCTGGCTGCCTTCCTGTGCCCAGAAAGGAAGGGG
CTATTGCCTCCTCCCAGCCACGTTCCCTTTCCTCCTCTCCCTCCTGTGGATTCTCCCATCAGCCATCTGGTTCTC
CTCTTAAGGCCAGTTGAAGATGGTCCCTTACAGCTTCCCAAGTTAGGTTAGTGATGTGAAATGCTCCTGTCCCTG
GCCCTACCTCCTTCCCTGTCCCCACCCCTGCATAAGGCAGTTGTTGGTTTTCTTCCCCAATTCTTTTCCAAGTAG
GTTTTGTTTACCCTACTCCCCAAATCCCTGAGCCAGAAGTGGGGTGCTTATACTCCCAAACCTTGAGTGTCCAGC
CTTCCCCTGTTGTTTTTAGTCTCTTGTGCTGTGCCTAGTGGCACCTGGGCTGGGGAGGACACTGCCCCGTCTAGG
TTTTTATAAATGTCTTACTCAAGTTCAAACCTCCAGCCTGTGAATCAACTGTGTCTCTTTTTTGACTTGGTAAGC
AAGTATTAGGCTTTGGGGTGGGGGGAGGTCTGTAATGTGAAACAACTTCTTGTCTTTTTTTCTCCCACTGTTGTA
AATAACTTTTAATGGCCAAACCCCAGATTTGTACTTTTTTTTTTTTCTAACTGCTAAAACCATTCTCTTCCACCT
GGTTTTACTGTAACATTTGGAAAAGGAATAAATGTCGTCCCTTTTTAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MGSQSSKAPRGDVTAEEAAGASPAKANGQENGHVKSNGDLSPKGEGESPPVNGTDEAAGATGDAIEPAPPSQGAE
AKGEVPPKETPKKKKKFSFKKPFKLSGLSFKRNRKEGGGDSSASSPTEEEQEQGEIGACSDEGTAQEGKAAATPE
SQEPQAKGAEASAASEEEAGPQATEPSTPSGPESGPTPASAEQNE

FIGURE 154

GCTCCCATTGGCTGATGTTGGCGCGAAGGTGCGCGAGTCAGCCCTCGCGCTGGGGGCGCAGGAAACAATAGAGGC
CGCGCGCACAGAGCGAGCTCTTGCAGCCTCCCCGCCCCTCCCGCAACGCTCGACCCCAGGATTCCCCCGGCTCGC
CTGCCCGCCATGGCCGACAAGGAAGCAGCCTTCGACGACGCAGTGGAAGAACGAGTGATCAACGAGGAATACAAA
ATATGGAAAAAGAACACCCCTTTTCTTTATGATTTGGTGATGACCCATGCTCTGGAGTGGCCCAGCCTAACTGCC
CAGTGGCTTCCAGATGTAACCAGAATTTGGAGGTTTTGGTTCAGTTAGTGGAAAAATTGAAATAGAAATCAAGAT
CAACCATGAAGGAGAAGTAAACAGGGCCCGTTATATGCCCCAGAACCCTTGTATCATCGCAACAAAGACTCCTTC
CAGTGATGTTCTTGTTTTTGACTATACAAAACATCCTTCTAAACCAGATCCTTCTGGAGAGTGCAACCCAGACTT
GCGTCTCCGTGGACATCAGAAGGAAGGCTATGGGCTTTCTTGGAACCCAAATCTCAGTGGGCACTTACTTAGTGC
TTCAGATGACCATACCATCTGCCTGTGGGACATCAGTGCCGTTCCAAAGGAGGGAAAAGTGGTAGATGCGAAGAC
CATCTTTACAGGGCATACGGCAGTAGTAGAAGATGTTTCCTGGCATCTACTCCATGAGTCTCTGTTTGGGTCAGT
TGCTGATGATCAGAAACTTATGATTTGGGATACTCGTTCAAACAATACTTCCAAACCAAGCCACTCAGTTGATGC
TCACACTGCTGAAGTGAACTGCCTTTCTTTCAATCCTTATAGTGAGTTCATTCTTGCCACAGGATCAGCTGACAA
GACTGTTGCCTTGTGGGATCTGAGAAATCTGAAACTTAAGTTGCATTCCTTTGAGTCACATAAGGATGAAATATT
CCAGGTTCAGTGGTCACCTCACAATGAGACTATTTTAGCTTCCAGTGGTACTGATCGCAGACTGAATGTCTGGGA
TTTAAGTAAAATTGGAGAGGAACAATCCCCAGAAGATGCAGAAGACGGGCCACCAGAGTTGTTGTTTATTCATGG
TGGTCATACTGCCAAGATATCTGATTTCTCCTGGAATCCCAATGAACCTTGGGTGATTTGTTCTGTATCAGAAGA
CAATATCATGCAAGTGTGGCAAATGGAGTTAGTCCTTGACCACTAGTTTGATGCCATCTCCATTTTGGGTGACCT
GTTTCACCAGCAGGCCTGTTACTCTCCATGACTAACTGTGTAAGTGCTTAAAATGGAATAAATTGCTTTTCTACA
TAA

FIGURE 155A

GGCTCGCATCCCCATAGTGCTGGGTTACAGTGAAGGTACGCCCCGCGCTCTGCTCTGGAGAGGCAGGGTGGGATA
GGGAACGTCTCGAGTGGCGCCCGCAGTC**ATG**GTGGTGTTCGTTGGCCGCCGCCTCCCGGCGCTCCTAGGGCTGTT
TAAGAAGAAGGGCTCTGCCAAGGCTGAGAATGACAAACATCTAAGTGTAGGGCCTGGCCAGGGGCCAGGGTCTGC
AGTGGATGAGCACCAGGACAACGTCTTCTTTCCCAGTGGGCGACCCCCCCACCTGGAAGAGCTGCACACTCAGGC
CCAGGAGGGGCTCCGCTCCCTACAACACCAAGAGAAACAGAAACTGAACAAGGGTGGCTGGGACCATGGAGACAC
CCAGAGTATCCAGTCCTCCCGGACGGGGCCGGATGAAGACAACATCTCCTTCTGCAGTCAGACCACATCCTACGT
GGCTGAGAGCTCCACAGCAGAGGACGCGCTCTCCATCCGCTCGGAGATGATCCAGCGCAAAGGCTCCACCTTCCG
ACCCCATGACTCATTTCCCAAATCTGGAAAGTCAGGGCGGCGTCGGCGGGAGCGGCGGAGCACTGTGCTGGGACT
CCCGCAGCATGTGCAGAAGGAGCTTGGCCTGAGGAATGAGCGTGAGGCACCAGGCACGCCCCGGGCTCCTGGTGC
ACGGGATGCCGTACGCATCCCCACAGTGGACGGCCGCCCCCGAGGCACCTCAGGGATGGGGGCCCGGGTGTCCCT
GCAGGCGCTGGAGGCGGAGGCGGAGGCTGGCGCTGAGACAGAGGCCATGCTGCAGCGCCACATTGACCGTGTCTA
CCGGGATGACACCTTTGTTGGCCGGTCCACGGGTACCCGGGCCCCACCATTGACCCGGCCCATGTCCCTAGCAGT
GCCTGGATTGACAGGAGGGGCAGGCCTGCAGAGCCCCTGAGCCCGGCCATGTCCATCTCCCCCCAGGCCACCTA
CCTGTCGAAGTTGATTCCACATGCTGTGCTGCCGCCTACAGTGGACGTGGTGGCCCTAGGCCGCTGCAGCCTGCG
CACACTAAGCCGCTGCAGCCTGCACTCGGCCAGCCCAGCCTCAGTCCGCTCGCTGGGGCGCTTCTCCTCCGTCTC
CAGCCCACAGCCCCGCAGCCGCCACCCATCCTCCTCCAGTGACACCTGGAGCCACTCTCAATCCTCCGACACCAT
TGTGTCTGACGGTTCCACCCTCTCCTCTAAGGGTGGCTCTGAGGGCCAGCCGGAGAGCTCTACGGCTAGCAATAG
CGTGGTACCCCCTCCCCAGGGAGGCAGTGGGAGGGGCTCTCCCAGTGGGGGCAGCACTGCTGAGGCCTCAGACAC
ACTCAGCATTCGGAGCAGTGGGCAGTTGTCTGGCCGGAGTGTGTCCCTGCGTAAGCTGAAGCGGCCTCCACCCCC
TCCCCGCCGGACCCACTCCCTCCATCAGCGGGGCTTAGCAGTGCCTGATGGGCCATTAGGGTTGCCCCCTAAGCC
TGAGCGTAAGCAGCAGCCCCAGCTGCCTCGGCCACCCACCACTGGTGGCTCAGAAGGGGCGGGGGCAGCACCCTG
TCCACCCAACCCAGCCAACAGCTGGGTACCTGGCTTGTCTCCGGGTGGTTCCCGGCGCCCCCCACGGTCCCCAGA
ACGGACACTTTCGCCCTCCAGTGGATACTCGAGCCAAAGTGGTACTCCCACCCTCCCTCCCAAGGGCCTGGCAGG
TCCCCCTGCTTCCCCAGGCAAGGCCCAGCCCCCTAAACCAGAGCGTGTCACGTCTCTTCGCTCCCCTGGGGCCTC
CGTCTCCTCTTCCCTCACGTCTTTATGTTCCTCCTCCTCTGACCCAGCCCCCTCAGACCGCTCTGGGCCACAGAT
ATTGACCCCCCTGGGTGACAGGTTTGTCATACCTCCTCACCCCAAGGTGCCTGCCCCCTTCTCCCCACCTCCCTC
CAAGCCCAGGAGCCCTAACCCAGCTGCCCCTGCTCTAGCCGCCCCTGCTGTGGTTCCTGGGCCTGTTTCTACCAC
TGACGCCAGTCCTCAGTCCCCTCCCACTCCCCAGACAACCTTGACTCCACTGCAGGAGTCTCCTGTCATCTCCAA
AGACCAGTCACCCCCACCTTCCCCACCCCCATCTTATCATCCACCCCCACCACCCACTAAGAAGCCAGAGGTGGT
TGTGGAGGCACCATCTGCCTCAGAGACTGCTGAGGAGCCCCTCCAAGATCCCAACTGGCCCCCTCCCCCACCCCC
TGCCCCTGAGGAGCAGGACCTGTCCATGGCTGACTTCCCCCCACCAGAGGAGGCTTTTTTCTCTGTGGCCAGCCC
TGAGCCTGCAGGCCCTTCAGGCTCCCCAGAGCTTGTCAGCTCCCCGGCTGCTTCGTCCTCCTCAGCTACTGCTTT
GCAGATTCAGCCCCCGGGTAGCCCAGACCCTCCTCCAGCTCCGCCAGCCCCAGCTCCTGCTAGTTCCGCCCCAGG
GCATGTGGCCAAGCTCCCTCAGAAGGAACCGGTGGGCTGTAGCAAGGGTGGTGGGCCTCCCAGGGAGGACGTAGG
TGCGCCCCTGGTCACGCCCTCGCTCCTGCAGATGGTGCGGCTGCGCTCCGTGGGTGCTCCAGGAGGGGCTCCCAC
CCCAGCACTGGGGCCATCGGCCCCCCAGAAACCACTGCGAAGGGCCCTGTCAGGGCGGGCCAGCCCAGTGCCTGC
CCCCTCCTCAGGGCTCCATGCTGCGGTCCGACTCAAGGCCTGCAGCCTGGCCGCCAGTGAAGGCCTCTCAAGTGC
TCAGCCCAACGGACCGCCTGAGGCAGAGCCACGGCCTCCCCAGTCCCCTGCCTCAACGGCCAGTTTCATCTTCTC
CAAGGGCTCTAGGAAGCTGCAGCTGGAGCGGCCCGTGTCCCCTGAGACCCAGGCTGACCTCCAGCGGAATCTGGT
GGCAGAACTCCGGAGCATCTCAGAGCAGCGGCCACCCCAGGCCCCAAAGAAGTCACCTAAGGCTCCCCCACCTGT
GGCCCGCAAGCCGTCTGTGGGAGTCCCCCCACCCGCCTCCCCCAGTTACCCTCGAGCTGAGCCCCTTACTGCTCC
TCCCACCAATGGGCTCCCTCACACCCAGGACAGGACTAAGAGGGAGCTGGCGGAGAATGGAGGTGTCCTGCAGCT
GGTGGGCCCAGAGGAGAAGATGGGCCTCCCGGGCTCAGACTCACAGAAAGAGCTGGCC**TGA**CCACCAGGCACCTC
ACTGGCACTGCTGACCCATCCCAGAAACACAATCTCAGGGACCCGAGCAGCTCCAAGGACGAGAGGATACAGCAG
ACACAACCTAATAGAGAGGGCGCCTGCAGCCTTAACCTCCACGGCCTTCGATACTTATGCAAGCCTGGTGTTGCT
CCTGTCCTCAGAGTCATCCTGCGCTCATGCCTTTTCCCGAATGGGTTCACCTCTGGCAGTTGCCGCTTCAGTCTT
GGCCTTAGCCTCATCTTGAAGTGGGTAGCTGGCGGGAGAGGGTGGCTGCGCCCCCTGCTGGCCCTGAGGCTGCAG
AGTTGGGAGCAGGACACCTCACCTGAGTTTCATTTTTTTTCATGTCCAAACCATGCACATACTATAGTCCAGAAT

FIGURE 155B

CAAAGCACTTTTGAAAAGTGGCTGCATGGCCATCCTCCAGGGCCCAGGAAGTTGCATTCCAAGGGCCTGTTTACA
TGGCAGCAGAATCCATCCCCGGCAGTCAGCCCATAGCTTGGGACCAGTCTGTGCCCTCCTGCCCAGTCCAGTTTA
CTCCTCTTGGTTCCTGAAGGTGGCCAAGTCATTGTGTTCCCACAGGCTTCTCTAGGCTGGGGGCAGGTGTGGGGC
TGTGGAATTCCAAAGCACAAAAGGTGCAGAGGGGATTGGCCTTCCTGTGCCTCAACTCACCAACCACCCTCCTGC
CTTCCAGTTCTGCCAGGTGCTCCATGCTGGGGACAAGTAGGAGACTGCCAGGGCCCAAAGAAATGGGTGAGCAGT
AGAGTCATCTCGGGGCACTTGGCAGTGTCAAGCACCTGCCCCTTGCCTCCTTGACCACACTGGGGTGGGTGGGCC
CCCAGCACTTCAGAGGCAGGAGCCTTTGGGCTGAGCAAGCACTGAGGAGGTGGATGGAAGGGAGCATCTGGAGGG
GGGGAGCTTCCTTGAGCAGTGGGCCCAGGCCTGGCCCTCCACACTTCATTCTCTGACCTTTCTCTCTCCTCATTT
CGGTGCATGTCCTTTCTGCAGCTGCCTTTCAGCACAGGTGGTTCCACTGGGGGCAGCTAACGCTGAGTGACAAGG
ATGGGAAGCCACAGGTGCATTTTACTCAAGTCTTCTCTAGTCAATGAGGGGCACCCAGTGCTTCTAGGGCAGGCT
GGGTGGTGGTCCCCTAGGTATCAGCCTCTCTTACTGTACTCTCCGGGAATGTTAACCTTTCTATTTTCAGCCTGT
GCCACCTGTCTAGGCAAGCTGGCTTCCCCATTGGCCCCTGTGGGTCCACAGCAGCGTGGCTGCCCCCCAGGGCCA
CCGCTTCTTTCTTGATCCTCTTTCCTTAACAGTGACTTGGGCTTGAGTCTGGCAAGGAACCTTGCTTTTAGCTTC
ACCACCAAGGAGAGAGGTTGACATGACCTCCCCGCCCCCTCACCAAGGCTGGGAACAGAGGGGATGTGGTGAGAG
CCAGGTTCCTCTGGCCCTCTCCAGGGTGTTTTCCACTAGTCACTACTGTCTTCTCCTTGTAGCTAATCAATCAAT
ATTCTTCCCTTGCCTGTGGGCAGTGGAGAGTGCTGCTGGGTGTACGCTGCACCTGCCCACTGAGTTGGGGAAAGA
GGATAATCAGTGAGCACTGTTCTGCTCAGAGCTCCTGATCTACCCCACCCCCTAGGATCCAGGACTGGGTCAAAG
CTGCATGAAACCAGGCCCTGGCAGCAACCTGGGAATGGCTGGAGGTGGGAGAGAACCTGACTTCTCTTTCCCTCT
CCCTCCTCCAACATTACTGGAACTCTATCCTGTTAGGATCTTCTGAGCTTGTTTCCCTGCTGGGTGGGACAGAGG
ACAAAGGAGAAGGGAGGGTCTAGAAGAGGCAGCCCTTCTTTGTCCTCTGGGGTAAATGAGCTTGACCTAGAGTAA
ATGGAGAGACCAAAAGCCTCTGATTTTTAATTTCCATAAAATGTTAGAAGTATATATATACATATATATATTTCT
TTAAATTTTTGAGTCTTTGATATGTCTAAAAATCCATTCCCTCTGCCCTGAAGCCTGAGTGAGACACATGAAGAA
AACTGTGTTTCATTTAAAGATGTTAATTAAATGATTGAAACTTG

FIGURE 156

MVVFVGRRLPALLGLFKKKGSAKAENDKHLSVGPGQGPGSAVDEHQDNVFFPSGRPPHLEELHTQAQEGLRSLQH
QEKQKLNKGGWDHGDTQSIQSSRTGPDEDNISFCSQTTSYVAESSTAEDALSIRSEMIQRKGSTFRPHDSFPKSG
KSGRRRRERRSTVLGLPQHVQKELGLRNEREAPGTPRAPGARDAVRIPTVDGRPRGTSGMGARVSLQALEAEAEA
GAETEAMLQRHIDRVYRDDTFVGRSTGTRAPPLTRPMSLAVPGLTGGAGPAEPLSPAMSISPQATYLSKLIPHAV
LPPTVDVVALGRCSLRTLSRCSLHSASPASVRSLGRFSSVSSPQPRSRHPSSSSDTWSHSQSSDTIVSDGSTLSS
KGGSEGQPESSTASNSVVPPPQGGSGRGSPSGGSTAEASDTLSIRSSGQLSGRSVSLRKLKRPPPPPRRTHSLHQ
RGLAVPDGPLGLPPKPERKQQPQLPRPPTTGGSEGAGAAPCPPNPANSWVPGLSPGGSRRPPRSPERTLSPSSGY
SSQSGTPTLPPKGLAGPPASPGKAQPPKPERVTSLRSPGASVSSSLTSLCSSSSDPAPSDRSGPQILTPLGDRFV
IPPHPKVPAPFSPPPSKPRSPNPAAPALAAPAVVPGPVSTTDASPQSPPTPQTTLTPLQESPVISKDQSPPPSPP
PSYHPPPPPTKKPEVVVEAPSASETAEEPLQDPNWPPPPPPAPEEQDLSMADFPPPEEAFFSVASPEPAGPSGSP
ELVSSPAASSSSATALQIQPPGSPDPPPAPPAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLL
QMVRLRSVGAPGGAPTPALGPSAPQKPLRRALSGRASPVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAE
PRPPQSPASTASFIFSKGSRKLQLERPVSPETQADLQRNLVAELRSISEQRPPQAPKKSPKAPPPVARKPSVGVP
PPASPSYPRAEPLTAPPTNGLPHTQDRTKRELAENGGVLQLVGPEEKMGLPGSDSQKELA

FIGURE 157

ATGGGGGACGCTCCCAGCCCTGAAGAGAAACTGCACCTTATCACCCGGAACCTGCAGGAGGTTCTGGGGGAAGAG
AAGCTGAAGGAGATACTGAAGGAGCGGGAACTTAAAATTTACTGGGGAACGGCAACCACGGGCAAACCACATGTG
GCTTACTTTGTGCCCATGTCAAAGATTGCAGACTTCTTAAAGGCAGGGTGTGAGGTAACAATTCTGTTTGCGGAC
CTCCACGCATACCTGGATAACATGAAAGCCCCATGGGAACTTCTAGAACTCCGAGTCAGTTACTATGAGAATGTG
ATCAAAGCAATGCTGGAGAGCATTGGTGTGCCCTTGGAGAAGCTCAAGTTCATCAAAGGCACTGATTACCAGCTC
AGCAAAGAGTACACACTAGATGTGTACAGACTCTCCTCCGTGGTCACACAGCACGATTCCAAGAAGGCTGGAGCT
GAGGTGGTAAAGCAGGTGGAGCACCCTTTGCTGAGTGGCCTCTTATACCCCGGACTGCAGGCTTTGGATGAAGAG
TATTTAAAAGTAGATGCCCAATTTGGAGGCATTGATCAGAGAAAGATTTTCACCTTTGCAGAGAAGTACCTCCCT
GCACTTGGCTATTCAAAACGGGTCCATCTGATGAATCCTATGGTTCCAGGATTAACAGGCAGCAAAATGAGCTCT
TCAGAAGAGGAGTCCAAGATTGATCTCCTTGATCGGAAGGAGGATGTGAAGAAAAAACTGAAGAAGGCCTTCTGT
GAGCCAGGAAATGTGGAGAACAATGGGGTTCTGTCCTTCATCAAGCATGTCCTTTTTCCCCTTAAGTCCGAGTTT
GTGATCCTACGAGATGAGAAATGGGGTGGAAACAAAACCTACACAGCTTACGTGGACCTGGAAAAGGACTTTGCT
GCTGAGGTTGTACATCCTGGAGACCTGAAGAATTCTGTTGAAGTCGCACTGAACAAGTTGCTGGATCCAATCCGG
GAAAAGTTTAATACCCCTGCCCTGAAAAAACTGGCCAGCGCTGCCTACCCAGATCCCTCAAAGCAGAAGCCAATG
GCCAAAGGCCCTGCCAAGAATTCAGAACCAGAGGAGGTCATCCCATCCCGGCTGGATATCCGTGTGGGGAAAATC
ATCACTGTGGAGAAGCACCCAGATGCAGACAGCCTGTATGTAGAGAAGATTGACGTGGGGGAAGCTGAACCACGG
ACTGTGGTGAGCGGCCTGGTACAGTTCGTGCCCAAGGAGGAACTGCAGGACAGGCTGGTAGTGGTGCTGTGCAAC
CTGAAACCCCAGAAGATGAGAGGAGTCGAGTCCCAAGGCATGCTTCTGTGTGCTTCTATAGAAGGGATAAACCGC
CAGGTTGAACCTCTGGACCCTCCGGCAGGCTCTGCTCCTGGTGAGCACGTGTTTGTGAAGGGCTATGAAAAGGGC
CAACCAGATGAGGAGCTCAAGCCCAAGAAGAAAGTCTTCGAGAAGTTGCAGGCTGACTTCAAAATTTCTGAGGAG
TGCATCGCACAGTGGAAGCAAACCAACTTCATGACCAAGCTGGGCTCCATTTCCTGTAAATCGCTGAAAGGGGGG
AACATTAGC**TAG**CCAGCCCAGCATCTTCCCCCCTTCTTCCACCACTGAGTCATCTGCTGTCTCTTCAGTCTGCTC
CATCCATCACCCATTTACCCATCTCTCAGGACA

FIGURE 158

MGDAPSPEEKLHLITRNLQEVLGEEKLKEILKERELKIYWGTATTGKPHVAYFVPMSKIADFLKAGCEVTILFAD
LHAYLDNMKAPWELLELRVSYYENVIKAMLESIGVPLEKLKFIKGTDYQLSKEYTLDVYRLSSVVTQHDSKKAGA
EVVKQVEHPLLSGLLYPGLQALDEEYLKVDAQFGGIDQRKIFTFAEKYLPALGYSKRVHLMNPMVPGLTGSKMSS
SEEESKIDLLDRKEDVKKKLKKAFCEPGNVENNGVLSFIKHVLFPLKSEFVILRDEKWGGNKTYTAYVDLEKDFA
AEVVHPGDLKNSVEVALNKLLDPIREKFNTPALKKLASAAYPDPSKQKPMAKGPAKNSEPEEVIPSRLDIRVGKI
ITVEKHPDADSLYVEKIDVGEAEPRTVVSGLVQFVPKEELQDRLVVVLCNLKPQKMRGVESQGMLLCASIEGINR
QVEPLDPPAGSAPGEHVFVKGYEKGQPDEELKPKKKVFEKLQADFKISEECIAQWKQTNFMTKLGSISCKSLKGG
NIS

FIGURE 159

GCGCGAGCAAG**ATG**GCCACCACCAAGCGCGTCTTGTACGTGGGTGGACTGGCAGAGGAAGTGGACGACAAAGTTC
TTCATGCTGCGTTCATTCCTTTTGGAGACATCACAGATATTCAGATTCCTCTGGATTATGAAACAGAAAAGCACC
GAGGATTTGCTTTTGTTGAATTTGAGTTGGCAGAGGATGCTGCAGCAGCTATCGACAACATGAATGAATCTGAGC
TTTTTGGACGTACAATTCGTGTCAATTTGGCCAAACCAATGAGAATTAAGGAAGGCTCTTCCAGGCCAGTTTGGT
CAGATGATGACTGGTTGAAGAAGTTTTCTGGGAAGACGCTTGAAGAGAATAAAGAGGAAGAAGGGTCAGAGCCTC
CCAAAGCAGAGACCCAGGAGGGAGAGCCCATTGCTAAAAAGGCCCGCTCAAATCCTCAGGTGTACATGGACATCA
AGATTGGGAACAAGCCGGCTGGCCGCATCCAGATGCTCCTGCGTTCTGATGTCGTGCCCATGACAGCAGAGAATT
TCCGCTGCCTGTGCACTCATGAAAAGGGCTTTGGCTTTAAGGGAAGCAGCTTCCACCGCATCATCCCCCAGTTCA
TGTGCCAGGGCGGTGATTTCACAAACCACAATGGCACTGGGGGCAAGTCCATCTATGGGAAGAAGTTCGATGATG
AAAACTTTATCCTCAAGCATACGGGACCAGGTCTACTATCCATGGCCAACTCTGGCCCAAACACCAATGGCTCTC
AGTTCTTCCTGACATGTGACAAGACAGACTGGCTGGATGGCAAGCATGTGGTGTTTGGAGAGGTCACCGAAGGCC
TAGATGTCTTGCGGCAAATTGAGGCCCAGGGCAGCAAGGACGGGAAGCCAAAGCAGAAGGTGATCATCGCCGACT
GTGGGGAGTACGTG**TGA**GGCGGCACTCTCTCTGCTTCCCCCTCCGCTCTTGACCCTGCATATCCAGGAAGGAACT
GCCAGCCTCAGAGGAGGCAGCACCGAGGGTGCCTGTTTGAAGCAAGCAGCATTTGGGATATGTGCCCTTCCTCAG
GGTCTGCTTGGAGCAGCTCCTCTGCAGGCACAGCCTGGACTATTCCCAGGCACAGCTGTGGGCCCAGGAGCCAGC
TCAGGTGCTCCCCTCCACCATGGGCAGGCTGTGCAAAAAAGCCACTGGCTTTTCTCAGCATTTGCTGCTGGGCCT
CTCCTGGGACTACCAGTGTGGCTCTTACGTGTTTTCTTTGCTAAAATAAACCCTAGTTCTTATATTAAAAAAAAA
AAAAAAAAAA

FIGURE 160

MATTKRVLYVGGLAEEVDDKVLHAAFIPFGDITDIQIPLDYETEKHRGFAFVEFELAEDAAAAIDNMNESELFGR
TIRVNLAKPMRIKEGSSRPVWSDDDWLKKFSGKTLEENKEEEGSEPPKAETQEGEPIAKKARSNPQVYMDIKIGN
KPAGRIQMLLRSDVVPMTAENFRCLCTHEKGFGFKGSSFHRIIPQFMCQGGDFTNHNGTGGKSIYGKKFDDENFI
LKHTGPGLLSMANSGPNTNGSQFFLTCDKTDWLDGKHVVFGEVTEGLDVLRQIEAQGSKDGKPKQKVIIADCGEY
V

FIGURE 161

TCAAAGCACCTGCAGCCCCAATTTGTGATCCAGCAGCAGCCACAGCCACAACAGCAGCAGCCGCCGCCCCAGCAG
TCACGGCCTGTGCTCCAAGCTGAGCCCCACCCCCAGCTCGCCTCAGTCTCTCCAAGCGTGGCCCTCCAGCCCAGC
TCAGAGGCCCATGCC**ATG**CCACTAGGCCCGGTTACACCCGCCCTGCCACTCCAGTGTCCCACTGCCAACCTGCAC
AAGCCTGGCGGCAGTCAGCAGTGTCACCCTCCCACACCTGATACTGGGCCTCAGAATGGACATCCCGAGGGCGTG
CCCCACACCCCTCAACGCAGGTTCCAGCACACTTCAGCTGTCATCTTACAACTGCAGCCTGCTTCACCAGTGCCC
CAGCAGTGTGTCCCTGATGACTGGAAAGAAGTGGCACCAGGGGAGAAAAGTGTGCCTGAGACGCGGTCTGGCCCA
TCACCACATCAGCAGGCTATTGTCACTGCCATGCCTGGTGGCCTGCCTGTACCCACGAGCCCTAACATCCAGCCG
TCCCCAGCTCACGAGACAGGGCAGGGCATTGTTCATGCACTGACCGACCTCAGCAGCCCCGGCATGACCTCAGGG
AACGGAAACTCTGCCTCCAGCATCGCCGGCACTGCCCCCCAGAATGGTGAGAATAAACCACCACAGGCCATTGTG
AAACCCCAAATCCTGACGCATGTTATCGAAGGGTTTGTGATCCAGGAGGGGGCGGAGCCTTTCCCGGTGGGACGC
TCGTCCCTGCTGGTGGGGAATCTCAAGAAGAAGTATGCACAGGGGTTCCTGCCTGAGAAACTTCCACAGCAGGAT
CACACCACCACCACTGACTCGGAGATGGAGGAGCCCTATCTGCAAGAATCCAAAGAGGAGGGTGCTCCCCTCAAA
CTCAAGTGTGAGCTCTGTGGCCGGGTGGACTTTGCCTATAAGTTCAAGCGTTCCAAGCGCTTCTGTTCCATGGCT
TGTGCAAAGAGGTACAACGTGGGATGCACCAAACGGGTGGGACTTTTCCACTCAGACCGGAGCAAGCTGCAGAAG
GCAGGAGCTGCGACCCACAACCGCCGTCGGGCCAGCAAAGCCAGTCTGCCACCACTTACCAAGGATACCAAGAAG
CAGCCAACAGGCACTGTGCCCCTTTCGGTTACTGCTGCTTTGCAGCTAACACACAGCCAGGAAGACTCCAGCCGT
TGCTCAGATAACTCAAGCTATGAGGAACCCTTGTCACCCATCTCAGCCAGCTCATCTACTTCCCGCCGGCGACAA
GGCCAGCGGGACCTGGAGCTCCCCGACATGCATATGCGGGACCTGGTGGGCATGGGACACCACTTCCTGCCAAGT
GAGCCCACCAAGTGGAATGTAGAAGACGTCTACGAATTCATCCGCTCTCTGCCAGGCTGCCAGGAGATAGCAGAG
GAATTCCGTGCCCAGGAAATCGACGGGCAAGCCCTGCTGCTGCTCAAGGAGGACCACCTGATGAGCGCCATGAAC
ATCAAGCTGGGGCCCGCCCTGAAGATCTACGCCCGCATCAGCATGCTCAAGGACTCC**TAG**GGCTGGTGGCAGCCA
GGATTCTGGCCCAGGGCGCCTCCTCCCGACTGAGCAGAGCCAGACAGACATTCCTGAGGGGCCCAGAAATGGGGC
CGGTTGGAGGGCAGGGGCTCTCCCTAGGGGCATAGCTGGTGAGGAGGTCTGGGCACCTCCTCCATGGCTCTCAGG
CGCCTTTCATTTCTGTGGGAGGGGCAGAGAGGTAGGTGGCACAGAAGATGGGGCTTTATGCTTGTAAATATTGAT
AGCACTGGCTTCCTCCAAAGTCCCAATACTCTAGCCCCGCTCTCTTCCCCTCTTTCTGTCCCCCATTTTCCAGGG
GGTATATGGTCAGGGCTCCCCAACCTGAGTTGGGTTACTTCAAGGGCAGCCAGCAGGCCTGGATGGAGGCCTAGA
AAGCCCTTGCCTTCCTTCCTCCCACTTCTTTCTCCAGGCCTGGTTAACTCTTCCGTTGTCAGCTTCTCCCCCTTC
AGCCTGTTTCTGCAGCAGCCAGGGTTCTCCCCCCTACACCCTCTGCAGGTGGAGAGAGAGAAGCTGGGCCCAGCC
GGGCCGTGCCTGCTGGCACAGACGCCTTAACGCTGTGTGTATGACTGTGTGACTGTGTGGGAGCCTGGACTGACA
GATAGGCCAAGGGCTACTCTCTGGCATCTCCAGGTGTTTTGTAGCAAACAGCCACTTAGTGCTTTGTCCTGGACT
CCACTCAGCCTCAGGATGGGGAATAGCCAAGAATGGCAGCCTCAGCGCAGAGGCAAGGTCAGAAAGAGACGGCGC
TTCAGAGTTTCCTTTCCAGACACCCCTCCCCGCACTGTGAAGTTCCCCTGACCGCCCTCCTGGTTCACAAAGAGC
ATTAAGAAAGCTGCGGTGGTCTGAGCAACATAGCCCAAAGGGCTGAGCCTCCTGGCCTGCCTGCCCGCCCACCCT
GGGAGTCCCAGTGGTGAGGCTCAGAGAACTGCTAAGGGGAAAGAACAGCTGGAGTTTCTGTTGATGTGAAGAAGG
CAGCTCTTGGCCTCCCACTCCCACACTTCTTTGCCTATAAATCTTCCTAGCAGCAATTTGAGCTACCTGAGGAGG
AGGCAGGGCAGAAAGGGCGAGGGCCTGCCTCTGACCTGCCGTGTCCTTTGCAGGAAGGAGGTAGGCACCTTTCTG
AGCTTATTCTATTCCCCACCCACACCCCCAGGCAGGGTTGGAAATGAAGGACTTTTTTAACCTTTGTTTTGTTTT
TTAAAAATAAATCTGTAAAATCTG

FIGURE 162

MPLGPVTPALPLQCPTANLHKPGGSQQCHPPTPDTGPQNGHPEGVPHTPQRRFQHTSAVILQLQPASPVPQQCVP
DDWKEVAPGEKSVPETRSGPSPHQQAIVTAMPGGLPVPTSPNIQPSPAHETGQGIVHALTDLSSPGMTSGNGNSA
SSIAGTAPQNGENKPPQAIVKPQILTHVIEGFVIQEGAEPFPVGRSSLLVGNLKKKYAQGFLPEKLPQQDHTTTT
DSEMEEPYLQESKEEGAPLKLKCELCGRVDFAYKFKRSKRFCSMACAKRYNVGCTKRVGLFHSDRSKLQKAGAAT
HNRRRASKASLPPLTKDTKKQPTGTVPLSVTAALQLTHSQEDSSRCSDNSSYEEPLSPISASSSTSRRRQGQRDL
ELPDMHMRDLVGMGHHFLPSEPTKWNVEDVYEFIRSLPGCQEIAEEFRAQEIDGQALLLLKEDHLMSAMNIKLGP
ALKIYARISMLKDS

FIGURE 163

AGACAAGGCAAATTTAAGTAGGCTC**ATG**GCTTTTCCAGTTGGGTTGGAAAGTTCCTCTCCGATGACTGTTATATT
CTCAAAGAAATATGAGGAGAGGGGCAGGGCATGGTGGCTCACATCCGTAATCCTAGCAAATCATAGTGGCCTACA
GCCAACGCCTTCTTCGCTCACTGGCCAACTGGAAACTTCAGTCCCCCCATGCCTCCCGCCTCTCACCCAGGGGCC
AATAGGAATGATCAGAGGTTCGCAACTTAGTGTCATCAAGCATAGTAATTGCAATTGGCTATTGGAGCTGTCGAT
CGTGGAG**TAG**GCGGGGCCGTGCCAGCTGGCCTATATAAGACGAGGACAAAGGCGGCGCGCCGCCTGTGTCATCCG
CCATTTTGTGAGAAGCAAGGTGGCCTCCACGTTTCCTGAGCGTCTTCTTCGCTTTTGCCTCGACCGCCCCTTGAC
CACAGACATGTCTCGGGATCGGTTCCGGAGTCGTGGCGGTGGCGGTGGTGGCTTCCACAGGCGTGGAGGAGGCGG
CGGCCGCGGCGGCCTCCACGACTTCCGTTCTCCGCCGCCCGGCATGGGCCTCAATCAGAATCGCGGCCAGGCCCG
ACTCCGACCCCGCCGCCTGCAGTCACCTCGGCCCCTCCCGGGGCGCCGCCACCCACCCCGCCAAGCAGCGGGGTC
CCTACCACACCTCCTCAGGCCGGAGGCCCGCCGCCTCCGCCCGCGGCAGTCCCGGGCCCGGGTCCAGGGCCTAAG
CAGGGCCCAGGTCCGGGTGGTCCCAAAGGCGGCAAAATGCCTGGCGGGCCGAAGCCAGGTGGCGGCCCGGGCCTA
AGTACGCCTGGCGGCCACCCCAAGCCGCCGCATCGAGGCGGCGGGGAGCCCCGCGGGGGCCGCCAGCACCACCCG
CCCTACCACCAGCAGCATCACCAGGGGCCCCCGCCCGGCGGGCCCGGCGGCCGCAGCGAGGAGAAGATCTCGGAC
TCGGAG

FIGURE 164

MAFPVGLESSSPMTVIFSKKYEERGRAWWLTSVILANHSGLQPTPSSLTGQLETSVPPCLPPLTQGPIGMIRGSQ
LSVIKHSNCNWLLELSIVE

FIGURE 165

GGCGAGCAGTCTGCGCGCGG**ATG**GCCGCAGCGGCGATGGCGGCAGCGGCAGGTGGAGGGGCTGGCGCGGCCCGCT
CCCTCTCGCGCTTCCGAGGCTGCCTGGCTGGTGCGCTGCTCGGGGACTGCGTGGGCTCCTTCTACGAGGCCCACG
ACACCGTCGACCTGACGTCAGTCCTGCGTCATGTCCAGAGTCTGGAGCCGGACCCCGGCACGCCCGGGAGTGAGC
GGACAGAAGCCTTGTACTACACAGATGACACAGCCATGGCCAGGGCCCTGGTGCAGTCCCTGCTAGCCAAGGAGG
CCTTTGACGAGGTGGACATGGCTCACAGATTTGCTCAGGAGTACAAGAAAGACCCTGACAGGGGCTATGGTGCTG
GAGTAGTCACTGTCTTCAAGAAGCTCCTGAACCCCAAATGTCGCGATGTCTTTGAGCCTGCCCGGGCCCAGTTTA
ACGGGAAAGGCTCCTATGGCAATGGAGGTGCCATGCGGGTGGCTGGCATCTCCCTGGCCTATAGCAGTGTCCAGG
ATGTGCAGAAGTTTGCCCGGCTCTCGGCCCAGCTGACACACGCCTCCTCCCTGGGTTACAATGGCGCCATCCTGC
AGGCCCTGGCTGTGCACCTGGCCTTGCAGGGCGAGTCTTCCAGCGAGCACTTTCTCAAGCAACTCCTGGGCCACA
TGGAGGATCTGGAGGGTGATGCCCAGTCCGTCTTGGATGCCAGGGAGTTGGGCATGGAGGAGCGTCCATACTCCA
GCCGCCTGAAGAAGATTGGAGAGCTTCTAGACCAGGCATCGGTGACCAGGGAGGAAGTGGTGTCTGAGCTAGGGA
ATGGCATTGCTGCCTTTGAGTCGGTACCCACCGCCATCTACTGCTTCCTACGCTGCATGGAGCCAGACCCTGAGA
TCCCTTCTGCCTTCAATAGCCTCCAAAGGACTCTCATTTATTCCATCTCACTTGGTGGGGACACAGACACCATTG
CCACCATGGCTGGGGCCATTGCTGGTGCCTACTATGGGATGGATCAGGTGCCAGAGAGCTGGCAGCAAAGCTGTG
AAGGCTACGAGGAGACAGACATCCTGGCCCAAAGCCTGCACCGTGTCTTCCAGAAGAGT**TGA**TGAGGGCTACAGC
TGTTGGGGCTCTGCCAGGTCCCCTGGGACCAACTACAGCTCCAATCAGAAACCCTGCGCTTCCTTGAGTGTGGCT
TCCCACTTTTCCTGCATTGTGGAGCTGACTGAGTACACCGGTGAGGCTGGGGTCTCTGCAGGGGAGGTCACTGGA
ACAGCGAGCAAGGGACTGGTGCCTCGCTGGTGCTGGGTCTCTGGTTTGCTGCAGAGCCGTAGGACACTCCTGGCT
CCTCAGTAGGACAGACAGACGCAGGCGGGTTTATTTTGGAGGGGTACTTGTGGCATTTTCCTGTATTGTCTTGGA
CATGGGATGTGGGGAGGTGGAAATGATGAGCAGTAGCATCATTTCTCCCTGTTGGGTTTTAGCCAGTTTGCCAGC
AAGCGCATCCTAGCAGGGTCCCCGAGCAGCAGGTTGTGTGGATGAAGGGACAGGCACTTGCATCCAGCTGATCTA
GGTCACACCTGGCTCTTGGCTGCCATGTGGCTTATTAACAGCTTCCAGTGGAAGTCGCAATAAACAGTTTTTGGT
AAATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDTVDLTSVLRHVQSLEPDPGTPGSERTEALYY
TDDTAMARALVQSLLAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCRDVFEPARAQFNGKGSYG
NGGAMRVAGISLAYSSVQDVQKFARLSAQLTHASSLGYNGAILQALAVHLALQGESSSEHFLKQLLGHMEDLEGD
AQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVSELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNS
LQRTLIYSISLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILAQSLHRVFQKS

FIGURE 167

CCGTGGCTAGGCGAGTGGGGCGGGGCGGCCGGCACC**<u>ATG</u>**TCGAGGCAGGCGAACCGTGGCACCGAGAGCAAGAAA
ATGAGCTCTGAGCTCTTCACCCTGACCTATGGTGCCCTGGTCACCCAGCTATGTAAGGACTATGAAAATGATGAA
GATGTGAATAAACAGCTGGACAAAATGGGCTTTAACATTGGAGTCCGGCTGATTGAAGATTTCTTGGCTCGGTCA
AATGTTGGGAGGTGCCATGACTTTCGGGAAACTGCGGATGTCATTGCCAAGGTGGCGTTCAAGATGTACTTGGGC
ATCACTCCAAGCATTACTAATTGGAGCCCAGCTGGTGATGAATTCTCCCTCATTTTGGAAAATAACCCCTTGGTG
GACTTTGTGGAACTTCCTGATAACCACTCATCCCTTATTTATTCCAATCTCTTGTGTGGGGTGTTGCGGGGAGCT
TTGGAGATGGTCCAGATGGCTGTGGAGGCCAAGTTTGTCCAGGACACCCTGAAAGGAGACGGTGTGACAGAAATC
CGGATGAGATTCATCAGGCGGATTGAGGACAATCTTCCAGCTGGAGAGGAA**<u>TAA</u>**CCATCCCTACAACTCGAGGAT
AGCCATCAGGAGCACTGTTGGAATCAGCAGGCCTCTGTGCTCCCTCTGCCCTCCAGAACTCAGTGACTCTTGAAC
ATGGATGTTATATATTCTTATAACCTGTTTCCATTCTCCATTCAAATAAAGAGCAGACTGCGATATAGTCCATTT
ACCCCATGTGTGCACATTCAGGAGCGACAGTCTCTGCCCCCATTCCCTTGAGAGGGGCTGGATGTAATCACCTTT
GGTTGGACTAGAAAGAGCTCAAACCATTTTACATTCCTGTTTGAATTTTCCAAAGCAAAACTCACTTTGACCCCA
TTAAGAGGCAAGCCTGGCACATCTATCCCTGGGCCTTTAGAAAGCCATTTGCCTCAAATGGCTATAGGGTTGTGG
GGTGGAGGGAGGAAGGGCTGGGAGGGAGTGGGGAGGAATTGCTAGCTGTAGTGTGACACATTGTAGTGTTTGCCA
GGAAAGGAGCCAGTCATGCCGGAAACACTGACTTCTGGGAAGCCACCCAGGTCTCATTCCTCCCTGCTGTTGGAG
GCAACATCTCCTCTTTTTACAGAGGGTACATCCTTTTTTCTTACAAATTCTTCAATAAAGACACATTCTTGAGTG
AAATCCCTAAAAAAAAA

FIGURE 168

MSRQANRGTESKKMSSELFTLTYGALVTQLCKDYENDEDVNKQLDKMGFNIGVRLIEDFLARSNVGRCHDFRETA
DVIAKVAFKMYLGITPSITNWSPAGDEFSLILENNPLVDFVELPDNHSSLIYSNLLCGVLRGALEMVQMAVEAKF
VQDTLKGDGVTEIRMRFIRRIEDNLPAGEE

FIGURE 169A

ACTTACTATTGGAGGCAGTGGGCAGCGCAGGACAGGCCCAGGGCCGCCGACCCTGGCAATGACTGTCACCAGCTG
GAGGGAAGAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCGGCCAGGGCCAAGGCTCT
AGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTCATCCTTGGTCCCCGTCTGGGCAACTCACC
GGTGCCAAGCATAGTGCAGTGTTTGGCGAGGAAAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCT
GGAGGAGAGGGGGGACCAAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTC
ACTGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACCGCACCTGTGAAAT
CGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGCGCATCTGCCTCGTCCTGGACTGCCTCTG
TGCTCATGACTTCAGCGATAAGACCGCTGACCTCATCAACCTGCAGCACTACGTCATCAAGGAGAAGAGGCTCAG
CGAGAGGGAGACTGTGGTAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGCA
CAGAGACCTGAAGCTGGGGAACATGGTGCTCAACAAGAGGACACATCGGATAACCATCACCAACTTCTGCCTCGG
GAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGAGCCCTGCCTACATCAGTCCCGACGTGCT
CAGCGGCCGGCCGTACCGTGGCAAGCCCAGTGACATGTGGGCCCTGGGCGTGGTGCTCTTCACCATGCTGTATGG
CCAGTTCCCCTTCTACGACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGA
GGATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCCTTGACCCCCAGCAGCGCCTGGC
CGCCGCCGACGTCCTGGAGGCCCTCAGTGCCATCATTGCATCATGGCAGTCCCTGTCATCTCTGAGTGGGCCTTT
GCAAGTGGTTCCTGACATTGATGACCAAATGAGCAATGCGGATAGCTCCCAGGAGGTGAGTTGGGGAGGGCAGAT
GGGCCATTACCCAGCCCCAAGGGACAGGCTTCTGGGGGCAGGCAGGGCAAGGGCAGAGGTGGCAGCTACCCGCAG
GCCACAGAGTTTCCTTGGTCTTCTTCCCCAGCCTTGGGGTGGGAAAGGGAGACTTCAGTCCTCAGCCTGAGCTGC
CTGGGGCCTGCCTTGGGCTTGGTGTAGCTGGAGATCTTTGGCCAGAGAGACCTGTGAGACAGCCGAGCTGGAGCC
AGTGCCCAAGTGGCCCAGGCCAGCCCTCTCAGCTTCCTCCTGCTGCCCAAGTCACATTTCTCTGCCCCCTGACTC
AGAGTTCTCTCTCACCCTTCCTGCTTTTCATTTTTCAGATGATTCATTTCTCCCTATTTCTTTCCTCCCCATTCC
CTGCACTGGAGAAAGTGTTGGGCCTAGGGTGGGGGCAGAGACTTGGGCACCAGGCAGCAGAGGGCAGGTGATCTT
AGGGTGCCCCCTGGAGGGCAGGGCTTGGCCGAGCAACAGCATTGCTGGGCCCTGGATATTGGAAGGACCTTCCCT
CCCTGGCCCACCTTGGAGCTCCACAGTGAGCAGTGTGCAGGTAGGACCAGGAGGGGCCGTGCCTGGGAGAGCCTC
CCAGAGCCTCCTGGCCCCCGAGGAAAGAGAGTTCCAATCCCTACCCACCTCCAGCTTCCACCCTTTAGCTGTTTG
GCTAAAATCATCATCACTAGCCCGCAGTGAGTGCCTACCCCGAGGGCACCTCATTCAGCCCTCACTGCGGGCCTG
CGTGGCCTGTGTTCTTAGCCCCATGTTACAGAAGAGGAAACAGGGTTAGAGAGGACTTTCCCAAAGCCACACAGC
TTAGAAGTAGTGGAGCTAAGCCTTGAACCCAAGTCTCATCCGGAAGCCCTGCTGTCTCCTGTGGTGACTGGCACG
GGGACACCACTTCAGCTTCTGTTACCATCTGCCTAGACCATCCCAGGGAGCTCAGCATGGGGCCCTGCGTATGTG
GCTCCTCCAGGTGCTGCGCCCCCAGCCCAGGGCTTGCTCGTACCTCTTGACGTGCATTAGCCGCCTCAGGGCTCA
GAGAACCTTTGCGAGGGGCCAGACAGCTAAGGCTTCTGAGGTAAAGTGACCTCTCACGCAGCCAGTGAGTTAGGA
AGCATGAGTCTGCGTCAGTCCCGGGTCCGCAGGGCGGCCTGCAAGGGGAGTTGAGGTTGGCTGGAGGGGGTCAGG
GACCCACCCTCAGCGCCACTCCCACCCCCGGCCTTGAGGCCTGAGGGTGTGGTGCCTGGAAGGGTGACTGCAGGA
GCCAGGCTGCCAGCACTCTTGCCTGCCCTCCTGTCTGCTGCGCTGCCTTCATCTGGGTTTATCTTTGTCTCCTTC
CCACCCTCCCCGCCTCAAAGGCGAAGGTGACGGAGGAGTGCTCCCAGTACGAGTTTGAGAACTACATGCGTCAGC
AGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACGCCCGGAGCTGGGTACCCAAGCGGCAGTTCGGCAGCG
CACCACCGGTGCGACGGCTGGGCCACGACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCT
ACCTGCGGAAATAACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCGTGG
CTGTCAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGCAGGGACAGGGACAGCCCA
GGTCACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTTTGGGATGATTGCTCGATTGTTTGGTTTTTAAAT
CTGAGAAGCCTAGATAACTAATCTGCTTTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTC
TCTGGACTGAGCAAGAGGGAGGAGGGAGCCTGCTCACCCCACTCCAGGGCCTTCCCCAGCGGCCACCAACTGACC
TGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGCAGCTCGCTGCAGGCCCCAGAGCGAGCTTCCCCTCC
TCCCTGCTCTCCCAGGCCCCTGCCACAGCCTCTTTCCGTCCCTCTCTTTCTGATCCAGGCCCCTCAGTCCAAGCT
TTGGAAAACCTTCACCTCATCTTAAACCGAACTCAAATATATTTATTTTTTTACCATACCAACTTCTCTCCCATC
TCTAGGTGGCTCAGTCCATGGCCACTCCCTGCCCCCAGCCTGGCTGGACAGCAAGGAATCCACAGCCCACACGTG
AGCTCCCTCCTCACCCCCAGGCAGGGAAGCCCCTCCTGCCAGTCCCTGTCCCCTTTCAGCCCACCAGTCCCTCTC
TGCTGCCGGTGATGGGAGGCCTTTCTAGACCTGGCTCTTTCTCTCCCGTCTCAGTGGCTTCTCTGAGGTGCTGTA

FIGURE 169B

CACGCGCGTTAACCTGTTCCCTTCTCTATCCTTCCCCGTGGTACTGAGCTCACGTGGACTCCCAGTGCGAAGGGG
CCCATGGGTTGGGCTGCAGGCCTGGCCGTGAGCGGGGGCTGCCTGCACGCTCCCCTAGCCTACTCTTGTGTTTAG
GGGATGGTGGGAACATATCCCAGTGCCCTTGCCTCATAATAGATGTGGTGACTCTCCCGGTAGACCCTAGCAAGG
GTCCTCCATGGTGGTGAGGGACTCAGGAGAATTGTAGGGATTGGGGGACCCTGCCTGCCTGGCTTGAGAACAGCC
CTGCTGCCCTTTTGAGCCGAGATTTTGAAGTGGATGCCCGTCTTGCCAGAAATGCTGTTCTCACCAGAATGCCCC
CTCCCCTTGCCCTTACTGGACTTGGCCCTGCCTGATGCCAAGCAAAGACCCTTCCCCAGAGGCCTACCCCCCATA
TGTCCTCAGAGAGGCTGAGTGTCCCCTCCAGGCAGTCATGGGCCCTGAGGCCCCTCCTGCCTGGCCCTGCTCCCC
AGTGGGGAGGTGACTGTGTTTCCCAGAGTGTGAGCCGCTCTCCTCCCCCTAAAAAGCTGACTCACTGTGAGTGAC
CTTGGGCAAGTTCCCAAACCTCCTTGTGCCTCAGTTTCCCCATCTGGAAAAAATGGGGCCACCTCTTGCCAGCAG
TAGCAGGGCTGCCCACGCCCCTTTCTCCCCATGCCCCATCCAGCACTTGGGCGACTCATGCCTCTGCCTCAGTGG
GCCTGTGGGAGCCTACTGGAGCCCAGCACTTACTCCCCCTGAGCAGCGAGCCTGCGTCTGTCTCAGCTGTCCAGC
GCTGAGGGCCAGGGTCTTGTGCTGTGGGGCTGGGGGATGCCCTCTTTTCTATATTTATTTCATAGAAAGTCTCCT
GCGGGAGCGGAAATGCAGTCCGGCCTAGGGCTCCCAGCCCTTGACTGTCCTCCTGTGAGGGCCTGAAGCTGGGCC
AGGGCCCGTCGCAGCGGAGCCCCCTCTCAGCAGCCCACCGGGTCCCTCCAGGCTGCTGCCCGTGCGTGGTCTTTC
TCCTCCTTTTCAAAGCAATAGCCGCCGGGTCTGCAAAGCCCTGTCAGACAGACTGGGCCCTTCCAAGGTCAAGCC
ATGTGTCTGATGACATTCCTGGTGAAGCAAAGGAGAGGAGGATGGGTCAGCCCTCACTGGGTGTCACACACTGAG
AGAAGTCCTATTGTAAAGAAACGGAAAAAGTCACAAAAAAGTTTGTATAAAGACATATTTTTGTACTACATGGGG
ACTCTTCCTGCATGTCAGCAATAAAACTTCCTGATCTGG

FIGURE 170

MKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLARKDGTDDFYQLKILTLEERGD
QGIESQEERQGKMLLHTEYSLLSLLHTQDGVVHHHGLFQDRTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFS
DKTADLINLQHYVIKEKRLSERETVVIFYDVVRVVEALHQKNIVHRDLKLGNMVLNKRTHRITITNFCLGKHLVS
EGDLLKDQRGSPAYISPDVLSGRPYRGKPSDMWALGVVLFTMLYGQFPFYDSIPQELFRKIKAAEYTIPEDGRVS
ENTVCLIRKLLVLDPQQRLAAADVLEALSAIIASWQSLSSLSGPLQVVPDIDDQMSNADSSQEVSWGGQMGHYPA
PRDRLLGAGRARAEVAATRRPQSFLGLLPQPWGGKGRLQSSA

FIGURE 171

ATTGGGACGCTGCGGCCTGGCCTTCAGGCCACTGGCTACCGAACCCCGGGGCTCTTCACCAGTCCAGCTCGTTTC
CAGCACC<u>**ATG**</u>TCGGTGCGGACGCTACCGCTGCTCTTCTTGAACTTGGGCGGGGAGATGCTTTACATCCTCGACCA
ACGGCTGCGGGCCCAGAACATCCCGGGAGACAAGGCCCGCAAAGTTCTGAATGACATCATCTCCACCATGTTCAA
TAGAAAGTTTATGGAGGAATTATTCAAGCCTCAAGAGCTCTACTCCAAGAAGGCCCTGAGGACTGTCTATGAGCG
CCTGGCTCATGCCTCCATTATGAAACTGAACCAGGCCAGCATGGATAAGCTCTATGACCTGATGACCATGGCTTT
CAAATATCAAGTATTGCTGTGTCCCCGACCCAAGGATGTGCTGCTGGTCACTTTCAATCACTTGGATACCATCAA
GGGATTCATCCGAGACTCCCCAACCATCCTGCAGCAAGTGGACGAGACTTTGCGGCAGCTGACAGAAATATATGG
TGGTCTCTCTGCAGGGGAGTTCCAGCTGATCCGGCAGACACTCCTCATCTTCTTCCAAGACCTGCACATCCGAGT
ATCCATGTTTCTAAAGGACAAAGTTCAGAATAATAACGGTCGCTTTGTGTTGCCGGTGTCCGGGCCTGTTCCTTG
GGGAACTGAAGTTCCAGGACTCATCAGAATGTTCAACAACAAAGGTGAAGAAGTGAAGAGGATAGAATTCAAGCA
TGGTGGAAACTATGTCCCTGCACCCAAAGAAGGTTCTTTTGAACTTTATGGAGACCGAGTCCTGAAACTGGGAAC
TAACATGTACAGCGTGAATCAGCCTGTGGAAACTCATGTGTCTGGATCATCAAAGAACTTAGCCTCATGGACCCA
GGAAAGCATTGCTCCAAACCCTCTTGCTAAAGAAGAGCTGAATTTCTTGGCCAGGCTGATGGGAGGGATGGAGAT
TAAGAAACCCAGTGGCCCTGAGCCCAGATTCCGGTTGAATCTCTTTACCACCGATGAAGAAGAGGAACAAGCAGC
GCTAACCAGGCCAGAAGAGTTATCCTATGAAGTTATCAACATACAAGCCACCCAGTCTCTTTTCAGCAATCTGGC
CACCATTCAGGGGGGCCTGACTGGG<u>**TGA**</u>CAGATGAATGGGAAGGTTCTGACCTGTTTTGAGTCCGGCTCCCACCT
TGCTGTCACATATCAGAATGTCACTGCTCTGAGTGTGTCCCAGGGCCTTGGAGGTGGGCCGTGAGGTGCCGAGAA
GCAGCCGCAGCCTCCTCCCTCCACCTATCCCAGAGCGATGCTGGTGATTTCAAACGTATCTGTCCTATCAGTAAA
TAAACAAGATGCAGATCTCTGGT

FIGURE 172

MSVRTLPLLFLNLGGEMLYILDQRLRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALRTVYERLA
HASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVLLVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGL
SAGEFQLIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGTEVPGLIRMFNNKGEEVKRIEFKHGG
NYVPAPKEGSFELYGDRVLKLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNFLARLMGGMEIKK
PSGPEPGFRLNLFTTDEEEEQAALTRPEELSYEVINIQATQSLFSNLATIQGGLTG

FIGURE 173

GAAGCTGGACTGCAGCTGGTTTCAGGAACTTCTCTTGACGAGAAGAGAGACCAAGGAGGCCAAGCAGGGGCTGGG
CCAGAGGTGCCAACATGGGGAAACTGAGGCTCGGCTCGGAAAGGTGAAGTAACTTGTCCAAGATCACAAAGCTGG
TGAACATCAAGTTGGTGCT**ATG**GCAAGGCTGGGAAACTGCAGCCTGACTTGGGCTGCCCTGATCATCCTGCTGCT
CCCCGGAAGTCTGGAGGAGTGCGGGCACATCAGTGTCTCAGCCCCCATCGTCCACCTGGGGGATCCCATCACAGC
CTCCTGCATCATCAAGCAGAACTGCAGCCATCTGGACCCGGAGCCACAGATTCTGTGGAGACTGGGAGCAGAGCT
TCAGCCCGGGGGCAGGCAGCAGCGTCTGTCTGATGGGACCCAGGAATCTATCATCACCCTGCCCCACCTCAACCA
CACTCAGGCCTTTCTCTCCTGCTGCCTGAACTGGGGCAACAGCCTGCAGATCCTGGACCAGGTTGAGCTGCGCGC
AGGCTACCCTCCAGCCATACCCCACAACCTCTCCTGCCTCATGAACCTCACAACCAGCAGCCTCATCTGCCAGTG
GGAGCCAGGACCTGAGACCCACCTACCCACCAGCTTCACTCTGAAGAGTTTCAAGAGCCGGGGCAACTGTCAGAC
CCAAGGGGACTCCATCCTGGACTGCGTGCCCAAGGACGGGCAGAGCCACTGCTGCATCCCACGCAAACACCTGCT
GTTGTACCAGAATATGGGCATCTGGGTGCAGGCAGAGAATGCGCTGGGGACCAGCATGTCCCCACAACTGTGTCT
TGATCCCATGGATGTTGTGAAACTGGAGCCCCCCATGCTGCGGACCATGGACCCCAGCCCTGAAGCGGCCCCTCC
CCAGGCAGGCTGCCTACAGCTGTGCTGGGAGCCATGGCAGCCAGGCCTGCACATAAATCAGAAGTGTGAGCTGCG
CCACAAGCCGCAGCGTGGAGAAGCCAGCTGGGCACTGGTGGGCCCCCTCCCCTTGGAGGCCCTTCAGTATGAGCT
CTGCGGGCTCCTCCCAGCCACGGCCTACACCCTGCAGATACGCTGCATCCGCTGGCCCCTGCCTGGCCACTGGAG
CGACTGGAGCCCCAGCCTGGAGCTGAGAACTACCGAACGGGCCCCCACTGTCAGACTGGACACATGGTGGCGGCA
GAGGCAGCTGGACCCCAGGACAGTGCAGCTGTTCTGGAAGCCAGTGCCCCTGGAGGAAGACAGCGGACGGATCCA
AGGTTATGTGGTTTCTTGGAGACCCTCAGGCCAGGCTGGGGCCATCCTGCCCCTCTGCAACACCACAGAGCTCAG
CTGCACCTTCCACCTGCCTTCAGAAGCCCAGGAGGTGGCCCTTGTGGCCTATAACTCAGCCGGGACCTCTCGCCC
CACCCCGGTGGTCTTCTCAGAAAGCAGAGGCCCAGCTCTGACCAGACTCCATGCCATGGCCCGAGACCCTCACAG
CCTCTGGGTAGGCTGGGAGCCCCCCAATCCATGGCCTCAGGGCTATGTGATTGAGTGGGGCCTGGGCCCCCCAG
CGCGAGCAATAGCAACAAGACCTGGAGGATGGAACAGAATGGGAGAGCCACGGGGTTTCTGCTGAAGGAGAACAT
CAGGCCCTTTCAGCTCTATGAGATCATCGTGACTCCCTTGTACCAGGACACCATGGGACCCTCCCAGCATGTCTA
TGCCTACTCTCAAGAAATGGCTCCCTCCCATGCCCCAGAGCTGCATCTAAAGCACATTGGCAAGACCTGGGCACA
GCTGGAGTGGGTGCCTGAGCCCCCTGAGCTGGGGAAGAGCCCCCTTACCCACTACACCATCTTCTGGACCAACGC
TCAGAACCAGTCCTTCTCCGCCATCCTGAATGCCTCCTCCCGTGGCTTTGTCCTCCATGGCCTGGAGCCCGCCAG
TCTGTATCACATCCACCTCATGGCTGCCAGCCAGGCTGGGGCCACCAACAGTACAGTCCTCACCCTGATGACCTT
GACCCCAGAGGGGTCGGAGCTACACATCATCCTGGGCCTGTTCGGCCTCCTGCTGTTGCTCACCTGCCTCTGTGG
AACTGCCTGGCTCTGTTGCAGCCCCAACAGGAAGAATCCCCTCTGGCCAAGTGTCCCAGACCCAGCTCACAGCAG
CCTGGGCTCCTGGGTGCCCACAATCATGGAGGAGGATGCCTTCCAGCTGCCCGGCCTTGGCACGCCACCCATCAC
CAAGCTCACAGTGCTGGAGGAGGATGAAAAGAAGCCGGTGCCCTGGGAGTCCCATAACAGCTCAGAGACCTGTGG
CCTCCCCACTCTGGTCCAGACCTATGTGCTCCAGGGGGACCCAAGAGCAGTTTCCACCCAGCCCCAATCCCAGTC
TGGCACCAGCGATCAGGTCCTTTATGGGCAGCTGCTGGGCAGCCCCACAAGCCCAGGGCCAGGGCACTATCTCCG
CTGTGACTCCACTCAGCCCCTCTTGGCGGGCCTCACCCCCAGCCCCAAGTCCTATGAGAACCTCTGGTTCCAGGC
CAGCCCCTTGGGGACCCTGGTAACCCCAGCCCCAAGCCAGGAGGACGACTGTGTCTTTGGGCCACTGCTCAACTT
CCCCCTCCTGCAGGGGATCCGGGTCCATGGGATGGAGGCGCTGGGGAGCTTC**TAG**GGCTTCCTGGGGTTCCCTTC
TTGGGCCTGCCTCTTAAAGGCCTGAGCTAGCTGGAGAAGAGGGGAGGGTCCATAAGCCCATGACTAAAAACTACC
CCAGCCCAGGCTCTCACCATCTCCAGTCACCAGCATCTCCCTCTCCTCCCAATCTCCATAGGCTGGGCCTCCCAG
GCGATCTGCATACTTTAAGGACCAGATCATGCTCCATCCAGCCCCACCCAATGGCCTTTTGTGCTTGTTTCCTAT
AACTTCAGTATTGTAAAC

FIGURE 174

MARLGNCSLTWAALIIILLLPGSLEECGHISVSAPIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQ
QRLSDGTQESIITLPHLNHTQAFLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEPGPET
HLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVV
KLEPPMLRTMDPSPEAAPPQAGCLQLCWEPWQPGLHINQKCELRHKPQRGEASWALVGPLPLEALQYELCGLLPA
TAYTLQIRCIRWPLPGHWSDWSPSLELRTTERAPTVRLDTWWRQRQLDPRTVQLFWKPVPLEEDSGRIQGYVVSW
RPSGQAGAILPLCNTTELSCTFHLPSEAQEVALVAYNSAGTSRPTPVVFSESRGPALTRLHAMARDPHSLWVGWE
PPNPWPQGYVIEWGLGPPSASNSNKTWRMEQNGRATGFLLKENIRPFQLYEIIVTPLYQDTMGPSQHVYAYSQEM
APSHAPELHLKHIGKTWAQLEWVPEPPELGKSPLTHYTIFWTNAQNQSFSAILNASSRGFVLHGLEPASLYHIHL
MAASQAGATNSTVLTLMTLTPEGSELHIILGLFGLLLLLTCLCGTAWLCCSPNRKNPLWPSVPDPAHSSLGSWVP
TIMEEDAFQLPGLGTPPITKLTVLEEDEKKPVPWESHNSSETCGLPTLVQTYVLQGDPRAVSTQPQSQSGTSDQV
LYGQLLGSPTSPGPGHYLRCDSTQPLLAGLTPSPKSYENLWFQASPLGTLVTPAPSQEDDCVFGPLLNFPLLQGI
RVHGMEALGSF

FIGURE 175

GGGTCGCGCGGAGATTGCTGGGCGGTTCTTGCCGGAAGCGGAGAGCGGCTGATCGCAGTCCGGAGGTGAGGCGGA
ACTCTGAGGCAGATATCCTCCCTTTCCTCCTCGGCTGCTGCTCTTACTTTGACAAGCCAGGCTAACATTGAAGGT
GGTCCATTATGGCTGACATGCAAAATCTGGTAGAAAGATTGGAGAGGGCAGTGGGCCGCCTGGAGGCAGTATCTC
ATACCTCTGACATGCACCGTGGGTATGCAGACAGTCCTTCAAAAGCAGGAGCAGCTCCATATGTGCAGGCATTTG
ACTCGCTGCTTGCTGGTCCTGTGGCAGAGTACTTGAAGATCAGTAAAGAGATTGGGGGAGACGTGCAGAAACATG
CGGAGATGGTCCACACAGGTTTGAAGTTGGAGCGAGCTCTGTTGGTTACAGCTTCTCAGTGTCAACAGCCAGCAG
AAAATAAGCTTTCCGATTTGTTGGCACCCATCTCAGAGCAGATCAAAGAAGTGATAACCTTTCGGGAGAAGAACC
GAGGCAGCAAGTTGTTTAATCACCTGTCAGCTGTCAGCGAAAGTATCCAGGCCCTGGGCTGGGTGGCTATGGCTC
CCAAGCCTGGCCCTTATGTGAAAGAAATGAATGATGCCGCCATGTTTTATACAAACCGAGTCCTCAAAGAGTACA
AAGATGTGGATAAGAAGCATGTAGACTGGGTCAAAGCTTATTTAAGTATATGGACAGAGCTGCAGGCTTACATTA
AGGAGTTCCATACCACCGGACTGGCCTGGAGCAAAACGGGGCCTGTGGCAAAAGAACTGAGCGGACTGCCATCTG
GACCCTCTGCCGGATCATGTCCTCCTCCCCCTCCACCATGCCCCCCTCCTCCCCCAGTCTCTACCATTTCATGCT
CATATGAGTCTGCTTCCCGCTCATCACTGTTCGCGCAGATTAATCAGGGGGAGAGCATTACACATGCCCTGAAAC
ATGTATCTGATGACATGAAGACTCACAAGAACCCTGCCCTGAAGGCTCAGAGTGGTCCAGTACGCAGTGGCCCCA
AACCATTCTCTGCACCTAAACCCCAAACCAGCCCATCCCCCAAACGAGCCACAAAGAAGGAGCCAGCTGTACTTG
AACTGGAGGGCAAGAAGTGGAGAGTGGAAAATCAGGAAAATGTTTCCAACCTGGTGATTGAGGACACAGAGCTGA
AACAGGTGGCTTACATATACAAGTGTGTCAACACGACATTGCAAATCAAGGGCAAAATTAACTCCATTACAGTAG
ATAACTGTAAGAAACTTGGCCTGGTATTCGATGACGTGGTGGGCATTGTGGAGATAATCAACAGTAAGGATGTCA
AAGTTCAGGTAATGGGTAAAGTGCCAACCATATCCATCAACAAAACAGATGGCTGCCATGCTTACCTGAGCAAGA
ATTCCCTGGATTGTGAAATAGTCAGTGCCAAATCTTCCGAGATGAATGTCCTCATTCCTACAGAAGGCGGTGACT
TTAATGAATTCCCAGTTCCTGAGCAGTTCAAGACCCTATGGAACGGGCAGAAGTTGGTCACCACAGTGACAGAAA
TTGCTGGATAAGCGAAGTGCCACTGGGTTCTTTGCCCTCCCTTCACACCATGGGATAAATCTGTATCAAGACGGT
TCTTTTCTAGATTTCCTCTACCTTTTTGCTCTTAAAACTGCTTCTCTGCTCTGAGAAGCACAGCTACCTGCCTTC
ACTGAAATATACCTCAGGCTGAAATTTGGGGTGGGATAGCAGGTCAGTTGATCTTCTGCAGGAAGGTGCAGCTTT
TCCATATCAGCTCAACCACGCCGCCAGTCCATTCTTAAGGAACTGCCGACTAGGACTGATGATGCATTTTAGCTT
TGAGCTTTTGGGGGTTATTCTACCAACAAACAGTCCATTGGAAAGAAAACAGTCCCTGGAATTAACAGATCAGAA
TGTTCACACTGGTTAATCTTTTTTAACAATGAGCATGAAGGTAGCAGAAGCTGGTGTGTTTCCAGATGGTTCTT
CTAACCAAACTAATTTTTCACTGTTGACAAGCGAGGCAAGGGTTGCACTGGACCAAAGGCTGAGGCTTGGCCATC
TAGCATTCCATACAAAATTGTTTCCTATAAGCATTCCTTTTATTCTCTATTCTATCCTGGGTCTGCCTCAACCGT
GAGATAGGAGAGTCTCTGGTACTAGCTGCTGTAGCAGTGCCCTTCATCCAGGGCAGTTAATGGAGTCTTGGACCC
TTTCTTTCTCTGGGATCCCTGCCCAGCACCTTCCTATAGAGATGACTTTAAAAGGAAAAAAAAAAAAAAAAAAAC
CCACATGATTTCAAGGAGTCTGGCATTCCTGAATCCTTCTTCCCTGCCAGGTGCCTGTCACCTGTCTTCACTGCC
TCCTTTTCCCTGTCATGCTCATCAGCTTATGGCTTCTGTCTAAGCACCTGAACAGAGGACTGAAACCTCCACTGC
AGGCTGGTTTTAGGTCTTGAATTATGTAAGAATCTTGCACAGCACTGCTAATGTAAATTTCAGTTGTTTTTCCCT
CTAGGACAAACACTTACCAAAATATGCAACTTTTTTTTGGTGGGAAGAGAGATTGTCCTGTGATTTCTACCCATT
TCCTGAGGCCTGTGGAAATAAACCTTTATGTACTTAAAGTTATACAGAAAATAGAATAAAGTTAATACCAAACTT
G

FIGURE 176

CCGGAGTCTCGCGCCCGCGGTCATGTGACACAGCGAAG**ATG**GCGTCGCCCGGCTGCCTGTGGCTCTTGGCTGTGG
CTCTCCTGCCATGGACCTGCGCTTCTCGGGCGCTGCAGCATCTGGACCCGCCGGCGCCGCTGCCGTTGGTGATCT
GGCATGGGATGGGAGACAGCTGTTGCAATCCCTTAAGCATGGGTGCTATTAAAAAAATGGTGGAGAAGAAAATAC
CTGGAATTTACGTCTTATCTTTAGAGATTGGGAAGACCCTGATGGAGGACGTGGAGAACAGCTTCTTCTTGAATG
TCAATTCCCAAGTAACAACAGTGTGTCAGGCACTTGCTAAGGATCCTAAATTGCAGCAAGGCTACAATGCTATGG
GATTCTCCCAGGGAGGCCAATTTCTGAGGGCAGTGGCTCAGAGATGCCCTTCACCTCCCATGATCAATCTGATCT
CGGTTGGGGGACAACATCAAGGTGTTTTTGGACTCCCTCGATGCCCAGGAGAGAGCTCTCACATCTGTGACTTCA
TCCGAAAAACACTGAATGCTGGGGCGTACTCCAAAGTTGTTCAGGAACGCCTCGTGCAAGCCGAATACTGGCATG
ACCCCATAAAGGAGGATGTGTATCGCAACCACAGCATCTTCTTGGCAGATATAAATCAGGAGCGGGGTATCAATG
AGTCCTACAAGAAAAACCTGATGGCCCTGAAGAAGTTTGTGATGGTGAAATTCCTCAATGATTCCATTGTGGACC
CTGTAGATTCGGAGTGGTTTGGATTTTACAGAAGTGGCCAAGCCAAGGAAACCATTCCCTTACAGGAGACCTCCC
TGTACACACAGGACCGCCTGGGGCTAAAGGAAATGGACAATGCAGGACAGCTAGTGTTTCTGGCTACAGAAGGGG
ACCATCTTCAGTTGTCTGAAGAATGGTTTTATGCCCACATCATACCATTCCTTGGA**TGA**AACCCGTATAGTTCAC
AATAGAGCTCAGGGAGCCCCTAACTCTTCCAAACCACATGGGAGACAGTTTCCTTCATGCCCAAGCCTGAGCTCA
GATCCAGCTTGCAACTAATCCTTCTATCATCTAACATGCCCTACTTGGAAAGATCTAAGATCTGAATCTTATCCT
TTGCCATCTTCTGTTACCATATGGTGTTGAATGCAAGTTTAATTACCATGGAGATTGTTTTACAAACTTTTGATG
TGGTCAAGTTCAGTTTTAGAAAAGGGAGTCTGTTCCAGATCAGTGCCAGAACTGTGCCCAGGCCCAAAGGAGACA
ACTAACTAAAGTAGTGAGATAGATTCTAAGGGCAAACATTTTTCCAAGTCTTGCCATATTTCAAGCAAAGAGGTG
CCCAGGCCTGAGGTACTCACATAAATGCTTTGTTTTGCTGGTGATTTAACCAGTGCTTGGAAAAATCTTGCTTGG
CTATTTCTGCATCATTTCTTAAGGCTGCCTTCCTCTCTCAGTACGTTGCCCTCTGTGCTATCATCTTATCATCAA
TTATTAGACAAATCCCACTGGCCTACAGTCTTGCTTCTGCAGCACCCACTTTGTCTCCTCAGGTAGTGATGAATT
AGTTGCTGTCACAAAAGGAGGGAAGTAGCACCCAAATTAAGTTGCTTAAGAGAGGAAATGTACATCTTGTATAAC
TTAGGGAGCGAAGAAAATGTAGGCGCGAAAGTGAAAAGTGAGGCAGCTAGTTCTTCCTATTCCATTCTCGACCAA
CCTGCCCTTTCTTAATATGACTAGTGGTCTTGATGCTAGAGTCAACTTACTCTGTTGCTGGCTTTAGCAGAGAAT
AGGAGGAACCATATGAAAAAGATCAGGCTTTCTGACTTCCATCCCCAAAACACATTTACCAGCATACTCCAAACT
GTTTCTGATGTGTTCCATGAGAAAAGGATTGTTTGCTCAAAAAGCTTGGAAAATACTACACACTCCCTTTCTCCT
TCTGGAGATCAACCCACATTAGAGTGTCTAAGGACTCCTGAGAATTCCTGTTACAGTAAACAAAACTAACGTAAT
CTACCATTTCCTACACTATTTGAGCATGGAAATCATAGTCCCCACTCTGTGAAAACTTAACGCTTTTTGGAAGAC
ATTTCTGTAGCATGTCAGTTTGGAGAAATGATGAGCTACGCCTTGATGAAAGAACCGTGTTGGTGCTGCTAAGTT
TAGCCATTATGGTTTTTCCTTTCTCTCTCTTAAGCCTTATTCTTCAACTAAAAGATGAGGATTAAGAGCAAGAAG
TTGGGGGGGATGTGAAAATAATTTTATGAGGTTGTCTAAAAT

FIGURE 177

MASPGCLWLLAVALLPWTCASRALQHLDPPAPLPLVIWHGMGDSCCNPLSMGAIKKMVEKKIPGIYVLSLEIGKT
LMEDVENSFFLNVNSQVTTVCQALAKDPKLQQGYNAMGFSQGGQFLRAVAQRCPSPPMINLISVGGQHQGVFGLP
RCPGESSHICDFIRKTLNAGAYSKVVQERLVQAEYWHDPIKEDVYRNHSIFLADINQERGINESYKKNLMALKKF
VMVKFLNDSIVDPVDSEWFGFYRSGQAKETIPLQETSLYTQDRLGLKEMDNAGQLVFLATEGDHLQLSEEWFYAH
IIPFLG

FIGURE 178

CCTTACGGCCAGAAACGCCACCTTCCAGTAATTCGCCAAA**ATG**ACAAACACAAAGGGAAAGAGGAGAGGCACCCG
ATACATGTTCTCTAGGCCTTTTAGAAAACATGGAGTTGTTCCTTTGGCCATGTATATGCGAATCTATAAGAAAGG
TGATATTGTAGACATCAAGGGAATGGGTACTGTTCAAAAAGGAATGTCCCACAAGTGTTACCATGGCAAAACTGG
AAGAGTCTACAATGTTCCCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAA
GAGAATTAATGTGTGTATTGAGCACATTAAGCACTCTAAAAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAA
TGATCCTCCACCCAGAGAAGCACAGTGTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAAACTATTCCCTA
TGAATTCATGGCA**TAA**TAGGTGTT

FIGURE 179

MTNTKGKRRGTRYMFSRPFRKHGVVPLAMYMRIYKKGDIVDIKGMGTVQKGMSHKCYHGKTGRVYNVPQHAVGIV
VNKQVKGKILAKRINVCIEHIKHSKSRDSFLKRVKENDPPPREAQCVRTNGKEPELLETIPYEFMA

FIGURE 180A

CGGACGCGTGGGCTGCTGCGGAGCCGGCAGCGCAGGCGGGCGGAGCGGAGCTGCCCCCGTGGTGGCGGGCGATGC
CCCCGTGAGCCTCCCTCGCCGCCCCTCCCCGCCCCGCGTGCCTATCCACTCGGAGTCCGCGCCAGCCTGGGGCCG
GGCCGCGCCTACTGCCGGGTTCGCGGGGCGGGGTCCCGGGGCAGCACCTGCCCCGCCTTGCGGAGCCGCCTCGGC
CTGTGGAGGCCCCCTCCCTGTCTGGACCCCGGCCCCACCTCCGGACCCTTTTATCACATCGCCTCCTCTGGGAGC
CTGCCCTGATTGCCTTCACCTCATTTCTTGAAAATTGGTGTTTTGGCAGAAGTCAATTGAAGCCTTGTGCAAATG
CCCTAGGGGTGTGCTGTTGGGAGGCAGCCCCCTGTGATGCGGAACACCAGGCTCAGATTCATCAGTTCGAGCTGC
CTGAGGCCCTGCCACCCCGGGGACC**ATG**TTTAACGGGGAGCCAGGTCCTGCCTCATCTGGGGCCTCCAGGAATGT
GGTGCGGAGCTCCAGCATTGGCGGTGAAATCTGCGGATCCCAGCAAGCCGGGGGCGGGGCTGGGACCACCACCGC
CAAGAAGCGGCGGAGCAGCCTGGGTGCCAAGATGGTGGCCATCGTGGGCCTGACTCAGTGGAGCAAGAGCACACT
CCAGCTTCCGCAGCCTGAAGGGGCCACCAAGAAGCTGCGCAGCAACATCCGCCGGAGCACGGAGACAGGCATCGC
GGTGGAGATGCGGAGCCGGGTCACACGCCAGGGCAGCCGGGAGTCCACCGATGGGAGCACCAACAGCAACAGCTC
CGACGGCACGTTCATCTTCCCCACTACCCGGCTAGGGGCTGAAAGCCAGTTCAGCGATTTCCTGGATGGGCTGGG
ACCAGCTCAGATTGTGGGGCGACAGACACTGGCAACACCACCCATGGGAGATGTGCACATTGCCATCATGGACCG
GAGTGGCCAGCTGGAGGTGGAAGTGATTGAAGCTCGGGGCCTGACCCCCAAACCAGGCTCCAAATCCCTCCCAGC
CACCTATATCAAGGTTTACCTGCTGGAGAATGGGGCCTGCTTGGCCAAGAAGAAGACAAAGATGACCAAGAAGAC
CTGTGATCCCCTGTACCAGCAGGCTCTGCTCTTTGACGAGGGACCCCAGGGCAAGGTGCTGCAGGTGATCGTCTG
GGGAGACTATGGCCGCATGGACCACAAGTGCTTCATGGGCATGGCCCAGATCATGCTGGACGAGCTGGACCTCAG
CGCCGCGGTCACCGGCTGGTACAAACTCTTCCCCACCTCCTCAGTGGCAGACTCCACACTCGGATCCCTCACCAG
GCGCCTGTCCCAGTCTTCCCTGGAGAGTGCCACCAGCCCCTCATGCTCT**TAA**GGATGTCAGGAAGAGGCCAGGAT
GGTGGTGTGGGGAGGGGTGCCTGCTGGCCCCATGTCCTCCCCTGTACATAGTCTTCGTGTCTTTCTGGACCCCTT
GTCCTGCTGCATGCCTGTTGGCTACTGGGCTCATCCCAGCTGGCAGTGGAGACTGTAGTGTGTGCGTGTGTGCGT
GCGTGTGTGTGTGTGTGTACGTGACCACGTTCTATCTGTTCATTTGTCTGGGTATAGTCACTCCTGGTGATGATA
TGGGCTGAAATGTCTCCACGTCTCTTTGTGTCTTGTTGAAAAGAAACCCAAAGGAGTGTTGTGTGGACATGACTC
ACCCTGAGGAGTCTCCAGGGATGGAGGTGGGGCATGCGGCCACTGGTCGGTGCTGCCTGGTCCTGGCCTGGGGCA
GAGCCTGTGTGTTCTTCACCTGTGCCTGCTCCTGGTGGTCTCTGCTTTGTTTTCTGTCTTGTCTTTTGTTCCACT
CTTGACTCTCCCGGCTCTGCCACTGTTTTCTGAGAAATGTAGCATCCGCTGCAGCTGGCCACACTGAGGGCCCTC
TGGGAACCCCACCCCACTGGAGCCGCTCCGGCAGCTCTTCCTGCCACTGAATGCGTTCTGCAGCATGTAGCATGC
CCACCTAGCTCCCTGGCCAGGGCCCTGGGGAGGCAGAGGGTACCCAGGGGACTGAGGGCTTAGAAATGACTTTCT
CTATGAGGCTGGAACCTCCTCCTTCTTCCAGTGAAGCACGAGGTCTTGGTTCCAGGGTTCCTGGCCAGGTGCCCC
CTTAGCATTTGTTCTTCATCTCCTGTCTCTTCAAGCCTCCCCACTCCACCGTGCCGAAGGAGCTCTGCCAGTGGG
CCTGGGCAGGCAGCCACAGAGGGCATGTTATCTGCTAAAGCAAACAGTCCTCCTGAGGCCCTGAGGGTGGCCCTG
ACCCCCTCAGGGCTCATTCCTGGTGGGCATGACTCGGTAAGGAGGTTCTGTGGGTAGGGCTGTTTGCTGGAATAA
GGAGGGCTGAGGCTGAGTTGTTCCCCGCCACTGTTGAGGATCCCATCTGACATTTGGGGATTCACTGCATGAAGT
TGTTCATTTGGGGCTCCAGTTTTTGTGCATTTCCAGACCAGGGTCCCTGTCTGGGAGCTCAGACTTAGCTGGGCT
CCAGCAGCCTGGCTCCGGACTCTCGTCTGCCACCATCACCAGCTCTGTCTAAGCAATACTTACCCCTCCGGGCTT
CCCTGCTTTCCTGTGCCCCACTGCTGCCCTCTGCAGAGCCATCTGCTCCAGGCACCCACCTGCCTCTGCTTGCTT
TCTCACCCATGTCTGGTTGGAGCTTCTCACAGCCACTCAAACCCTGACTTGATTTGACAACTGGGCCCTGTTGGT
GGAGACCAGTGCCTGAACTGGACCCTGTGAAATCTGTCCCGTGGGAATCCTGAAGTCTGACTCAGGAATGCCCAG
ACCTGTCCCTGTCCCTCCTCAGCTCTAGGGTGAAAGGCGAGAGGTTGCACAGGACATGGACAGAGCAGCCCTTGG
GTTTGTATCTGGTAGGGGAGAAAGCAGCAGGACAGTGGAGGTGTGTGGAAGGCACTCTTTCCACCTCTCTCCAGG
CATTATCCCCAGGTGCTGAAATGGCTGTGGCCCCAGCACCTGAGGCAGGGGTACGCTACCTGGGGTAGCAGTAGA
AAGGTCTTGGGGTCTGAATGACTTGGGGCCTCCATTCATAACCAAAGTTGTAGGGGCATGGAGGCAGTGGCGCCT
TATGGATAGGTCATCTCAGCCCAAAGGGCCTCCTTGGCTGGCATGGTTCTGTGTTACGTTGAAGCCAGAGTCTTA
TAACACCTCCCAAGAAAAGATAGGGGAAGAAGCCAGAACCCCACCTGGCCTGCCCACAGGACAAGAAGTGGGTAAG
GGCAGGAAGGAAATGAACGGAGTTAGCTCCCAGGCTCCTATCTCTGCCTGAGCCTCTATTCTTATATTATCAGAG
AAAGGGACCATTGGGTGCATAGAGATGGGGAGGAGGCCACTGGGCTGAATTTTCTCTTTAGGCGGAAATGCTCTC
CCCAGGCCCATTGCGTTCGTCAAGTTCTTGGAAATGGACAAAGGGCTCTGTCCTCCTCGACCCTAGTGGGGGATC
AAGAAGGAAACTCCGTTGCAAAAGGGTATTTTAATCTCCTGTTTATGATATATTCACCTCTAGAGCAGTCACTGT

FIGURE 180B

CAGGGTGTTGCGAAAATACTCTACACCTTTGGGATGATAGGGTTGTTAGTGACCCACAGGACAGTATAGATGTTT
GTGGATGTAGCACTGAGTGGTGATACCCAGACCAGCAGTCACCCCAGGAAGTGGGGGCTACCCATACCCTCATTC
CTCTGGTGGGGAGCTGCCTGCAGAGAGGCCTGCCACTGGGGGTTCCAGGCCGTGGTGACCCTTGCCTCTGGGGAA
GGGTTAGCACAGGGGAGGTTCTAGCTGGAGGAGGGGTCTGATGTGCTGGTAACTTGGGCTGACCTACCTACAGTC
CCTGGCTGCCAAAACTGCTCAGCAGTTGGGCCACTCCACTATTCCACCTCTCTAAAAGAAGGTAATTTCCTCCCC
AAATTGACCTTGGGGAATTATTCTTTAACCCTTTGCACCAAATAAGTTACTCATCCCCACCTGGATTTTACCCC
ATGAGGGTAAAGTTGTGTGAGGCTGACACGTCTGTGTGATGCAGTGTGGCTGCACTTAAGGGTCTGTTTCTCAGC
ATCATGGATGCAGGGGCTTGTCTGAAAAGCCACTCTGGACCTAGCCTGTCCCAGAAGAGGAGAATGCACAAGTGT
AACTCCTGGTTGTTTGCTGGGGTGGGGGAGCATCTGCTGTTTGAGGACGGGGGGTGGGGAAGGAAGGAACATGAT
CCCTCCAGAAGTCTCCCACCCTGGGGCCAACTCACTGCCATGTTCAGTGTCCCGGCTCCAAATGCCCCCTTGCCC
AGATGAAACCCTGCAGTGGTTACAGGAATGGAGCTCTTTGTCATTCCACCTCCTCTGGTCAGGCGAGGTTCACTG
TGCATATGGCAGAGACAGGAGTGGCCCTGCAGTGATGTTGGGTTGTGGGCAGGGACAGTGATGGATGACTCAGAG
CGTCTGTCTTTGTATTTCTGCTCTGTTCATTCTGTCCCACTTTCTTCATAGACTCCTTTTCCCTGCAATGGGTTT
TTGGTATGAAAAAGGCTCCAGTAAATGGAGCCAAGTCTTGGTTTGACAAGGGGAACTTGATCCTTCAGGGAAGAA
TCATCTCCAAAATGACTCCCCATCTGGTTTCTTCTACCACCCAATTCTACTAGGAAAGGAGCACTTAGGAGGCTC
TTGGGATGCAGCAAGTCCCAGGCAATGCCAGCATTTCATGGGGGCTGAGGCAGAACCCAGGAGCTCCAAGAAAGG
CCACCCATAGAGCTCATCCTCTGTGGAATCACTGCCGGTTAGAACACTGAGGTCAAGCCAGTCCTCCCATGGTCA
TGCCACCCACCAGGGAAGCATGCCTGATCTCTTCTTTACTGCCAGCCTTGAGGAGAGCAGAAGCCTCCATTTTTA
AAGACAATAAAGACCTCCAAGGGTACTTCTTTGGAAATGAAATGTAGCACAATCTTAGCCTACGTTACCAGGAGC
CCTGACATGCAACCAGGGTCCCTCTTCCATGCCCTGCTGCCCAGGAGTTGCTGAGCTCCTCTTCCCCTGGGGTTC
CAGCCCTCCTAATACCTCATATTCCCCATCTTCCTCAGCCCAGAAAGCAATGGGGCTTTAGTGATGCTCCTCTTT
TGTGTCTCTCTGGTTGCCTCTAGCACTGTGCAAACTCTGCAAGAAATTGCTGCCTTTGCTTGATGTTGTAGATGA
GTTGCCCTCCACCTGGCTGGAGAGATGGCACATCATTCAGGGCCAGAAGGTTGTCCAGCAGTGTTTCTGCAGTGG
CTGCAGGGAGATGGAAAAGAAGAGCCCTGCTTCCCTGCCTCCTCCTACCTTTCTCTTCCACTCCTCAGAGTTTTC
TTCTCCAGTATCCTGACATGTAAAGAGATTCTTTAAAATGCTGCTTCTTCTACTGGACTGTCTTTCACTGAGTAG
TCAGGGAGGAGATGAAAATGTGGACACATCCCCCCGCCTTCTCCCTCAACCTTTTCACTCACGTCAGAAGAGGTT
GGGGCAAAACAAAACAAGCATGATTGAAGAGCAGGGGAAGCCCACACAATCAGGTGAGCCCTGATGGGGGCTGGA
CTGGCCTGGTCTGGCTGGGAAAGGATTCTTTTAAAAGCGTGCCTGAGCATCTCAGAGCAATGTCAGTGATGCCAA
AGAGAGCAACTTGGCCTCCTTGGGCACCAACTCTGATGGCTGAGTTGCACAAACGTGGCTCAGATGTTGGCATGC
CCGATGGTGGGACCTTGTTCTCTGATAAAGGGCTTAATCTTTCCATGTAGCAAAGCAACTTTCCCTCCCTCCCCT
CCCCCCGAACCCTGAGCTTGGGCTTGTGTGGGCCCAGCATGGCTGTGCCTGTGAGGGAAGCCACATCAGTGAGAG
AAAGTTGCATTCTCTCAGGGGCCTAGATTGGCTTGGGGCAGGTGCTTGTTGAAAAGCATGAGTGTTTCTGCTTTG
GGAAACCCTTCCAGGGCTCTGGTTGGAAACTTGGCCAGTAAGGACAGGGCCTTGGGCCTCCCAAGGAGTTCACAA
TGATGCCAGGAAGGGTCCCTGAGCCTGGGTTCCAGTCAGCTTGGCTAACAGAATGGGGCTTGGGAATTCCAGGGG
CAACTGAGCATCCACCCCATTAGCCAGTGATCTGGACAGGGACAGCTGGCTACAGGGAATCAAAGGCTGTTCTGT
ACAGTTTTACCAGAAACTGTGACCTTGGGTAAGGCTCCTCACTTTTCTGGGCCTCAACTTCCTCATCTGCAAAAT
CAGAGCATTAGCTGCTCTCCCCATGATTCCCTCCCAGTTTTAATTAAAAGTCTCTGATCTGGAGCACATGAGGGT
TGCGAGCCTGGTGCACCTGGTTCCTGTCTCCGTGGGCTGGTTTCCTTCAGCCCCTGATGCCCAGGCTGGGTGCAG
GCTCTCATCTGGTCCATGCCCAGATGCTGCCTCAGACAAGAACTCTGGGAATCCTAACAGACTCTGCTTTCCTCT
CTTCGTGGTTTGTCCTCCCTCTTTTATTCTTGTGTAATGATGAGACATAATTAAGGGTCATCTACAATGGACAAT
TTTCAAGGTGCTGATGTGATGTCACAACCTCCGCTACATCCTGAGTAAGTCAGTGTCCCCAACAGCAGATGAGGC
TGGGTCTTTCCTCATTTCTGCTTCTGGGATGACATCAGTGGGAGAGTTGAAGATCTGAGAATTCTAAAGGAAATG
TTCTCTGATGGGAGGAGAGAGGGAACTTATTTCCCTTCAAAGTAGTTTGCTTCTTAAGACCACTCCTCCCTCCAG
AATGTCTTTAACCAGACATCATTTCAGAAGGTGGGGCAGCTGCTTCCTTAGGAAGAGTGGGCCTGATAGCTCAAC
CAACTCCTTTAGCATGTAAACTCACAGAAGGCAAGAACCCCTTTTTTTAGACTTTCCAAATGCATCCTGCAAAGA
GAGAGATAGCTGATAGGGACTGACAAGCACACTGTTTAGATAAGAAGCAATTACCCTTTTATATCTGTGCTCTAT
ACATTTTCTATGTGCAGCATCTTTCCTAACTTGTTGTGGTTCCCGGGTGGCAGGTGCACAGCTGGGAGGGACTGC
CGGCTGTTTCGTACAACATTCTTGCCAATTCCCTTGAGGAGAAAATTCTTCACATGGCTTCTGCATGTACAGTAT

FIGURE 180C

TTGGGCAGCAAAACATGATTAAAGTCAGTTTGAAAATGG

FIGURE 181

MFNGEPGPASSGASRNVVRSSSIGGEICGSQQAGGGAGTTTAKKRRSSLGAKMVAIVGLTQWSKSTLQLPQPEGA
TKKLRSNIRRSTETGIAVEMRSRVTRQGSRESTDGSTNSNSSDGTFIFPTTRLGAESQFSDFLDGLGPAQIVGRQ
TLATPPMGDVHIAIMDRSGQLEVEVIEARGLTPKPGSKSLPATYIKVYLLENGACLAKKKTKMTKKTCDPLYQQA
LLFDEGPQGKVLQVIVWGDYGRMDHKCFMGMAQIMLDELDLSAAVTGWYKLFPTSSVADSTLGSLTRRLSQSSLE
SATSPSCS

FIGURE 182

AAGCTGCTGACATCCTGGATCTAGGGTTGTAAAGAAGATTACATGAGCTAATGGATGTGAAAACATCTTAAAAAC
TCTCAAATACTTTTCAACTTTGGAGGATTATTATGATTTTCATTCTGTTCAGCGGCTATACTCAGACTTTACTCT
AAAAGTCAAATCTTCTGACATTCTTTGAAGTGAAGCATTCTATGAATGTGAGCTGAAGAAATGAATGAAATGAAA
TAATGCAGCATCTAGTGCTTTTTGCATGGCCCAAAGGGGCTCTGTGCTGCTCCACTACAGAGGAAACTTCAAGAA
ATGCTGGTTTGCTACAGTGTTTTAGCTTGTGAGATTCTCTGGGACCTTCCCTGCTCCATCATGGGGTCACCTCTA
GGTCATTTTACCTGGGACAAATACCTAAAAGAAACATGTTCAGTCCCAGCGCCTGTCCATTGCTTCAAGCAGTCC
TACACACCTCCAAGCAACGAGTTCAAGATCAGTATGAAATTGGAAGCACAGGACCCCAGGAACACCACATCCACC
TGTATTGCCACAGTAGTTGGACTGACAGGTGCCCGCCTTCGCCTGCGCCTTGATGGGAGCGACAACAAAAATGAC
TTCTGGCGGCTGGTTGACTCAGCTGAAATCCAGCCTATTGGGAACTGTGAAAAGAATGGGGGTATGCTACAGCCA
CCTCTTGGATTTCGGCTGAATGCGTCTTCTTGGCCCATGTTCCTTTTGAAGACGCTAAATGGAGCAGAGATGGCT
CCCATCAGGATTTTCCACAAGGAGCCACCATCGCCTTCCCACAACTTCTTCAAAATGGGAATGAAGCTAGAAGCT
GTGGACAGGAAGAACCCTCATTTCATTTGCCCAGCCACTATTGGGGAGGTTCGGGGCTCAGAGGTGCTTGTCACT
TTTGATGGGTGGCGAGGGGCCTTTGACTACTGGTGCCGCTTCGACTCCCGAGACATCTTCCCTGTGGGCTGGTGT
TCCTTGACTGGAGACAACCTGCAGCCTCCTGGCACCAAAGTTGTGATTCCAAAGAATCCCTATCCTGCCTCCGAT
GTGAATACTGAGAAGCCCAGCATCCACAGCAGCACCAAAACTGTCTTGGAACATCAACCAGGGCAGAGGGGGCGT
AAACCAGGAAAGAAGCGGGGCCGGACACCCAAGACCCTAATTTCCCATCCCATCTCTGCCCCATCCAAGACAGCT
GAACCTTTGAAATTCCCAAAGAAGAGAGGTCCCAAACCTGGCAGCAAGAGGAAACCTCGGACTTTGCTGAACCCA
CCACCTGCCTCACCAACAACCAGCACTCCTGAACCGGATACCAGCACTGTACCCCAGGATGCTGCCACCATCCCC
AGCTCAGCCATGCAGGCCCCAACAGTTTGTATCTACTTGAACAAGAATGGCAGCACAGGCCCCCACTTAGATAAG
AAGAAGGTCCAGCAACTCCCTGACCATTTTGGACCAGCCCGTGCCTCTGTGGTGTTGCAGCAGGCTGTCCAGGCC
TGTATCGACTGTGCTTATCACCAGAAAACCGTCTTCAGCTTCCTCAAGCAAGGCCATGGTGGTGAGGTTATCTCA
GCCGTGTTTGACCGGGAACAGCATACCCTCAACCTCCCAGCAGTCAACAGCATCACCTACGTCCTCCGCTTCCTG
GAGAAACTCTGCCACAACCTTCGTAGTGACAATCTGTTTGGCAACCAGCCCTTTACACAGACTCACTTGTCACTC
ACTGCCATAGAGTACAGCCACAGCCACGACAGGTACCTACCAGGTGAAACCTTTGTCCTGGGGAATAGTCTGGCC
CGCTCCTTGGAACCACACTCAGACTCAATGGACTCTGCCTCAAATCCCACCAACCTTGTCAGCACCTCCCAAAGG
CACCGGCCCTTGCTTTCATCCTGTGGCCTCCCACCAAGCACTGCCTCAGCTGTGCGCAGGCTATGCTCCAGGGGA
GTGTTAAAAGGATCAAATGAAAGAAGGGATATGGAATCATTTTGGAAACTAAATCGTTCCCCAGGGTCGGACCGA
TACCTGGAGAGCCGCGATGCCTCTCGACTGAGTGGCCGGGACCCCTCCTCATGGACAGTCGAGGATGTGATGCAG
TTTGTCCGGGAAGCTGATCCTCAGCTTGGACCCCACGCTGACCTGTTTCGCAAACACGAGATCGATGGCAAGGCC
CTGCTGCTGCTGCGCAGTGACATGATGATGAAGTACATGGGCCTGAAGCTGGGGCCTGCACTCAAGCTCTCCTAC
CACATTGACCGGCTGAAGCAGGGCAAGTTCTGAACCAGGAGAGGCAGCCTAGACAACCAAGTGGCAGCAGGTGGG
GGCATTCTTCTAGGAATGAGGGGCATCAGCCCACCCCAGGCACCTCAGTGGGGTTCCGGGCCACCTCAGGACTCC
AAGAGGCTGTGTGGAGCCACCACTCCTAGCCACAGCTGCCATGATAAGTCCTTCCATGAAGGACTGAGGAGGGAG
AGTGGGGGTCCAGGGCTGGTGCTGCTCTTCCCTCAGCTCTGCCGGGGCTCTAAGGTCCCTCTATTTATTTCTCAA
CCCTGGCTGGCCTCTCACCAGGAGTTTAGGCTGAATGCCTTCCACGTGATGGAGGAAAAGGCCAACTCTGTCCTG
GTCTTGCTGTGGCACCCCATCGCCCCACAGCTCGTACCTTCTCACCAGATTCCCCTGAATCCAAACTCGTGGTGC
AAACCTCTACCTTTTTTACAAAAAGATCTTATTGTTAATTTATTGTTTCTGGCACTTGGGCAAACCCTGTAGTTA
ATACTCCTCCCACACTAGACACTGGGTTTCAGGAGGAGGGAGACTGCCCTGCTTTGGTCCCAGAGAGGCCCTCTG
CAGATAGGCGTGGCCCCTCTTCAGAGGACACTACCCTAGGGCACTTTCTCTTTGAGGTGGAGAGACCCATAAAGC
CTTGACCACATCACTCCATATGGGGAGGAGAAGGATCCCTGTCACCTTCTCCTCTCTTCACGGGGCCCTTTTGCA
GCCCTAGGCCTCATCTGTGGGAAGGGAGTCCCTGGCTTATACTGCCCCCACCACAGCTCCTTGCCCTGGCCAGAA
CTGCTGTCGAAGAAAATCAGGCCGGAAGGCCAAGAAGGCGCTAAGGGGGATGGGAGGGCAGGTTTTCCAGGCTGG
AGTCGGTTCCACCCACTCGCCTGTCCACAGGCTTCCTTGTAAGCAAGTCAGCAGCACAGCTACTCACGCTGCCAT
CTGGACTTATTTTATGTCAATCTGTTTATAAATAAAAACCAATATAGAT

FIGURE 183

GCTGCAG**<u>ATG</u>**GCGGAAATGGATCCGGTAGCCGAGTTCCCCCAGCCTCCCGGTGCTGCGCGCTGGGCTGAGGTTAT
GGCTCGCTTCGCGGCCAGGCTGGGCGCGCAGGGCCGGCGGGTGGTGTTGGTTACGTCAGGCGGCACCAAGGTCCC
ACTGGAAGCGCGGCCGGTGCGCTTCCTGGACAACTTCAGCAGCGGGCGGCGCGGTGCAACCTCGGCCGAGGCCTT
CCTAGCCGCCGGCTACGGGGTCCTGTTCTTGTATCGCGCTCGCTCTGCCTTCCCCTATGCCCACCGCTTCCCACC
CCAGACTTGGCTGTCCGCTCTGCGGCCTTCGGGCCCAGCCCTTTCGGGCTTGCTGAGCCTGGAGGCCGAGGAGAA
TGCACTTCCGGGTTTTGCTGAGGCTCTGAGGAGCTACCAGGAGGCTGCGGCTGCAGGCACCTTCCTGGCAGTAGA
GTTCACCACTTTGGCGGACTATTTGCATCTGTTGCAGGCTGCGGCCCAGGCACTCAATCCGCTAGGCCCTTCTGC
GATGTTTTACCTGGCTGCGGCTGTGTCAGATTTCTATGTTCCTGTCTCTGAAATGCCTGAACACAAGATCCAGTC
ATCTGGGGGCCCACTGCAGATAACAATGAAGATGGTGCCAAAACTGCTTTCTCCTTTGGTTAAAGATTGGGCTCC
CAAAGCATTTATAATTTCCTTTAAGTTGGAGACTGACCCCGCCATTGTAATTAATCGAGCTCGGAAGGCTTTGGA
AATTTATCAGCATCAAGTGGTGGTGGCTAATATCCTTGAGTCACGACAGTCCTTTGTGTTTATTGTAACCAAAGA
CTCGGAAACCAAGTTATTGCTATCAAGGAAGAAA**<u>TAG</u>**AAAAAGGCGTAGAGATAGAAGAGAAGATAGTGGATAAT
CTTCAGTCTCGACACACAGCTTTTATAGGTGACAGAAACTGAAGTAAAAAGCCCTTATAGGATTAAAAATTGTTC
AGGGCTCTTAGAGATGGTGAAAACTACAAAAAAAACCATGGCTTTCATATGGACAGAGAAAATGAAAGAAAGGGA
AAAGGCAGTGGTGTGTAGGCAAATATGGTTTGGCATTCGTCTTTTAATGACACCTGATATGATGTCATTTTGATT
TTGAAATTGAACACTAGAACTGTTAATCACCTTTAAAAAGAAGAGCTTATTGGGAATTATATATTCCTTAAAATA
TACATGGGGGCCTGAATGTCAGCCATCTTTATACTATAGAAAAAGGATTATGGATGCATGAATGGTCATGCTTTG
GAGATCAAATATTGGTTGAATGCCTATGTATGTCAGGCCCTGTGCTGAGCCATGAGGATTAAAAAGATGAATAAA
CATATCTTGTTTAGGAAATGGATGTATAAAAAAATCAAGTGCAATAAAGTGTGTGTCCAAAAGCTGACACAATGG
AAAGG

FIGURE 184

MAEMDPVAEFPQPPGAARWAEVMARFAARLGAQGRRVVLVTSGGTKVPLEARPVRFLDNFSSGRRGATSAEAFLA
AGYGVLFLYRARSAFPYAHRFPPQTWLSALRPSGPALSGLLSLEAEENALPGFAEALRSYQEAAAAGTFLAVEFT
TLADYLHLLQAAAQALNPLGPSAMFYLAAAVSDFYVPVSEMPEHKIQSSGGPLQITMKMVPKLLSPLVKDWAPKA
FIISFKLETDPAIVINRARKALEIYQHQVVVANILESRQSFVFIVTKDSETKLLLSRKK

FIGURE 185

CGGGAGCGGAGAGCGGACCCCAGAGAGCCCTGAGCAGCCCCACCGCCGCCGCCGGCCTAGTTACCATCACACCCC
GGGAGGAGCCGCAGCTGCCGCAGCCGGCCCCAGTCACCATCACCGCAACCATGAGCAGCGAGGCCGAGACCCAGC
AGCCGCCCGCCGCCCCCCCCGCCGCCCCCGCCCTCAGCGCCGCCGACACCAAGCCCGGCACTACGGGCAGCGGCG
CAGGGAGCGGTGGCCCGGGCGGCCTCACATCGGCGGCGCCTGCCGGCGGGGACAAGAAGGTCATCGCAACGAAGG
TTTTGGGAACAGTAAAATGGTTCAATGTAAGGAACGGATATGGTTTCATCAACAGGAATGACACCAAGGAAGATG
TATTTGTACACCAGACTGCCATAAAGAAGAATAACCCCAGGAAGTACCTTCGCAGTGTAGGAGATGGAGAGACTG
TGGAGTTTGATGTTGTTGAAGGAGAAAAGGGTGCGGAGGCAGCAAATGTTACAGGTCCTGGTGGTGTTCCAGTTC
AAGGCAGTAAATATGCAGCAGACCGTAACCATTATAGACGCTATCCACGTCGTAGGGGTCCTCCACGCAATTACC
AGCAAAATTACCAGAATAGTGAGAGTGGGGAAAAGAACGAGGGATCGGAGAGTGCTCCCGAAGGCCAGGCCCAAC
AACGCCGGCCCTACCGCAGGCGAAGGTTCCCACCTTACTACATGCGGAGACCCTATGGGCGTCGACCACAGTATT
CCAACCCTCCTGTGCAGGGAGAAGTGATGGAGGGTGCTGACAACCAGGGTGCAGGAGAACAAGGTAGACCAGTGA
GGCAGAATATGTATCGGGGATATAGACCACGATTCCGCAGGGGCCCTCCTCGCCAAAGACAGCCTAGAGAGGACG
GCAATGAAGAAGATAAAGAAAATCAAGGAGATGAGACCCAAGGTCAGCAGCCACCTCAACGTCGGTACCGCCGCA
ACTTCAATTACCGACGCAGACGCCCAGAAAACCCTAAACCACAAGATGGCAAAGAGACAAAAGCAGCCGATCCAC
CAGCTGAGAATTCGTCCGCTCCCGAGGCTGAGCAGGGCGGGGCTGAGTAAATGCCGGCTTACCATCTCTACCATC
ATCCGGTTTAGTCATCCAACAAGAAGAAATATGAAATTCCAGCAATAAGAAATGAACAAAAGATTGGAGCTGAAG
ACCTAAAGTGCTTGCTTTTTGCCCGTTGACCAGATAAATAGAACTATCTGCATTATCTATGCAGCATGGGGTTTT
TATTATTTTTACCTAAAGACGTCTCTTTTTGGTAATAACAAACGTGTTTTTTAAAAAAGCCTGGTTTTTCTCAAT
ACGCCTTTAAAGG

FIGURE 186

MSSEAETQQPPAAPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVLGTVKWFNVRNGYGFI
NRNDTKEDVFVHQTAIKKNNPRKYLRSVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSKYAADRNHYRRYPR
RRGPPRNYQQNYQNSESGEKNEGSESAPEGQAQQRRPYRRRRFPPYYMRRPYGRRPQYSNPPVQGEVMEGADNQG
AGEQGRPVRQNMYRGYRPRFRRGPPRQRQPREDGNEEDKENQGDETQGQQPPQRRYRRNFNYRRRRPENPKPQDG
KETKAADPPAENSSAPEAEQGGAE

FIGURE 187

GGCGGGTGGCTGGCGGTTCCGTTAGGTCTGAGGGAGCGATGGCGGTACGCGCGTTGAAGCTGCTGACCACACTGC
TGGCTGTCGTGGCCGCTGCCTCCCAAGCCGAGGTCGAGTCCGAGGCAGGATGGGGCATGGTGACGCCTGATCTGC
TCTTCGCCGAGGGGACCGCAGCCTACGCGCGCGGGGACTGGCCCGGGGTGGTCCTGAGCATGGAACGGGCGCTGC
GCTCCCGGGCAGCCCTCCGCGCCCTTCGCCTGCGCTGCCGCACCCAGTGTGCCGCCGACTTCCCGTGGGAGCTGG
ACCCCGACTGGTCCCCCAGCCCGGCCCAGGCCTCGGGCGCCGCCGCCCTGCGCGACCTGAGCTTCTTCGGGGGCC
TTCTGCGTCGCGCTGCCTGCCTGCGCCGCTGCCTCGGGCCGCCGGCCGCCCACTCGCTCAGCGAAGAGATGGAGC
TGGAGTTCCGCAAGCGGAGCCCCTACAACTACCTGCAGGTCGCCTACTTCAAGATCAACAAGTTGGAGAAAGCTG
TTGCTGCAGCACACACCTTCTTCGTGGGCAATCCTGAGCACATGGAAATGCAGCAGAACCTAGACTATTACCAAA
CCATGTCTGGAGTGAAGGAGGCCGACTTCAAGGATCTTGAGACTCAACCCCATATGCAAGAATTTCGACTGGGAG
TGCGACTCTACTCAGAGGAACAGCCACAGGAAGCTGTGCCCCACCTAGAGGCGGCGCTGCAAGAATACTTTGTGG
CCTATGAGGAGTGCCGTGCCCTCTGCGAAGGGCCCTATGACTACGATGGCTACAACTACCTTGAGTACAACGCTG
ACCTCTTCCAGGCCATCACAGATCATTACATCCAGGTCCTCAACTGTAAGCAGAACTGTGTCACGGAGCTTGCTT
CCCACCCAAGTCGAGAGAAGCCCTTTGAAGACTTCCTCCCATCGCATTATAATTATCTGCAGTTTGCCTACTATA
ACATTGGGAATTATACACAGGCTGTTGAATGTGCCAAGACCTATCTTCTCTTCTTCCCCAATGACGAGGTGATGA
ACCAAAATTTGGCCTATTATGCAGCTATGCTTGGAGAAGAACACACCAGATCCATCGGCCCCCGTGAGAGTGCCA
AGGAGTACCGACAGCGAAGCCTACTGGAAAAAGAACTGCTTTTCTTCGCTTATGATGTTTTTGGAATTCCCTTTG
TGGATCCGGATTCATGGACTCCAGAAGAAGTGATTCCCAAGAGATTGCAAGAGAAACAGAAGTCAGAACGGGAAA
CAGCCGTACGCATCTCCCAGGAGATTGGGAACCTTATGAAGGAAATCGAGACCCTTGTGGAAGAGAAGACCAAGG
AGTCACTGGATGTGAGCAGACTGACCCGGGAAGGTGGCCCCCTGCTGTATGAAGGCATCAGTCTCACCATGAACT
CCAAACTCCTGAATGGTTCCCAGCGGGTGGTGATGGACGGCGTAATCTCTGACCACGAGTGTCAGGAGCTGCAGA
GACTGACCAATGTGGCAGCAACCTCAGGAGATGGCTACCGGGGTCAGACCTCCCCACATACTCCCAATGAAAAGT
TCTATGGTGTCACTGTCTTCAAAGCCCTCAAGCTGGGGCAAGAAGGCAAAGTTCCTCTGCAGAGTGCCCACCTGT
ACTACAACGTGACGGAGAAGGTGCGGCGCATCATGGAGTCCTACTTCCGCCTGGATACGCCCCTCTACTTTTCCT
ACTCTCATCTGGTGTGCCGCACTGCCATCGAAGAGGTCCAGGCAGAGAGGAAGGATGATAGTCATCCAGTCCACG
TGGACAACTGCATCCTGAATGCCGAGACCCTCGTGTGTGTCAAAGAGCCCCCAGCCTACACCTTCCGCGACTACA
GCGCCATCCTTTACCTAAATGGGGACTTCGATGGCGGAAACTTTTATTTCACTGAACTGGATGCCAAGACCGTGA
CGGCAGAGGTGCAGCCTCAGTGTGGAAGAGCCGTGGGATTCTCTTCAGGCACTGAAAACCCACATGGAGTGAAGG
CTGTCACCAGGGGGCAGCGCTGTGCCATCGCCCTGTGGTTCACCCTGGACCCTCGACACAGCGAGCGGGTGAGAG
CAGCTCGAGCGGGTGAGAGCAGCTGGTGCTGTGGTGACCCGTTCCCAGAGCGCCCTTGGTTTGCCTTTCTCTTCC
CCAAATCCCATTGCCAGTGGCTGAGACACGAAAGGAGCACTTGGGACACCAGCTCCAACGCCCTGTCATTATGGT
CACATTGCCTTGTCCTCCCTGGGCCTGCTGTGAACGGGATCCAGGTGGGGAAAGAGGTCAAGACAGGGAGCGATG
CTGAGTTCTTGGTTCCCTCCTTGGGCCCCACTTCAGCTGTCCTTTTCCAGAGAGTAGGACCTGCTGGGAAGGAGA
TGAGCCTGGGGCCATTAAGGAACCTTCCTTGTCCCCTGGGAAGTAGCAGCTGAGAGATAGCGAGTGTCTGGAGCG
GAGGCCTCTCTGAATGGGCAGGGGTTTGTCCTTGCAGGACAGGGTGCAGGCAGATGACCTGGTGAAGATGCTCTT
CAGCCCAGAAGAGATGGACCTCTCCCAGGAGCAGCCCCTGGATGCCCAGCAGGGTCCCCCCGAACCTGCACAAGA
GTCTCTCTCAGGCAGTGAATCGAAGCCCAAGGATGAGCTATGACAGCGTCCAGGTCAGACGGATGGGTGACTAGA
CCCATGGAGAGGAACTCTTCTGCACTCTGAGCTGGCCAGCCCCTCGGGGCTGCAGAGCAGTGAGCCTACATCTGC
CACTCAGCCGAGGGGACCCTGCTCACAGCCTTCTACATGGTGCTACTGCTCTTGGAGTGGACATGACCAGACACC
GCACCCCCTGGATCTGGCTGAGGGCTCAGGACACAGGCCCAGCCACCCCCAGGGGCCTCCACAGGCCGCTGCATG
ACAGCGATACAGTACTTAAGTGTCTGTGTAGACAACCAAAGAATAAATGATTCATGGTTTTTTTT

FIGURE 188

TAGTCGCGGGTCCCCGAGTGAGCACGCCAGGGAGCAGGAGACCAAACGACGGGGGTCGGAGTCAGAGTCGCAGTG
GGAGTCCCCGGACCGGAGCACGAGCCTGAGCGGGAGAGCGCCGCTCGCACGCCCGTCGCCACCCGCGTACCCGGC
GCAGCCAGAGCCACCAGCGCAGCGCTGCC**ATG**GAGCCCAGCAGCAAGAAGCTGACGGGTCGCCTCATGCTGGCTG
TGGGAGGAGCAGTGCTTGGCTCCCTGCAGTTTGGCTACAACACTGGAGTCATCAATGCCCCCCAGAAGGTGATCG
AGGAGTTCTACAACCAGACATGGGTCCACCGCTATGGGGAGAGCATCCTGCCCACCACGCTCACCACGCTCTGGT
CCCTCTCAGTGGCCATCTTTTCTGTTGGGGGCATGATTGGCTCCTTCTCTGTGGGCCTTTTCGTTAACCGCTTTG
GCCGGCGGAATTCAATGCTGATGATGAACCTGCTGGCCTTCGTGTCCGCCGTGCTCATGGGCTTCTCGAAACTGG
GCAAGTCCTTTGAGATGCTGATCCTGGGCCGCTTCATCATCGGTGTGTACTGCGGCCTGACCACAGGCTTCGTGC
CCATGTATGTGGGTGAAGTGTCACCCACAGCCTTTCGTGGGGCCCTGGGCACCCTGCACCAGCTGGGCATCGTCG
TCGGCATCCTCATCGCCCAGGTGTTCGGCCTGGACTCCATCATGGGCAACAAGGACCTGTGGCCCCTGCTGCTGA
GCATCATCTTCATCCCGGCCCTGCTGCAGTGCATCGTGCTGCCCTTCTGCCCCGAGAGTCCCCGCTTCCTGCTCA
TCAACCGCAACGAGGAGAACCGGGCCAAGAGTGTGCTAAAGAAGCTGCGCGGGACAGCTGACGTGACCCATGACC
TGCAGGAGATGAAGGAAGAGAGTCGGCAGATGATGCGGGAGAAGAAGGTCACCATCCTGGAGCTGTTCCGCTCCC
CCGCCTACCGCCAGCCCATCCTCATCGCTGTGGTGCTGCAGCTGTCCCAGCAGCTGTCTGGCATCAACGCTGTCT
TCTATTACTCCACGAGCATCTTCGAGAAGGCGGGGGTGCAGCAGCCTGTGTATGCCACCATTGGCTCCGGTATCG
TCAACACGGCCTTCACTGTCGTGTCGCTGTTTGTGGTGGAGCGAGCAGGCCGGCGGACCCTGCACCTCATAGGCC
TCGCTGGCATGGCGGGTTGTGCCATACTCATGACCATCGCGCTAGCACTGCTGGAGCAGCTACCCTGGATGTCCT
ATCTGAGCATCGTGGCCATCTTTGGCTTTGTGGCCTTCTTTGAAGTGGGTCCTGGCCCCATCCCATGGTTCATCG
TGGCTGAACTCTTCAGCCAGGGTCCACGTCCAGCTGCCATTGCCGTTGCAGGCTTCTCCAACTGGACCTCAAATT
TCATTGTGGGCATGTGCTTCCAGTATGTGGAGCAACTGTGTGGTCCCTACGTCTTCATCATCTTCACTGTGCTCC
TGGTTCTGTTCTTCATCTTCACCTACTTCAAAGTTCCTGAGACTAAAGGCCGGACCTTCGATGAGATCGCTTCCG
GCTTCCGGCAGGGGGGAGCCAGCCAAAGTGATAAGACACCCGAGGAGCTGTTCCATCCCCTGGGGGCTGATTCCC
AAGTG**TGA**GTCGCCCCAGATCACCAGCCCGGCCTGCTCCCAGCAGCCCTAAGGATCTCTCAGGAGCACAGGCAGC
TGGATGAGACTTCCAAACCTGACAGATGTCAGCCGAGCCGGGCCTGGGGCTCCTTTCTCCAGCCAGCAATGATGT
CCAGAAGAATATTCAGGACTTAACGGCTCCAGGATTTTAACAAAAGCAAGACTGTTGCTCAAATCTATTCAGACA
AGCAACAGGTTTTATAATTTTTTTATTACTGATTTTGTTATTTTTATATCAGCCTGAGTCTCCTGTGCCCACATC
CCAGGCTTCACCCTGAATGGTTCCATGCCTGAGGGTGGAGACTAAGCCCTGTCGAGACACTTGCCTTCTTCACCC
AGCTAATCTGTAGGGCTGGACCTATGTCCTAAGGACACACTAATCGAACTATGAACTACAAAGCTTCTATCCCAG
GAGGTGGCTATGGCCACCCGTTCTGCTGGCCTGGATCTCCCCACTCTAGGGGTCAGGCTCCATTAGGATTTGCCC
CTTCCCATCTCTTCCTACCCAACCACTCAAATTAATCTTTCTTTACCTGAGACCAGTTGGGAGCACTGGAGTGCA
GGGAGGAGAGGGGAAGGGCCAGTCTGGGCTGCCGGGTTCTAGTCTCCTTTGCACTGAGGGCCACACTATTACCAT
GAGAAGAGGGCCTGTGGGAGCCTGCAAACTCACTGCTCAAGAAGACATGGAGACTCCTGCCCTGTTGTGTATAGA
TGCAAGATATTTATATATATATTTTTGGTTGTCAATATTAAATACAGACACTAAGTTATAGTATATCTGGACAAGCC
AACTTGTAAATACACCACCTCACTCCTGTTACTTACCTAAACAGATATAAATGGCTGGTTTTTAGAAACATGGTT
TTGAAATGCTTGTGGATTGAGGGTAGGAGGTTTGGATGGGAGTGAGACAGAAGTAAGTGGGGTTGCAACCACTGC
AACGGCTTAGACTTCGACTCAGGATCCAGTCCCTTACACGTACCTCTCATCAGTGTCCTCTTGCTCAAAAATCTG
TTTGATCCCTGTTACCCAGAGAATATATACATTCTTTATCTTGACATTCAAGGCATTTCTATCACATATTTGATA
GTTGGTGTTCAAAAAAACACTAGTTTTGTGCCAGCCGTGATGCTCAGGCTTGAAATCGCATTATTTTGAATGTGA
AGGGAA

FIGURE 189

MEPSSKKLTGRLMLAVGGAVLGSLQFGYNTGVINAPQKVIEEFYNQTWVHRYGESILPTTLTTLWSLSVAIFSVG
GMIGSFSVGLFVNRFGRRNSMLMMNLLAFVSAVLMGFSKLGKSFEMLILGRFIIGVYCGLTTGFVPMYVGEVSPT
AFRGALGTLHQLGIVVGILIAQVFGLDSIMGNKDLWPLLLSIIFIPALLQCIVLPFCPESPRFLLINRNEENRAK
SVLKKLRGTADVTHDLQEMKEESRQMMREKKVTILELFRSPAYRQPILIAVVLQLSQQLSGINAVFYYSTSIFEK
AGVQQPVYATIGSGIVNTAFTVVSLFVVERAGRRTLHLIGLAGMAGCAILMTIALALLEQLPWMSYLSIVAIFGF
VAFFEVGPGPIPWFIVAELFSQGPRPAAIAVAGFSNWTSNFIVGMCFQYVEQLCGPYVFIIFTVLLVLFFIFTYF
KVPETKGRTFDEIASGFRQGGASQSDKTPEELFHPLGADSQV

FIGURE 190

CACGTCGTTCACGGCCTTCTTCGGCCCCTCTAGCACGACATTGAGGCCTGGCTTCAGAAGCCCTCGGGAAAACGC
ATCCTGCAACTCTCTGTCTGTGACAAGGGATTCATCGGATTCCGACTCCGAATCCGAGAGCGGGGGAGTGTCCAT
CTCGCCGCACGCACGTCCCACACAGCTACTGCTCAACTTTTGATTGGGACTTCCGCTTCCGGCGGCAAACCATAC
TTCCGGTTTGTCGTTGCTATAGGAACCGCTACGGCGTTTGAAAGTGTCCGGGTTGCTTAGGATCCCTACAGGTAG
CGCCTCTGGATACATGCGTGGTCTGCTGACCCAGAGAGAAACGAAAGCAGAACTGTTTGGCGGGAGATC**ATG**TCA
GCCGTGGTAGCTCAGACGCTGCATGTTTTTGGTCTTCGATCCCACGTGGCCAACAATATCTTCTACTTCGATGAA
CAGATCATTATATTTCCTTCAGGAAATCACTGTGTGAAGTACAATGTGGATCAGAAATGGCAAAAATTCATTCCA
GGCTCAGAGAAGAGTCAGGGCATGTTGGCCTTGTCCATCAGTCCCAATCGGCGGTACCTCGCTATCTCTGAGACT
GTGCAAGAAAAACCTGCCATCACCATTTATGAATTGTCATCCATCCCTTGCCGGAAGCGCAAAGTTCTTAATAAT
TTTGACTTCCAAGTTCAGAAATTTATTAGCATGGCTTTTTCTCCAGACTCCAAATACCTATTGGCTCAGACGTCA
CCTCCAGAGTCAAATCTTGTCTACTGGCTGTGGGAAAAACAGAAAGTAATGGCCATTGTTAGAATCGACACTCAG
AACAACCCTGTCTACCAGGTGAGCTTCAGTCCACAGGATAACACTCAGGTGTGTGTCACTGGAAATGGGATGTTT
AAGCTTCTCCGTTTTGCTGAGGGAACCCTGAAGCAAACCAGCTTTCAGAGGGGAGAACCCCAAAACTATCTAGCC
CACACCTGGGTGGCTGATGACAAGATTGTCGTTGGCACTGACACAGGCAAACTCTTCCTCTTTGAATCTGGAGAT
CAGCGTTGGGAGACCAGCATAATGGTCAAGGAACCTACCGATGGCTCAAAGAGCCTGGATGTCATTCAGGAATCA
GAGAGCCTGATTGAATTTCCACCAGTCAGTTCTCCACTCCCTTCCTATGAACAGATGGTGGCGGCCAGTAGCCAT
AGCCAGATGTCCATGCCCCAGGTGTTTGCCATTGCAGCCTATTCAAAGGGATTTGCCTGTTCTGCTGGGCCAGGG
AGAGTTCTGCTGTTTGAGAAGATGGAAGAAAAGGATTTTTACCGTGAGAGCAGAGAAATCAGGATTCCTGTGGAC
CCGCAGAGCAATGATCCAAGTCAGTCTGACAAACAGGACGTTCTCTGCCTGTGCTTCAGCCCCTCAGAGGAAACT
CTGGTTGCCAGCACCAGTAAGAACCAACTCTACAGCATCACCATGTCCCTGACAGAGATCAGCAAGGGAGCCTGC
TCACTTTGAGTATTTGATGTATCCATTGCACTCAGCACCCATCACCGGTCTAGCTACCTGCATCCGCAAACCCCT
TATAGCCACCTGTTCTCTGGATCGATCCATCCGCCTTTGGAATTATGAAACAAACACCCTGGAACTATTTAAGGA
ATACCAAGAAGAGGCATATTCCATCAGCCTTCATCCATCTGGACACTTCATTGTAGTAGGGTTTGCTGACAAACT
ACGCCTCATGAATCTACTCATTGATGATATACGTTCTTTCAAAGAATACTCTGTTAGAGGATGCGGAGAGTGTTC
CTTTAGCAATGGAGGTCACCTGTTTGCTGCAGTCAATGGAAATGTGATTCACGTTTACACCACCACGAGCCTAGA
GAACATCTCAAGCCTGAAAGGACACACAGGGAAGATTCGCTCAATTGTGTGGAATGCAGA**TGA**TAGCAAACTGAT
TTCTGGTGGCACAGATGGTGCTGTGTATGAATGGAATCTGTCCACAGGAAAGAGAGAGACAGAATGCGTGCTCAA
GTCTTGCAGCTACAACTGTGTTACTGTCTCCCCCGATGCCAAAATTATCTTTGCTGTTGGATCAGACCACACCCT
CAAGGAGATTGCAGATTCCTTGCCTTCGAGAGATATCGGCGTTTGATGTCACCTACACCGCCATTGTCATCTCGC
ATTCTGGACGCATGATGTTTGTGGGCACCTCGGTGGGAACCATTCGTGCCATGAAGTACCCTCTGCCTCTGCAGA
AGGAATTCAATGAGTACCAGGCCCATGCCGGTCCTATCACCAAGGTGAGCAGGGCCCTCTCCCCAGGAACCCAGT
CCCACACCTGCCTGCTACGTGCCTTGTTCATCCCTTCAACCTCCCAATGTCTTTTCTCTCTCCTTCTTCTCTCTT
ATTTATTCATCCATCATTCATTGAATCACCATCTATTGACTATGAATATACTCTTTGTTTAAACTACTTCCAGGA
ATTTAGCCTAGGAAATCATCAGAGATACACCTAAAAATGTATGTACAACGTTTTCACCATAATATTATGCATAAT
AAGGGGCCGTTTGGTGGATGCCGTAGCTGCCGTGAGTGTGGGCTGCACTTGACCACAGCTGCCTCCTCCTCCAGA
GAATGCCCCAGACTGAAAGGAGCCATAGCCCTGAAGATTGGCCCCTACCTCTCCCTGAGGGTACAAAAGGCCACC
CCAGGGGCAATACCATGAGTACACATTTGTAAATTGTCCTTCCATTCACCCTTCTCATAAAGTAGTATCTATGTT
CAACAGTCAAAATGTGGAAGCAACCAAGCATCCATCGACAGACGAATGCATAAGCAAAAGATGGTATATCTATAC
AATGGAACAATACCCTGCCTAAAAAGGAAGGGAATTCTGCAATGTGCTACCACATGGATGAACCTTGAGGATGTT
ATGCTAAATTAAATAAGGCCAACCACAAAAAGATAAGTACAGTGTGATTCCACTTTTAGGAGATACTTGGAGCAG
TCAGAATCACAAAGACAGAGTGGTGGTTGGCAGGGGCTGCAGGAAGGGGGAATGAGGAATGATTGTTTCATAGGT
ATAGAGTTTTGGTTTTACAAGACAAAAGGATTATGGGGGTAGTTGGTGGCAATGGCTGCACAACATTACAAATGT
ATTTAATAACATGAACTGTACACTTGAAAATGGTTAAGATAGCAAATTTTACAGAATATGTATTTTACGACAATT
TTAAAAATGAAATAAAAAAGAATTATCTTGC

FIGURE 191

MSAVVAQTLHVFGLRSHVANNIFYFDEQIIIFPSGNHCVKYNVDQKWQKFIPGSEKSQGMLALSISPNRRYLAIS
ETVQEKPAITIYELSSIPCRKRKVLNNFDFQVQKFISMAFSPDSKYLLAQTSPPESNLVYWLWEKQKVMAIVRID
TQNNPVYQVSFSPQDNTQVCVTGNGMFKLLRFAEGTLKQTSFQRGEPQNYLAHTWVADDKIVVGTDTGKLFLFES
GDQRWETSIMVKEPTNGSKSLDVIQESESLIEFPPVSSPLPSYEQMVAASSHSQMSMPQVFAIAAYSKGFACSAG
PGRVLLFEKMEEKDFYRESREIRIPVDPQSNDPSQSDKQDVLCLCFSPSEETLVASTSKNQLYSITMSLTEISKG
EPAHFEYLMYPLHSAPITGLATCIRKPLIATCSLDRSIRLWNYETNTLELFKEYQEEAYSISLHPSGHFIVVGFA
DKLRLMNLLIDDIRSFKEYSVRGCGECSFSNGGHLFAAVNGNVIHVYTTTSLENISSLKGHTGKSLNCVECR

FIGURE 192

GCGATTCGGTGGCACGTGGAGCCACGGCGTGGGAGTAGGGGGCTGAAGGCAGGCAGCAGCGGCCAGGGCCGCCCT
CTGCTAGCCGCTTGGGTCTCGGGATACCCCGTTTCTTCCTGTAGGTGTGGGACGTGCGTGCGGCGAG**ATG**GACAC
TCCCCCGCTCTCGGATTCGGAGTCGGAATCCGATGAATCCCTTGTCACAGACAGAGAGTTGCAGGATGCGTTTTC
CCGAGGGCTTCTGAAGCCAGGCCTCAATGTCGTGCTAGAGGGGCCGAAGAAGGCCGTGAACGACGTGAATGGCCT
GAAGCAATGTTTGGCAGAATTCAAGCGGGATCTGGAATGGGTTGAAAGGCTCGATGTGACACTGGGTCCGGTACC
GGAGATCGGTGGATCTGAGGCGCCAGCACCTCAGAACAAGGACCAGAAAGCTGTTGATCCAGAAGACGACTTCCA
GCGAGAGATGAGTTTCTATCGCCAAGCCCAGGCCGCAGTGCTTGCAGTCTTACCCCGCCTCCATCAGCTCAAAGT
CCCTACGAAGCGACCCACTGATTATTTTGCGGAAATGGCCAAATCTGATCTGCAGGTGCAGAAGATTCGACAGAA
GCTGCAGACTAAACAGGCTGCCATGGAGAGGTCTGAAAAAGCTAAGCAACTGCGAGCACTTAGGAAATACGGGAA
GAAGGTGCAAACGGAGGTTCTTCAGAAGAGGCAGCAGGAGAAAGCCCATATGATGAATGCTATTAAGAAATATCA
GAAAGGCTTCTCTGATAAACTGGATTTCCTTGAGGGAGATCAGAAACCTCTGGCACAGCGCAAGAAGGCAGGAGC
CAAAGGCCAGCAGATGAGGAAGGGGCCCAGTGCTAAACGACGGTATAAAAACCAGAAGTTTGGTTTTGGTGGAAA
GAAGAAAGGCTCAAAGTGGAACACTCGGGAGAGCTATGATGATGTATCTAGCTTCCGGGCCAAGACAGCTCATGG
CAGAGGCCTCAAGAGGCCTGGCAAGAAAGGGTCAAATAAGAGACCTGGAAAACGAACAAGAGAGAAGATGAAGAA
CAGAACACAC**TAA**ATAGCATCTTTGAATACAAAGAACCAAGAAAAAGGAATGAAGACTCGCAATTTCACGACACA
CTTTGATCCCTTCTGTTGGTGTCATGTTGTAAACATTTCTTTCAATAAACTAAAGAAAAATTATTAAAGGAACAC
ATACCTTTGGTTAAATAGTCTAGACTAAAAGATTGAGAAGTTACTTTCCATTGCTATCTATTGATAATTTAGACA
TTGAGTTCAAATTGCCTTCATTTTATGATAAATAATGATTTAACTGAAAA

FIGURE 193

MDTPPLSDSESESDESLVTDRELQDAFSRGLLKPGLNVVLEGPKKAVNDVNGLKQCLAEFKRDLEWVERLDVTLG
PVPEIGGSEAPAPQNKDQKAVDPEDDFQREMSFYRQAQAAVLAVLPRLHQLKVPTKRPTDYFAEMAKSDLQVQKI
RQKLQTKQAAMERSEKAKQLRALRKYGKKVQTEVLQKRQQEKAHMMNAIKKYQKGFSDKLDFLEGDQKPLAQRKK
AGAKGQQMRKGPSAKRRYKNQKFGFGGKKKGSKWNTRESYDDVSSFRAKTAHGRGLKRPGKKGSNKRPGKRTREK
MKNRTH

FIGURE 194

CCACGCGTCCGGGCGTAAGCCAGGCGTGTTAAAGCCGGTCGGAACTGCTCCGGAGGGCACGGGCTCCGTAGGCAC
CAACTGCAAGGACCCCTCCCCCTGCGGGCGCTCCC**ATG**GCACAGTTCGCGTTCGAGAGTGACCTGCACTCGCTGC
TTCAGCTGGATGCACCCATCCCCAATGCACCCCCTGCGCGCTGGCAGCGCAAAGCCAAGGAAGCCGCAGGCCCGG
CCCCCTCACCCATGCGGGCCGCCAACCGATCCCACAGCGCCGGCAGGACTCCGGGCCGAACTCCTGGCAAATCCA
GTTCCAAGGTTCAGACCACTCCTAGCAAACCTGGCGGTGACCGCTATATCCCCCATCGCAGTGCTGCCCAGATGG
AGGTGGCCAGCTTCCTCCTGAGCAAGGAGAACCAGTCTGAAAACAGCCAGACGCCCACCAAGAAGGAACATCAGA
AAGCCTGGGCTTTGAACCTGAACGGTTTTGATGTAGAGGAAGCCAAGATCCTTCGGCTCAGTGGAAAACCACAAA
ATGCGCCAGAGGGTTATCAGAACAGACTGAAAGTACTCTACAGCCAAAAGGCCACTCCTGGCTCCAGCCGGAAGA
CCTGCCGTTACATTCCTTCCCTGCCAGACCGTATCCTGGATGCGCCTGAAATCCGAAATGACTATTACCTGAACC
TTGTGGATTGGAGTTCTGGGAATGTACTGGCCGTGGCACTGGACAACAGTGTGTACCTGTGGAGTGCAAGCTCTG
GTGACATCCTGCAGCTTTTGCAAATGGAGCAGCCTGGGGAATATATATCCTCTGTGGCCTGGATCAAAGAGGGCA
ACTACTTGGCTGTGGGCACCAGCAGTGCTGAGGTGCAGCTATGGGATGTGCAGCAGCAGAAACGGCTTCGAAATA
TGACCAGTCACTCTGCCCGAGTGGGCTCCCTAAGCTGGAACAGCTATATCCTGTCCAGTGGTTCACGTTCTGGCC
ACATCCACCACCATGATGTTCGGGTAGCAGAACACCATGTGGCCACACTGAGTGGCCACAGCCAGGAAGTGTGTG
GGCTGCGCTGGGCCCCAGATGGACGACATTTGGCCAGTGGTGGTAATGATAACTTGGTCAATGTGTGGCCTAGTG
CTCCTGGAGAGGGTGGCTGGGTTCCTCTGCAGACATTCACCCAGCATCAAGGGGCTGTCAAGGCCGTAGCATGGT
GTCCCTGGCAGTCCAATGTCCTGGCAACAGGAGGGGGCACCAGTGATCGACACATTCGCATCTGGAATGTGTGCT
CTGGGGCCTGTCTGAGTGCCGTGGATGCCCATTCCCAGGTGTGCTCCATCCTCTGGTCTCCCCATTACAAGGAGC
TCATCTCAGGCCATGGCTTTGCACAGAACCAGCTAGTTATTTGGAAGTACCCAACCATGGCCAAGGTGGCTGAAC
TCAAAGGTCACACATCCCGGGTCCTGAGTCTGACCATGAGCCCAGATGGGGCCACAGTGGCATCCGCAGCAGCAG
ATGAGACCCTGAGGCTATGGCGCTGTTTTGAGTTGGACCCTGCGCGGCGGCGGGAGCGGGAGAAGGCCAGTGCAG
CCAAAAGCAGCCTCATCCACCAAGGCATCCGC**TGA**AGACCAACCCATCACCTCAGTTGTTTTTTATTTTTCTAAT
AAAGTCATGTCTCCCTTCATGTTTTTTTTTTTAAAA

FIGURE 195

MAQFAFESDLHSLLQLDAPIPNAPPARWQRKAKEAAGPAPSPMRAANRSHSAGRTPGRTPGKSSSKVQTTPSKPG
GDRYIPHRSAAQMEVASFLLSKENQSENSQTPTKKEHQKAWALNLNGFDVEEAKILRLSGKPQNAPEGYQNRLKV
LYSQKATPGSSRKTCRYIPSLPDRILDAPEIRNDYYLNLVDWSSGNVLAVALDNSVYLWSASSGDILQLLQMEQP
GEYISSVAWIKEGNYLAVGTSSAEVQLWDVQQQKRLRNMTSHSARVGSLSWNSYILSSGSRSGHIHHHDVRVAEH
HVATLSGHSQEVCGLRWAPDGRHLASGGNDNLVNVWPSAPGEGGWVPLQTFTQHQGAVKAVAWCPWQSNVLATGG
GTSDRHIRIWNVCSGACLSAVDAHSQVCSILWSPHYKELISGHGFAQNQLVIWKYPTMAKVAELKGHTSRVLSLT
MSPDGATVASAAADETLRLWRCFELDPARRREREKASAAKSSLIHQGIR

FIGURE 196

GGCACGAGGGAACCGTCCGCAGCCGCCGGAGCCGGGAGCCCTGCCCAAGTCGGAGCGGCGTCCCCTGCTGAGCCC
CGAGCGCCGGGCCAGCAGCCGGATGCCCGGGCCCACTGGGCGGGCCAGTGGCCGCCTGCGGG**ATG**AGCAGACTGC
TGGGGGGGACGCTGGAGCGCGTCTGCAAGGCTGTGCTCCTTCTCTGCCTGCTGCACTTCCTCGTGGCCGTCATCC
TCTACTTTGACGTCTACGCCCAGCACCTGGCCTTCTTCAGCCGCTTCAGTGCCCGAGGCCCTGCCCATGCCCTCC
ACCCAGCTGCTAGCAGCAGCAGCAGCAGCAGCAACTGCTCCCGGCCCAACGCCACCGCCTCTAGCTCCGGGCTCC
CTGAGGTCCCCAGTGCCCTGCCCGGTCCCACGGCTCCCACGCTGCCACCCTGTCCTGACTCGCCACCTGGTCTTG
CGGGTGCACAGGGAGAACCCAGGCGTGCTCATGGGCGGCCGATACACACCGCCCGACTGCACCCCAGCCCAGACG
GTGGCGGTCATCATCCCCTT**TAG**ACACCGGGAACACCACCTGCGCTACTGGCTCCACTATCTACACCCCATCTTG
AGGCGGCAGCGGCTGCGCTACGGCGTCTATGTCATCAACCAGCATGGTGAGGACACCTTCAACCGGGCCAAGCTG
CTTAACGTGGGCTTCCTAGAGGCGCTGAAGGAGGATGCCGCCTATGACTGCTTCATCTTCAGCGATGTGGACCTG
GTCCCCATGGATGACCGCAACCTATACCGCTGCGGCGACCAACCCCGCCACTTTGCCATTGCCATGGACAAGTTT
GGCTTCCGGCTTCCCTATGCTGGCTACTTTGGAGGTGTGTCAGGCCTGAGTAAGGCTCAGTTTCTGAGAATCAAT
GGCTTCCCCAATGAGTACTGGGGCTGGGGTGGCGAGGATGATGACATCTTCAACCGGATCTCCCTGACTGGGATG
AAGATCTCACGCCCAGACATCCGAATTGGCCGCTACCGCATGATCAAGCACGACCGCGACAAGCATAACGAACCT
AACCCTCAGAGGTTTACCAAGATTCAAAACACGAAGCTGACCATGAAGCGGGACGGCATTGGGTCAGTGCGGTAC
CAGGTCTTGGAGGTGTCTCGGCAACCACTCTTCACCAATATCACAGTGGACATTGGGCGGCCTCCGTCGTGGCCC
CCTCGGGGCTGACACTAATGGACAGAGGCTCTCGGTGCCGAAGATTGCCTGCCAGAGGACTGACCACAGCCTGGC
TGGCAGCTGCTCTGTGGAGGACCTCCAGGACTGAGACTGGGCTCTGTTTTCCAAGGGTCTTCACTAGGCCCCCTA
GCTACACCTGGAAGTTTCAGAACCCACTTTGGGGGGCCTCCTGCCTGGGCAGGCTCTTCAAGTGTGGCCCTCTTT
GGAGTCAACCCTCCTTCCCGACCCCCTCCCCCTAGCCCAGCCCCAGTCACTGTCAGGGTCGGGCCAGCCCCTGCA
CTGCCTCGCAGAGTGGCCTGGGCTAGGTCACTCCACCTCTCTGTGCCTCAGTTTCCCCCCCTTGAGTCCCCTAGG
GCCTGGAAGGGTGGAGGTATGTCTAGGGGGCAGTGTCTCTTCCAGGGGGAATTCTCAGCTCTTGGGAACCCCCT
TGCTCCCAGGGGAGGGGAAACCTTTTTCATTCAACATTGTAGGGGGCAAGCTTTGGTGCGCCCCCTGCTGAGGAG
CAGCCCCAGGAGGGGACCAGAGGGGATGCTGTGTCGCTGCCTGGGATCTTGGGGTTGGCCTTTGCATGGAGGCA
GGTGGGGCTTGGATCAGTAAGTCTGGTTCCCGCCTCCCTGTCTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTT
GTGTTTGTACATTGCACAGAAACTTGTGTGGGTGCTTTAGTAAAAAACGTGAATGGAAAAAAAAAAAAAAAAAA

FIGURE 197

MSRLLGGTLERVCKAVLLLCLLHFLVAVILYFDVYAQHLAFFSRFSARGPAHALHPAASSSSSSSNCSRPNATAS
SSGLPEVPSALPGPTAPTLPPCPDSPPGLAGAQGEPRRAHGRPIHTARLHPSPDGGGHHPL

FIGURE 198

CCCAGTGCCCTGCCCGGTCCCACGGCTCCCACGCTGCCACCCTGTCCTGACTCGCCACCTGGTCTTGTGGGCAGA
CTGCTGATCGAGTTCACCTCACCCATGCCCCTGGAGCGGGTGCAGAGGGCCTGGAAGGGTGGGAGGTATGTCTAG
GGGGCAGTGTCTCTTCCAGGGGGAATTCTCAGCTCTTGGGAACCCCCTTGCTCCCAGGGGAGGGGAAACCTTTTT
CATTCAACATTGTAGGGGGCAAGCTTTGGTGCGCCCCCTGCTGAGGAGCAGCCCCAGGAGGGGACCAGAGGGGAT
GCTGTGTCGCTGCCTGGGATCTTGGGGTTGGCCTTTGCATGGGAGGCAGGTGGGGCTTGGATCAGTAAGTCTGGT
TCCCGCCTCCCTGTCTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTTGTGTTTGTACATTGCACAGAAACTTGT
GTGGGTGCTTTAGTAAAAAACGTGAATGG

FIGURE 199

GCCAGCAGCCGGATGCCCGGGCCCACTGGGCGGGCCAGTGGCCGCCTGCGGG**ATG**AGCAGACTGCTGGGGGGGAC
GCTGGAGCGCGTCTGCAAGGCTGTGCTCCTTCTCTGCCTGCTGCACTTCCTCGTGGCCGTCATCCTCTACTTTGA
CGTCTACGCCCAGCACCTGGCCTTCTTCAGCCGCTTCAGTGCCCGAGGCCCTGCCCATGCCCTCCACCCAGCTGC
TAGCAGCAGCAGCAGCAGCAGCAACTGCTCCCGGCCCAACGCCACCGCCTCTAGCTCCGGGCTCCCTGAGGTCCC
CAGTGCCCTGCCCGGTCCCACGGCTCCCACGCTGCCACCCTGTCCTGACTCGCCACCTGGTCTTGTGGGCAGACT
GCTGATCGAGTTCACCTCACCCATGCCCCTGGAGCGGGTGCAGAGGGAGAACCCAGGCGTGCTCATGGGCGGCCG
ATACACACCGCCCGACTGCACCCCAGCCCAGACGGTGGCGGTCATCATCCCCTTTAGACACCGGGAACACCACCT
GCGCTACTGGCTCCACTATCTACACCCCATCTTGAGGCGGCAGCGGCTGCGCTACGGCGTCTATGTCATCAACCA
GCATGGTGAGGACACCTTCAACCGGGCCAAGCTGCTTAACGTGGGCTTCCTAGAGGCGCTGAAGGAGGATGCCGC
CTATGACTGCTTCATCTTCAGCGATGTGGACCTGGTCCCCATGGATGACCGCAACCTATACCGCTGCGGCGACCA
ACCCCGCCACTTTGCCATTGCCATGGACAAGTTTGGCTTCCGGCTTCCCTATGCTGGCTACTTTGGAGGTGTGTC
AGGCCTGAGTAAGGCTCAGTTTCTGAGAATCAATGGCTTCCCCAATGAGTACTGGGGCTGGGGTGGCGAGGATGA
TGACATCTTCAACCGGATCTCCCTGACTGGGATGAAGATCTCACGCCCAGACATCCGAATCGGCCGCTACCGCAT
GATCAAGCACGACCGCGACAAGCATAACGAACCTAACCCTCAGAGGTTTACCAAGATTCAAAACACGAAGCTGAC
CATGAAGCGGGACGGCATTGGGTCAGTGCGGTACCAGGTCTTGGAGGTGTCTCGGCAACCACTCTTCACCAATAT
CACAGTGGACATTGGGCGGCCTCCGTCGTGGCCCCCTCGGGGC**TGA**CACTAATGGACAGAGGCTCTCGGTGCCGA
AGATTGCCTGCCAGAGGACTGACCACAGCCTGGCTGGCAGCTGCTCTGTGGAGGACCTCCAGGACTGAGACTGGG
CTCTGTTTTCCAAGGGTCTTCACTAGGCCCCCTAGCTACACCTGGAAGTTTCAGAACCCACTTTGGGGGGCCTCC
TGCCTGGGCAGGCTCTTCAAGTGTGGCCCTCTTTGGAGTCAACCCTCCTTCCCGACCCCCTCCCCCTAGCCCAGC
CCCAGTCACTGTCAGGGTCGGGCCAGCCCCTGCACTGCCTCGCAGAGTGGCCTGGGCTAGGTCACTCCACCTCTC
TGTGCCTCAGTTTCCCCCCCTTGAGTCCCCTAGGGCCTGGAAGGGTGGGAGGTATGTCTAGGGGGCAGTGTCTCT
TCCAGGGGGAATTCTCAGCTCTTGGGAACCCCCTTGCTCCCAGGGGAGGGGAAACCTTTTTCATTCAACATTGTA
GGGGGCAAGCTTTGGTGCGCCCCCTGCTGAGGAGCAGCCCCAGGAGGGGACCAGAGGGGATGCTGTGTCGCTGCC
TGGGATCTTGGGGTTGGCCTTTGCATGGGAGGCAGGTGGGGCTTGGATCAGTAAGTCTGGTTCCCGCCTCCCTGT
CTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTTGTGTTTGTACATTGCACAGAAACTTGTGTGGGTGCTTTAGT
AAAAAACGTGAATGG

FIGURE 200

MSRLLGGTLERVCKAVLLLCLLHFLVAVILYFDVYAQHLAFFSRFSARGPAHALHPAASSSSSSSNCSRPNATAS
SSGLPEVPSALPGPTAPTLPPCPDSPPGLVGRLLIEFTSPMPLERVQRENPGVLMGGRYTPPDCTPAQTVAVIIP
FRHREHHLRYWLHYLHPILRRQRLRYGVYVINQHGEDTFNRAKLLNVGFLEALKEDAAYDCFIFSDVDLVPMDDR
NLYRCGDQPRHFAIAMDKFGFRLPYAGYFGGVSGLSKAQFLRINGFPNEYWGWGGEDDDIFNRISLTGMKISRPD
IRIGRYRMIKHDRDKHNEPNPQRFTKIQNTKLTMKRDGIGSVRYQVLEVSRQPLFTNITVDIGRPPSWPPRG

FIGURE 201

GCGGAGAAACAGTAGTTAGGATGGCTGAAGGGGATACTCACCGGCTGAAGGCCGACTGTGATTCCCCCTACCCCC
ACAAGGCGATTTTGACCCCCTGAGGGCTGCTCTAGAGGACTCAGGCCCCGAAGCTGTCCCAGGGAGGTCCCCGCT
GCATCCCACCACCCAAGCTGTGCCTCATGGAGTCGATGTTTAGCAGCCCTGCCGAGGCGGCGCTGCAGCGAGAGA
CCGGGGTGCCAGGACTGCTTACTCCTCTTCCGGACCTGGACGGAGTGTACGAGCTGGAGCGAGTCGCTGGATTTG
TCCGCGACCTGGGGTGTGAACGAGTTGCCTTGCAGTTCCCTGACCAGCTATTGGGAGATGCTGTGGCTGTGGCTG
CACGACTGGAGGAGACGACAGGGTCAAAGATGTTCATTCTGGGTGACACAGCCTACGGCAGCTGCTGCGTGGATG
TGCTGGGTGCTGAGCAAGCTGGAGCTCAGGCTCTCATACATTTTGGCCCTGCCTGCTTAAGCCCTCCAGCCCGCC
CACTGCCCGTTGCCTTCGTGCTTCGTCAACGTTCTGTGGCCTTGGAGCTCTGTGTCAAGGCCTTTGAGGCCCAGA
ACCCAGACCCCAAAGCGCCTGTGGTGCTGCTGAGTGAGCCGGCCTGTGCCCATGCCCTGGAGGCTTTGGCTACTC
TCCTGCGCCCACGGTACCTGGACCTGCTAGTCTCCAGCCCAGCTTTTCCCCAACCAGTGGGTTCCCTGAGTCCAG
AGCCTATGCCCCTAGAGCGTTTTGGGCGCCGCTTCCCCCTTGCCCCAGGGAGGCGTCTAGAAGAGTATGGTGCCT
TCTATGTAGGGGGCTCTAAGGCCAGCCCTGACCCAGACCTTGACCCAGACCTGAGTCGGCTGCTCTTGGGGTGGG
CACCAGGTCAACCCTTCTCCTCCTGCTGTCCAGATACAGGGAAGACTCAGGATGAGGGTGCCCGGGCTGGACGGC
TAAGGGCACGAAGACGATATCTGGTAGAGAGGGCCAGAGATGCCCGCGTGGTAGGGCTGCTGGCAGGCACACTGG
GTGTAGCCCAACACCGTGAGGCACTGGCCCACTTGCGGAACCTGACTCAGGCTGCTGGCAAGCGTAGCTATGTGT
TGGCCCTGGGGCGGCCCACCCCTGCCAAGCTTGCCAACTTCCCTGAGGTGGATGTCTTTGTGCTATTAGCCTGTC
CTCTGGGTGCTCTAGCCCCCCAGCTTTCTGGTAGCTTCTTCCAGCCTATACTGGCACCATGTGAGCTGGAAGCTG
CCTGCAACCCTGCCTGGCCACCTCCAGGCCTGGCTCCCCACCTCACACATTATGCGGACTTATTGCCTGGCTCTC
CCTTCCACGTGGCTCTCCCACCACCTGAGTCAGAGCTGTGGGAAACCCCAGACGTGTCACTCATTACTGGAGATC
TCCGACCCCCACCTGCCTGGAAGTCATCAAATGATCATGGAAGCTTGGCTCTGACCCCACGGCCCCAGCTGGAGC
TGGCTGAGAGCAGTCCTGCAGCCTCATTCCTTAGTTCCCGGAGCTGGCAAGGGCTGGAGCCCCGCCTGGGTCAGA
CGCCAGTGACAGAAGCTGTGAGTGGAAGACGAGGGATTGCCATCGCCTATGAGGATGAGGGAAGCGGCTGATACC
ATGTGGGGCTGGAGACATAGATGGACTTATGAATGGCTGCTAGGACCTTTAGTGCTCCCTGCACCAACCTCCCAT
CCCCCTGCCAAGATCCTTGAAGGACCCTGGAAGGAGGGAGAGCAGGCAGCCCTTCACAGGATAGGATCCGTCTCT
GTCCTGTCCTGGCACTGGCACAAGCTCAGCCCATGCCCAGTAATGCGTGTTGTTTGGCTGATGGAATAAAGGGCT
TAGGGACTTCCCTGAGGCCTCTGGACCCATCTGTCTTCCTGAGGGCAGCCCAGGACCTTTGGCCAATCCCAGTTC
CCAGGCTGCAGTTGAGGGTCTGTCCTTGTCAAAAGGCAGGTGCTAGACAGTCTAGACCAGGGTTTCTCAAACTCG
TACTTGACATTTGGGGCCAGATAATTCTTTGTTGTGGGGCTGTCTGGTGTATGGTAGGGTGCTCAGCAGCATCCC
TGGCCTCTGCCCACTAGACATCAGAAGCACTCCCCCAGTTGTGACAACCAAAAATATCTCCAGACCTTGGCAAAT
GTTATCTGTGGGGGAAAATTGCCCTCAATTGAGAACCACTGGTCTAGCTAGACCTGCACTGTCCAGTACAGTAGC
CACTAAATACATGTGGCTAAACTTAAATTTAAGTTAATTAAGATTAAAAGCTCAGTTTCTCAGTCACATTAGTCA
TTCAAGTGTTCAGACAGCCACATGAGGGGACAGTGCAGCTACAGGATATGCCATCATGGCAGAAAGTTCTGTTGG
TTGGACAGCGTTGGTCTATACTGACTCTTATTCTCAGGGAGATCACAGCAACCTAAATAAACCAGATACCTTTT
C

FIGURE 202A

GCCTTCGCCTGCTGGAAAAGCAGTAGGATCGGCCAGTGGCGACAGCAGGAGCTGAGCCTAAGCCCTGGCGGGGCT
TTGGGCTGTAGATTCCTGTCTGACTAAAGGGACCTCAAAAAGGAGGGAAA**ATG**GCTTCTGAGTCTGAAACTCTGA
ATCCCAGTGCTAGGATAATGACCTTTTATCCAACTATGGAAGAGTTCCGAAACTTCAGTAGATACATTGCCTACA
TTGAATCCCAAGGAGCTCATCGGGCAGGGCTAGCCAAGGTTGTTCCTCCAAAAGAGTGGAAGCCACGAGCATCCT
ATGATGACATTGATGATTTGGTCATTCCTGCCCCCATTCAACAGCTGGTGACGGGGCAGTCTGGCCTCTTTACTC
AGTACAACATACAGAAGAAAGCCATGACTGTTCGAGAGTTCCGCAAGATAGCCAATAGCGATAAGTACTGTACCC
CACGCTATAGTGAGTTTGAAGAGCTCGAGCGGAAATACTGGAAAAATCTTACATTCAATCCTCCAATCTATGGTG
CAGATGTGAATGGTACCCTCTATGAAAAGCATGTTGATGAGTGGAATATTGGCCGGCTGAGAACAATCCTGGACT
TGGTGGAAAAGGAGAGTGGGATCACCATTGAGGGTGTGAACACCCCATACCTGTACTTTGGCATGTGGAAGACAT
CCTTTGCTTGGCACACTGAAGACATGGACCTCTACAGCATCAACTACCTGCACTTTGGAGAACCAAAGTCCTGGT
ACTCTGTTCCACCTGAGCATGGAAAGCGGTTGGAACGCCTCGCCAAAGGCTTTTTCCCAGGAAGTGCTCAAAGCT
GTGAGGCATTTCTCCGCCACAAGATGACCCTGATTTCCCCGTTAATGCTGAAGAAATATGGAATTCCCTTTGACA
AGGTGACTCAAGAGGCTGGAGAGTTTATGATCACTTTCCCTTATGGTTACCATGCCGGCTTTAACCATGGTTTTA
ACTGTGCGGAGTCTACCAATTTTGCTACCCGTCGGTGGATTGAGTACGGCAAGCAAGCTGTGCTGTGCTCCTGTA
GAAAGGACATGGTGAAGATCTCCATGGATGTGTTTGTGAGAAAGTTCCAGCCAGAAAGGTACAAACTTTGGAAAG
CTGGGAAGGACAACACAGTTATTGACCATACTCTGCCCACGCCAGAAGCAGCTGAGTTTCTTAAGGAGAGTGAAC
TGCCTCCAAGAGCTGGCAACGAGGAGGAGTGCCCAGAGGAGGACATGGAAGGGGTGGAGGATGGAGAGGAAGGAG
ACCTGAAGACAAGCCTGGCCAAGCACCGAATAGGGACAAAGAGGCACCGAGTTTGTCTTGAAATACCACAGGAGG
TGAGTCAGAGTGAGCTCTTCCCCAAGGAGGATCTGAGTTCTGAGCAGTATGAGATGACGGAGTGCCCGGCAGCCC
TCGCCCCTGTGAGGCCCACCCATAGCTCTGTGCGGCAAGTTGAGGATGGTCTTACCTTCCCAGATTATTCTGACT
CCACTGAAGTCAAATTTGAAGAGCTTAAAAATGTCAAACTAGAAGAGGAGGATGAGGAGGAAGAACAAGAAGCAG
CTGCCTTGGATCTTTCTGTGAATCCTGCGTCTGTAGGGGGACGCCTTGTCTTCTCAGGCTCCAAAAAGAAATCAT
CTTCTAGCCTGGGCTCTGGCTCTTCACGGGATTCTATCTCTTCTGATTCAGAAACTAGTGAGCCTCTCTCCTGCC
GAGCCCAAGGGCAAACGGGAGTTCTCACTGTGCACAGTTATGCCAAAGGGGATGGCAGGGTCACTGTGGGAGAGC
CATGCACGAGGAAGAAAGGAAGCGCCGCTAGAAGTTTCAGTGAGCGGGAGCTGGCAGAGGTTGCAGATGAATACA
TGTTTTCCCTAGAAGAGAATAAGAAGTCCAAGGGACGCCGTCAGCCTTTAAGCAAGCTCCCCCGCCATCACCCAC
TTGTGCTGCAGGAGTGTGTCAGTGATGATGAGACATCTGAACAGCTGACCCCTGAGGAAGAGGCTGAGGAGACAG
AGGCCTGGGCCAAGCCTCTGAGCCAACTGTGGCAGAACCGACCTCCAAACTTTGAGGCTGAGAAGGAATTCAATG
AGACCATGGCCCAACAGGCCCCTCACTGCGCTGTCTGTATGATCTTCCAGACTTATCATCAGGTTGAATTTGGAG
GCTTTAATCAGAACTGTGGAAATGCTTCAGATTTAGCCCCCCAGAAGCAGAGGACCAAGCCATTGATTCCAGAAA
TGTGCTTCACTTCGACTGGCTGCAGCACGGACATCAACCTTTCTACTCCTTATCTTGAGGAGGATGGCACCAGCA
TACTCGTTTCCTGCAAGAAGTGCAGCGTCCGGGTCCATGCCAGTTGCTATGGGGTCCCCCCTGCAAAGGCTTCTG
AAGACTGGATGTGTTCTCGGTGTTCAGCCAATGCCCTAGAGGAGGACTGCTGTTTATGCTCATTACGAGGAGGGG
CCCTGCAGAGAGCAAATGATGACAGGTGGGTCCACGTTTCATGTGCTGTGGCAATTCTGGAAGCAAGGTTTGTCA
ACATTGCAGAAAGAAGTCCGGTGGATGTGAGCAAAATCCCCCTGCCCCGCTTCAAACTGAAATGTATCTTCTGTA
AGAAGCGGAGGAAAAGAACTGCTGGCTGCTGTGTGCAGTGTTCTCACGGCCGCTGCCCAACTGCCTTCCATGTGA
GCTGCGCCCAGGCTGCCGGTGTGATGATGCAGCCTGACGACTGGCCTTTTGTGGTCTTCATTACCTGCTTTCGGC
ACAAGATTCCTAATTTGGAGCGTGCCAAGGGGGCCTTGCAAAGCATCACTGCAGGCCAGAAAGTCATTAGCAAGC
ATAAGAACGGGCGCTTCTACCAGTGTGAAGTGGTCAGGCTCACCACCGAGACCTTCTATGAAGTCAACTTTGATG
ATGGCTCCTTCAGCGACAATCTTTATCCTGAGGACATAGTGAGCCAGGACTGTCTCCAGTTTGGTCCTCCTGCTG
AAGGGGAAGTGGTCCAAGTGAGATGGACAGACGGCCAAGTCTATGGAGCCAAGTTTGTGGCCTCCCACCCTATCC
AAATGTACCAGGTGGAGTTTGAGGATGGCTCACAACTTGTGGTTAAGAGAGATGATGTATACACACTGGATGAAG
AGCTTCCCAAGAGAGTCAAATCTAGACTGTCAGTAGCCTCAGACATGCGCTTCAATGAGATTTTCACAGAGAAAG
AGGTTAAGCAAGAAAAGAAACGGCAACGAGTTATCAACTCAAGATACCGGGAAGATTATATTGAGCCTGCACTAT
ACCGGGCCATCATGGAG**TAG**GTGCTTCCAGGGTCCAAGGGATTCTCAGCCATCCAGGCAAGAGCACTCTGGGTTC
CACAGCACAGCAGACATGGAACGCTGAAGTCTCTGAAAGTGAAGTTGTAAAAAGAAAAGGAATGAAATAACCGAC
CCATCATCTTCTCACCCACCCTCATTGCATTCCGCTGTAGTGAAAGGACGAGCCATTTCTGGGCACGTGGCAGCA
GTCGCTGATCTCCCAGCTGAGGGGCTGAGCACTGGAATGCTGTGGCTGCACTGGCCCCAGTCCATAGAGGGGTCA

FIGURE 202B

ACTATGCTGGCTGGACTGGCTGCCTTGTTCCTGGCCTAGGACTTAGCTTCATAACTATCACCTGCACCGACTAGG
CTGAGGTGCTGGTACTTGCCCCAACCCCTACTTTTGTATTTATATGTGTGTGTGTGTGCGTGCGTGCGTGCGT
GCGTGTATGTTTGGTCTGGACCAGCTTCTGCCAGCCCCTGGCCTTTACTTTCTTCCTTGCCTATGCAGGGCAAAC
AAAATGTGAAATTCTGCCCTCAGCTGAGCTGAGTAAGGGCTCCTGGGGGTTGGCTGGAGATGGGTGTGGCATCTG
TCCAGGCCTGGAACCGTCTCAAGACAGTGCTGGCAAAGCTGCAGTATTGAGATGCTAAGGAGCTGATGCCACCTC
TTTGTCTTCCCCTAAAGGAGAACATGGGGATAACATGGGTGTGTGCCCACAACACTCTAGGTGCAGAGCCCCTGT
GGCAAAGTATTACAGGGTGTGGGTGGGGATTACCCTGAATCGGGGATTTTAATGATGGAAGCAGGCAGAGCCTGG
TGGGTGATTCTGTCAACAGAAAATTGCAATCATGCAGGGGCTGGGAGGGTTAGGATGAAAAAACTGGGGCCATTG
GAGGCCCACTGTAGGTGGGAGGGAGCTGATTTTGGGGTGGGGGGTGGGACTAGAGGGCAATACTGAAGGGGTTAA
ACAGGTTTTTGCTCCTCAAGAATTTGTTTGCCTGGGCCCAGGATTGGAGGGCTTCACACCAATACCCTGTGTATA
CAAGAATCAGATTTATAATACTTCCCCTTTTTTGTTACGTATGAACACTATAAACCAAATTATTTTG

FIGURE 203

MASESETLNPSARIMTFYPTMEEFRNFSRYIAYIESQGAHRAGLAKVVPPKEWKPRASYDDIDDLVIPAPIQQLV
TGQSGLFTQYNIQKKAMTVREFRKIANSDKYCTPRYSEFEELERKYWKNLTFNPPIYGADVNGTLYEKHVDEWNI
GRLRTILDLVEKESGITIEGVNTPYLYFGMWKTSFAWHTEDMDLYSINYLHFGEPKSWYSVPPEHGKRLERLAKG
FFPGSAQSCEAFLRHKMTLISPLMLKKYGIPFDKVTQEAGEFMITFPYGYHAGFNHGFNCAESTNFATRRWIEYG
KQAVLCSCRKDMVKISMDVFVRKFQPERYKLWKAGKDNTVIDHTLPTPEAAEFLKESELPPRAGNEEECPEEDME
GVEDGEEGDLKTSLAKHRIGTKRHRVCLEIPQEVSQSELFPKEDLSSEQYEMTECPAALAPVRPTHSSVRQVEDG
LTFPDYSDSTEVKFEELKNVKLEEEDEEEEQEAAALDLSVNPASVGGRLVFSGSKKKSSSSLGSGSSRDSISSDS
ETSEPLSCRAQGQTGVLTVHSYAKGDGRVTVGEPCTRKKGSAARSFSERELAEVADEYMFSLEENKKSKGRRQPL
SKLPRHHPLVLQECVSDDETSEQLTPEEEAEETEAWAKPLSQLWQNRPPNFEAEKEFNETMAQQAPHCAVCMIFQ
TYHQVEFGGFNQNCGNASDLAPQKQRTKPLIPEMCFTSTGCSTDINLSTPYLEEDGTSILVSCKKCSVRVHASCY
GVPPAKASEDWMCSRCSANALEEDCCLCSLRGGALQRANDDRWVHVSCAVAILEARFVNIAERSPVDVSKIPLPR
FKLKCIFCKKRRKRTAGCCVQCSHGRCPTAFHVSCAQAAGVMMQPDDWPFVVFITCFRHKIPNLERAKGALQSIT
AGQKVISKHKNGRFYQCEVVRLTTETFYEVNFDDGSFSDNLYPEDIVSQDCLQFGPPAEGEVVQVRWTDGQVYGA
KFVASHPIQMYQVEFEDGSQLVVKRDDVYTLDEELPKRVKSRLSVASDMRFNEIFTEKEVKQEKKRQRVINSRYR
EDYIEPALYRAIME

FIGURE 204

AGTTACAGACAGCTGACC**ATG**GAAGCGAATGGGTTGGGACCTCAGGGTTTTCCGGAGCTGAAGAATGACACATTC
CTGCGAGCAGCCTGGGGAGAGGAAACAGACTACACTCCCGTTTGGTGCATGCGCCAGGCAGGCCGTTACTTACCA
GAGTTTAGGGAAACCCGGGCTGCCCAGGACTTTTTCAGCACGTGTCGCTCTCCTGAGGCCTGCTGTGAACTGACT
CTGCAGCCACTGCGTCGCTTCCCTCTGGATGCTGCCATCATTTTCTCCGACATCCTTGTTGTACCCCAGGCACTG
GGCATGGAGGTGACCATGGTACCTGGCAAAGGACCCAGCTTCCCAGAGCCATTAAGAGAAGAGCAGGACCTAGAA
CGCCTACGGGATCCAGAAGTGGTAGCCTCTGAGCTAGGCTATGTGTTCCAAGCCATCACCCTTACCCGACAACGA
CTGGCTGGACGTGTGCCGCTGATTGGCTTTGCTGGTGCCCCATGGACCCTGATGACATACATGGTTGAGGGTGGT
GGCTCAAGCACCATGGCTCAGGCCAAGCGCTGGCTCTATCAGAGACCTCAGGCTAGTCACCAGCTGCTTCGCATC
CTCACTGATGCTCTGGTCCCATATCTGGTAGGACAAGTGGTGGCTGGTGCCCAGGCATTGCAGCTGTTTGAGTCC
CATGCAGGGCATCTTGGCCCACAGCTCTTCAACAAGTTTGCACTGCCTTACATCCGTGATGTGGCCAAGCAAGTG
AAGGCCAGGTTGCGGGAGGCAGGCCTGGCACCAGTGCCCATGATCATCTTTGCTAAGGATGGGCATTTTGCCCTG
GAGGAGCTGGCCCAAGCTGGCTATGAGGTGGTTGGGCTTGACTGGACAGTGGCCCCAAAGAAAGCCCGGGAGTGT
GTGGGGAAGACGGTGACATTGCAGGGCAACCTGGACCCCTGTGCCTTGTATGCATCTGAGGAGGAGATCGGGCAG
TTGGTGAAGCAGATGCTGGATGACTTTGGACCACATCGCTACATTGCCAACCTGGGCCATGGGCTTTATCCTGAC
ATGGACCCAGAACATGTGGGCGCCTTTGTGGATGCTGTGCATAAACACTCACGTCTGCTTCGACAGAAC**TGA**GTG
TATACCTTTACCCTCAAGTACCACTAACACAGATGATTGATCGTTTCCAGGACAATAAAAGTTTCGGAGTTGAAC
TATTGTGTAGTTTTGTTTGTGAAAGATTGTGCCCATATCCTCAGTTCTTCTTAGCCTCTGCTCCTTCCCTGGGAA
CCCTCTCTATATCCTCTT

FIGURE 205

MEANGLGPQGFPELKNDTFLRAAWGEETDYTPVWCMRQAGRYLPEFRETRAAQDFFSTCRSPEACCELTLQPLRR
FPLDAAIIFSDILVVPQALGMEVTMVPGKGPSFPEPLREEQDLERLRDPEVVASELGYVFQAITLTRQRLAGRVP
LIGFAGAPWTLMTYMVEGGGSSTMAQAKRWLYQRPQASHQLLRILTDALVPYLVGQVVAGAQALQLFESHAGHLG
PQLFNKFALPYIRDVAKQVKARLREAGLAPVPMIIFAKDGHFALEELAQAGYEVVGLDWTVAPKKARECVGKTVT
LQGNLDPCALYASEEEIGQLVKQMLDDFGPHRYIANLGHGLYPDMDPEHVGAFVDAVHKHSRLLRQN

FIGURE 206

AGCTTTGCGCAGTGGCAGTATCGTAGCCAATGAGGTTTATCCGAGGCGCGATTATTGCTAATTGAAAACTTTTCC
CAATACCCCGCCATGACGACTTGAAATATAGTCGGCATTGGCAATTTTTGACAGTCTCTACGGAGACTGCATGTG
CTGGTGAAGCTCCTGGAAGTG**ATG**GAAGGAATGGACAAGGAGACGTTTGAGTTCAAGTTTGGGAAGGAACTAACA
TTCACCACTGTACTGAGTGACCAACAGGTGGTGGAGCTGATCCCTGGGGGTGCAGGCATCGTCGTGGGATATGGG
GACCGTTCTCGTTTCATCCAACTGGTCCAGAAGGCACGGCTAGAGGAGAGCAAGGAGCAGGTGGCAGCTATGCAG
GCAGGTCTGCTGAAGGTGGTACCACAGGCTGTGCTGGACTTGCTGACCTGGCAAGAGTTGGAGAAGAAAGTGTGT
GGGGATCCAGAGGTCACTGTGGATGCTCTGCGCAAGCTCACCCGGTTTGAGGACTTCGAGCCATCTGACTCGCGG
GTGCAGTATTTCTGGGAGGCACTGAACAACTTCACCAACGAGGACCGGAGCCGCTTCCTGCGCTTTGTCACGGGC
CGCAGTCGCCTGCCAGCACGGATCTACATCTACCCAGACAAGCTGGGCTACGAGACCACAGACGCGCTGCCCGAG
TCTTCCACTTGCTCCAGCACCCTCTTCCTGCCACACTATGCCAGTGCCAAGGTATGCGAGGAGAAGCTCCGCTAT
GCGGCCTACAACTGCGTGGCCATCGACACTGACATGAGCCCTTGGGAGGAG**TGA**GGCGTGCCGCCGGCTGTGGGA
CCAGCAAGACTGCACGTGTCCCTCTTGGCCTTGCCCAGGGCGAAGACACCTTCCCTGCCCTGGTTTGGCTGACGT
GCTCAGCAAAACCCCATGTGCCCTGCTCCTGTGTGCAGTTGGGGTAGGGGCAGCTGGCATGGTCAGGTAACACTA
GTGGCCCAGCCCCGCAGACCCACAAGCCCTACCCGTGCTGGGGCTTGCTTCCCGAGGTATTTCACCTCTTAAGAG
GGAATCTTCCACAAGCCCAGCACAAGCTGCCAGGCCTGAGCTACTTGAAGGGGGCCATCTAGGTCCCCAACCCAT
GGACTTTGCCTCCATTTTCAGCTCCGCCTTTTTTCTCCTATTTCTCTCTGGCTTTCTTCAGCCATGACTCACAA
CTAAAAACATAAAACACTGGAGGTTAGTGGAGGCCCCTCCCCAAGCAGGGAGCCTGGGATGGGCAGGGAGTGATA
GCCAAACTCCTTGGTCACCTGCTCCAAGAAGGAAGCAGTAGCTGAGCACCTGCCCTCACATACTGCTCTTTTCCC
CTCTCCCTCCACACCAGAGATGTGGTGAGCTCTGTTCTTCTACCAACCCAGTCTCAACACACAAAGTGCCACCAC
CTTCCCTGACTCAGAACCCACATCCACTCAATGTGAACTCTACTACCACGACCTCCCCATATTCCTCACTTCTCC
ATCACCTCCAGCCTGACTCCCTGTCTGCCCTTTCACCCCCAAGATTTTGCACAGGTTAAGGCCAGTTATGGCCTT
TTTGAAATCTGTAATAGCTCCCCTTTCCCCAACTCTAAAGCCTAGACCTTAAACCTGTTCCTAGAGCTATGCACA
CCCCTGCCCCAGTTTACCGTTCCTCCCTCAGGGCCTCCGTGACACTCCATGAAAAGAAGTTCTTGCATACCGGAA
AGTTGAATAAATGGATGAATTCAAAAAAAAAAAAAAAAA

FIGURE 207

MEGMDKETFEFKFGKELTFTTVLSDQQVVELIPGGAGIVVGYGDRSRFIQLVQKARLEESKEQVAAMQAGLLKVV
PQAVLDLLTWQELEKKVCGDPEVTVDALRKLTRFEDFEPSDSRVQYFWEALNNFTNEDRSRFLRFVTGRSRLPAR
IYIYPDKLGYETTDALPESSTCSSTLFLPHYASAKVCEEKLRYAAYNCVAIDTDMSPWEE

FIGURE 208

CACAATGGTGCGCATGAATGCCCTGGCAGATGCTCTCAAGAGCATCAACAATGCCGAAAAGAGAGGCAAACGCCA
GGTGCTTCTTAGGCCATGCTCCAAAGTCATCGTCCAGTTTCTCACTGTGATGATGAAGCATGGTTACATTGGCGA
ATTTGAAATCACTGATGATCACAGAGCTGGGAAAATTGTTGTGAACCTCACAGGCAGGCTAAACAAGTGTGGAGC
GATCAGCCCCAGATTTGATGTGCAACTCAAAGATCTGGAAAAATGGCAGAATAATCTGCTTCCATCCCGCCAGTT
TGATTTCATTGTACTGACAACCTCAGCTGGCATCATGGACCATGAAGCAAGACGAAAACACACAGGAGGGAAAAT
CCAGGGATTCTTTTTCTAGGGATGTAATACATATATTTACAAATAAAATGCCTCAAGGAC

FIGURE 209

MVRMNALADALKSINNAEKRGKRQVLLRPCSKVIVQFLTVMMKHGYIGEFEITDDHRAGKIVVNLTGRLNKCGAI
SPRFDVQLKDLEKWQNNLLPSRQFDFIVLTTSAGIMDHEARRKHTGGKIQGFFF

FIGURE 210

CTCTTTCCAGCCAGCGCCGAGCG**ATG**GGCATCTCTCGGGACAACTGGCACAAGCGCCGCAAAACCGGGGGCAAGA
GAAAGCCCTACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCCAGCTGCCAACACCAAGATTGGCCCCCGCCGCA
TCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGACGTGGGGAATTTCTCCTGGG
GCTCAGAGTGTTGTACTCGTAAAACAAGGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTA
CCAAGACCCTGGTGAAGAATTGCATCGTGCTCATCGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTATG
CGCTGCCCCTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTAAACAAAAAACGATCTA
AAAAAATTCAGAAGAAATATGATGAAAGGAAAAAGAATGCCAAAATCAGCAGTCTCCTGGAGGAGCAGTTCCAGC
AGGGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGGACAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGGCA
AAGAGTTGGAGTTCTATCTTAGGAAAATCAAGGCCCGCAAAGGCAAA**TAA**ATCCTTGTTTTGTCTTCACCCATGT
AATAAAGGTGTTTATTGTTTTGTTCCCACA

FIGURE 211

MGISRDNWHKRRKTGGKRKPYHKKRKYELGRPAANTKIGPRRIHTVRVRGGNKKYRALRLDVGNFSWGSECCTRK
TRIIDVVYNASNNELVRTKTLVKNCIVLIDSTPYRQWYESHYALPLGRKKGAKLTPEEEEILNKKRSKKIQKKYD
ERKKNAKISSLLEEQFQQGKLLACIASRPGQCGRADGYVLEGKELEFYLRKIKARKGK

FIGURE 212

ACGCTTGCGCGCGGGATTTAAACTGCGGCGGTTTACGCGGCGTTAAGACTTCGTAGGGTTAGCGAAATTGAGGTT
TCTTGGTATTGCGCGTTTCTCTTCCTTGCTGACTCTCCGAATGGCCATGGACTCGTCGCTTCAGGCCCGCCTGTT
TCCCGGTCTCGCTATCAAGATCCAACGCAGTAATGGTTTAATTCACAGTGCCAATGTAAGGACTGTGAACTTGGA
GAAATCCTGTGTTTCAGTGGAATGGGCAGAAGGAGGTGCCACAAAGGGCAAAGAGATTGATTTTGATGATGTGGC
TGCAATAAACCCAGAACTCTTACAGCTTCTTCCCTTACATCCGAAGGACAATCTGCCCTTGCAGGAAAATGTAAC
AATCCAGAAACAAAAACGGAGATCCGTCAACTCCAAAATTCCTGCTCCAAAAGAAAGTCTTCGAAGCCGCTCCAC
TCGCATGTCCACTGTCTCAGAGCTTCGCATCACGGCTCAGGAGAATGACATGGAGGTGGAGCTGCCTGCAGCTGC
AAACTCCCGCAAGCAGTTTTCAGTTCCTCCTGCCCCCACTAGGCCTTCCTGCCCTGCAGTGGCTGAAATACCATT
GAGGATGGTCAGCGAGGAGATGGAAGAGCAAGTCCATTCCATCCGAGGCAGCTCTTCTGCAAACCCTGTGAACTC
AGTTCGGAGGAAATCATGTCTTGTGAAGGAAGTGGAAAAAAATGAAGAACAAGCGAGAAGAGAAGAAGGCCCAGAA
CTCTGAAATGAGAATGAAGAGAGCTCAGGAGTATGACAGTAGTTTTCCAAACTGGGAATTTGCCCGAATGATTAA
AGAATTTCGGGCTACTTTGGAATGTCATCCACTTACTATGACTGATCCTATCGAAGAGCACAGAATATGTGTCTG
TGTTAGGAAACGCCCACTGAATAAGCAAGAATTGGCCAAGAAAGAAATTGATGTGATTTCCATTCCTAGCAAGTG
TCTCCTCTTGGTACATGAACCCAAGTTGAAAGTGGACTTAACAAAGTATCTGGAGAACCAAGCATTCTGCTTTGA
CTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTCACAGCAAGGCCACTGGTACAGACAATCTT
TGAAGGTGGAAAAGCAACTTGTTTTGCATATGGCCAGACAGGAAGTGGCAAGACACATACTATGGGCGGAGACCT
CTCTGGGAAAGCCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTCCCGGGACGTCTTCCTCCTGAAGAATCA
ACCCTGCTACCGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATGGGAAGCTGTTTGACCT
GCTCAACAAGAAGGCCAAGCTGCGCGTGCTGGAGGACGGCAAGCAACAGGTGCAAGTGGTGGGGCTGCAGGAGCA
TCTGGTTAACTCTGCTGATGATGTCATCAAGATGATCGACATGGGCAGCGCCTGCAGAACCTCTGGGCAGACATT
TGCCAACTCCAATTCCTCCCGCTCCCACGCGTGCTTCCAAATTATTCTTCGAGCTAAAGGGAGAATGCATGGCAA
GTTCTCTTTGGTAGATCTGGCAGGGAATGAGCGAGGCGCGGACACTTCCAGTGCTGACCGGCAGACCCGCATGGA
GGGCGCAGAAATCAACAAGAGTCTCTTAGCCCTGAAGGAGTGCATCAGGGCCCTGGGACAGAACAAGGCTCACAC
CCCGTTCCGTGAGAGCAAGCTGACACAGGTGCTGAGGGACTCCTTCATTGGGGAGAACTCTAGGACTTGCAGATT
GCCACGATCTCACCAGGCATAAGCTCCTGTGAATATACTTTAAACACCCTGAGATATGCAGACAGGGTCAAGGAG
CTGAGCCCCCACAGTGGGCCCAGTGGAGAGCAGTTGATTCAAATGGAAACAGAAGAGATGGAAGCCTGCTCTAAC
GGGGCGCTGATTCCAGGCAATTTATCCAAGGAAGAGGAGGAACTGTCTTCCCAGATGTCCAGCTTTAACGAAGCC
ATGACTCAGATCAGGGAGCTGGAGGAGAAGGCTATGGAAGAGCTCAAGGAGATCATACAGCAAGGACCAGACTGG
CTTGAGCTCTCTGAGATGACCGAGCAGCCAGACTATGACCTGGAGACCTTTGTGAACAAAGCGGAATCTGCTCTG
GCCCAGCAAGCCAAGCATTTCTCAGCCCTGCGAGATGTCATCAAGGCCTTGCGCCTGGCCATGCAGCTGGAAGAG
CAGGCTAGCAGACAAATAAGCAGCAAGAAACGGCCCCAGTGACGACTGCAAATAAAAATCTGTTTGGTTTGACAC
CCAGCCTCTTCCCTGGCCCTCCCCAGAGAACTTTGGGTACCTGGTGGGTCTAGGCAGGGTCTGAGCTGGGACAGG
TTCTGGTAAATGCCAAGTATGGGGGCATCTGGGCCCAGGGCAGCTGGGGAGGGGGTCAGAGTGACATGGGACACT
CCTTTTCTGTTCCTCAGTTGTCGCCCTCACGAGAGGAAGGAGCTCTTAGTTACCCTTTTGTGTTGCCCTTCTTTC
CATCAAGGGGAATGTTCTCAGCATAGAGCTTTCTCCGCAGCATCCTGCCTGCGTGGACTGGCTGCTAATGGAGAG
CTCCCTGGGGTTGTCCTGGCTCTGGGGAGAGAGACGGAGCCTTTAGTACAGCTATCTGCTGGCTCTAAACCTTCT
ACGCCTTTGGGCCGAGCACTGAATGTCTTGTACTTTAAAAAAATGTTTCTGAGACCTCTTTCTACTTTACTGTCT
CCCTAGAGATCCTAGAGGATCCCTACTGTTTTCTGTTTTATGTGTTTATACATTGTATGTAACAATAAAGAGAAA
AAATAAA

FIGURE 213A

TAGGCAGGCGGCTGAGCCGGCGGCGGGTGGCCTGCCCAACGTGTGCTGGGTGGGAGAAGGCGAGGCGTCAGCGAT
GCTGTCTCTTCCGTGAGGAGCGCAGAGGAGGTCGCGGCGCCGGAGGCCCCAGAAGGCTCGAAGGCGCCGCGGGCT
GGGGTCGGTGGCTTAGGGAGCCCGTCCGGCCATGGTGGCCGCGGGTGGTGGTTGGCGCGGCTGCGCTGCGGCCCG
GGGCAGTGCGGAGCCGGGACAGTCGCGGCGCTGACGCCCGCGGGCCCCAGCTGCAGATATGAAGCGGAGCCGCTG
CCGCGACCGACCGCAGCCGCCGCCGCCCGACCGCCGGGAGGATGGAGTTCAGCGGGCAGCGGAGCTGTCTCAGTC
TTTGCCGCCGCGCCGGCGAGCGCCGCCCGGGAGGCAGCGGCTGGAGGAGCGGACGGCCCCGCGGGGCCCGAGGG
CAAGGAGCAGGATGTAGTAACTGGAGTTAGTCCCCTGCTCTTCAGGAAACTCAGTAATCCTGACATATTTTCATC
CACTGGAAAAGTTAAACTTCAGCGACAACTGAGTCAGGATGATTGTAAGTTATGGAGAGGAAACCTGGCCAGCTC
TCTATCGGGTAAGCAGCTGCTCCCTTTGTCCAGCAGTGTACATAGCAGTGTGGGACAGGTGACTTGGCAGTCGTC
AGGAGAAGCATCAAACCTGGTTCGAATGAGAAACCAGTCCCTTGGACAGTCTGCACCTTCTCTTACTGCTGGCCT
GAAGGAGTTGAGCCTTCCAAGAAGAGGCAGCTTTTGTCGGACAAGTAACCGCAAGAGCTTGATTGTGACCTCTAG
CACATCACCTACACTACCACGGCCACACTCACCACTCCATGGCCACACAGGTAACAGTCCTTTGGACAGCCCCCG
GAATTTCTCTCCAAATGCACCTGCTCACTTTTCTTTTGTTCCTGCCCGTAGGACTGATGGGCGGCGCTGGTCTTT
GGCCTCTTTGCCCTCTTCAGGATATGGAACTAACACTCCTAGCTCCACTGTCTCATCATCATGCTCCTCACAGGA
AAAGCTGCATCAGTTGCCTTTCCAGCCTACAGCTGATGAGCTGCACTTTTTGACGAAGCATTTCAGCACAGAGAG
CGTACCAGATGAGGAAGGACGGCAGTCCCCAGCCATGCGGCCTCGCTCCCGGAGCCTCAGTCCCGGACGATCCCC
AGTATCCTTTGACAGTGAAATAATAATGATGAATCATGTTTACAAAGAAAGATTCCCAAAGGCCACCGCACAAAT
GGAAGAGCGACTAGCAGAGTTTATTTCCTCCAACACTCCAGACAGCGTGCTGCCCTTGGCAGATGGAGCCCTGAG
CTTTATTCATCATCAGGTGATTGAGATGGCCCGAGACTGCCTGGATAAATCTCGGAGTGGCCTCATTACATCACA
ATACTTCTACGAACTTCAAGATAATTTGGAGAAACTTTTACAAGATGCTCATGAGCGCTCAGAGAGCTCAGAAGT
GGCTTTTGTGATGCAGCTGGTGAAAAAGCTGATGATTATCATTGCCCGCCCAGCACGTCTCCTGGAATGCCTGGA
GTTTGACCCTGAAGAGTTCTACCACCTTTTAGAAGCAGCTGAGGGCCACGCCAAAGAGGGACAAGGGATTAAATG
TGACATTCCCCGCTACATCGTTAGCCAGCTGGGCCTCACCCGGGATCCCCTAGAAGAAATGGCCCAGTTGAGCAG
CTGTGACAGTCCTGACACTCCAGAGACAGATGATTCTATTGAGGGCCATGGGGCATCTCTGCCATCTAAAAAGAC
ACCCTCTGAAGAGGACTTCGAGACCATTAAGCTCATCAGCAATGGCGCCTATGGGGCTGTATTTCTGGTGCGGCA
CAAGTCCACCCGGCAGCGCTTTGCCATGAAGAAGATCAACAAGCAGAACCTGATCCTACGGAACCAGATCCAGCA
GGCCTTCGTGGAGCGTGACATACTGACTTTCGCTGAGAACCCCTTTGTGGTCAGCATGTTCTGCTCCTTTGATAC
CAAGCGCCACTTGTGCATGGTGATGGAGTACGTTGAAGGGGGAGACTGTGCCACTCTGCTGAAGAATATTGGGGC
CCTGCCTGTGGACATGGTGCGTCTATACTTTGCGGAAACTGTGCTGGCCCTGGAGTACTTACACAACTATGGCAT
CGTGCACCGTGACCTCAAGCCTGACAACCTCCTAATTACATCCATGGGGCACATCAAGCTCACGGACTTTGGACT
GTCCAAAATTGGCCTCATGAGTCTGACAACGAACTTGTATGAGGGTCATATTGAAAAGGATGCCCGGGAATTCCT
GGACAAGCAGGTATGCGGGACCCCAGAATACATTGCGCCTGAGGTGATCCTGCGCCAGGGCTATGGGAAGCCAGT
GGACTGGTGGGCCATGGGCATTATCCTGTATGAGTTCCTGGTGGGCTGCGTCCCTTTTTTTGGAGATACTCCGGA
GGAGCTCTTTGGGCAGGTGATCAGTGATGAGATTGTGTGGCCTGAGGGTGATGAGGCACTGCCCCCAGACGCCCA
GGACCTCACCTCCAAACTGCTCCACCAGAACCCTCTGGAGAGACTTGGCACAGGCAGTGCCTATGAGGTGAAGCA
GCACCCATTCTTTACTGGTCTGGACTGGACAGGACTTCTCCGCCAGAAGGCTGAATTTATTCCTCAGTTGGAGTC
AGAGGATGATACTAGCTATTTTGACACCCGCTCAGAGCGATACCACCACATGGACTCGGAGGATGAGGAAGAAGT
GAGTGAGGATGGCTGCCTTGAGATCCGCCAGTTCTCTTCCTGCTCTCCAAGGTTCAACAAGGTGTACAGCAGCAT
GGAGCGGCTCTCACTGCTCGAGGAGCGCCGGACACCACCCCCGACCAAGCGCAGCCTGAGTGAGGAGAAGGAGGA
CCATTCAGATGGCCTGGCAGGGCTCAAAGGCCGAGACCGGAGCTGGGTGATTGGCTCCCCTGAGATATTACGGAA
GCGGCTGTCGGTGTCTGAGTCATCCCACACAGAGAGTGACTCAAGCCCTCCAATGACAGTGCGACGCCGCTGCTC
AGGCCTCCTGGATGCGCCTCGGTTCCCGGAGGGCCCTGAGGAGGCCAGCAGCACCCTCAGGAGGCAACCACAGGA
GGGTATATGGGTCCTGACACCCCCATCTGGAGAGGGGGTATCTGGGCCTGTCACTGAACACTCAGGGGAGCAGCG
GCCAAAGCTGGATGAGGAAGCTGTTGGCCGGAGCAGTGGTTCCAGTCCAGCTATGGAGACCCGAGGCCGTGGGAC
CTCACAGCTGGCTGAGGGAGCCACAGCCAAGGCCATCAGTGACCTGGCTGTGCGTAGGGCCCGCCACCGGCTGCT
CTCTGGGGACTCAACAGAGAAGCGCACTGCTCGCCCTGTCAACAAAGTGATCAAGTCCGCCTCAGCCACAGCCCT
CTCACTCCTCATTCCTTCGGAACACCACACCTGCTCCCCGTTGGCCAGCCCCATGTCCCCACATTCTCAGTCGTC
CAACCCATCATCCCGGGACTCTTCTCCAAGCAGGGACTTCTTGCCAGCCCTTGGCAGCATGAGGCCTCCCATCAT

FIGURE 213B

CATCCACCGAGCTGGCAAGAAGTATGGCTTCACCCTGCGGGCCATTCGCGTCTACATGGGTGACTCCGATGTCTA
CACCGTGCACCATATGGTGTGGCACGTGGAGGATGGAGGTCCGGCCAGTGAGGCAGGGCTTCGTCAAGGTGACCT
CATCACCCATGTCAATGGGGAACCTGTGCATGGCCTGGTGCACACGGAGGTGGTAGAGCTGATCCTGAAGAGTGG
AAACAAGGTGGCCATTTCAACAACTCCCCTGGAGAACACATCCATTAAAGTGGGGCCAGCTCGGAAGGGCAGCTA
CAAGGCCAAGATGGCCCGAAGGAGCAAGAGGAGCCGCGGCAAGGATGGGCAAGAAAGCAGAAAAAGGAGCTCCCT
GTTCCGCAAGATCACCAAGCAAGCATCCCTGCTCCACACCAGCCGCAGCCTTTCTTCCCTTAACCGCTCCTTGTC
ATCAGGGGAGAGTGGGCCAGGCTCTCCCACACACAGCCACAGCCTTTCCCCCCGATCTCCCACTCAAGGCTACCG
GGTGACCCCCGATGCTGTGCATTCAGTGGGAGGGAATTCATCACAGAGCAGCTCCCCCAGCTCCAGCGTGCCCAG
TTCCCCAGCCGGCTCTGGGCACACACGGCCCAGCTCCCTCCACGGTCTGGCACCCAAGCTCCAACGCCAGTACCG
CTCTCCACGGCGCAAGTCAGCAGGCAGCATCCCACTGTCACCACTGGCCCACACCCCTTCTCCCCCACCCCCAAC
AGCTTCACCTCAGCGGTCCCCATCGCCCCTGTCTGGCCATGTAGCCCAGGCCTTTCCCACAAAGCTTCACTTGTC
ACCTCCCCTGGGCAGGCAACTCTCACGGCCCAAGAGTGCGGAGCCACCCCGTTCACCACTACTCAAGAGGGTGCA
GTCGGCTGAGAAACTGGCAGCAGCACTTGCCGCCTCTGAGAAGAAGCTAGCCACTTCTCGCAAGCACAGCCTTGA
CCTGCCCCACTCTGAACTAAAGAAGGAACTGCCGCCCAGGGAAGTGAGCCCTCTGGAGGTAGTTGGAGCCAGGAG
TGTGCTGTCTGGCAAGGGGGCCCTGCCAGGGAAGGGGGTGCTGCAGCCTGCTCCCTCACGGGCCCTAGGCACCCT
CCGGCAGGACCGAGCCGAACGACGGGAGTCGCTGCAGAAGCAAGAAGCCATTCGTGAGGTGGACTCCTCAGAGGA
CGACACCGAGGAAGGGCCTGAGAACAGCCAGGGTGCACAGGAGCTGAGCTTGGCACCTCACCCAGAAGTGAGCCA
GAGTGTGGCCCCTAAAGGAGCAGGAGAGAGTGGGGAAGAGGATCCTTTCCCGTCCAGAGACCCTAGGAGCCTGGG
CCCAATGGTCCCAAGCCTATTGACAGGGATCACACTGGGGCCTCCCAGAATGGAAAGTCCCAGTGGTCCCCACAG
GAGGCTCGGGAGCCCACAAGCCATTGAGGAGGCTGCCAGCTCCTCCTCAGCAGGCCCCAACCTAGGTCAGTCTGG
AGCCACAGACCCCATCCCTCCTGAAGGTTGCTGGAAGGCCCAGCACCTCCACACCCAGGCACTAACAGCACTTTC
TCCCAGCACTTCGGGACTCACCCCCACCAGCAGTTGCTCTCCTCCCAGCTCCACCTCTGGGAAGCTGAGCATGTG
GTCCTGGAAATCCCTTATTGAGGGCCCAGACAGGGCATCCCCAAGCAGAAAGGCAACCATGGCAGGTGGGCTAGC
CAACCTCCAGGATTTGGAAAACACAACTCCAGCCCAGCCTAAGAACCTGTCTCCCAGGGAGCAGGGGAAGACACA
GCCACCTAGTGCCCCCAGACTGGCCCATCCATCTTATGAGGATCCCAGCCAGGGCTGGCTATGGGAGTCTGAGTG
TGCACAAGCAGTGAAAGAGGATCCAGCCCTGAGCATCACCCAAGTGCCTGATGCCTCAGGTGACAGAAGGCAGGA
CGTTCCATGCCGAGGCTGCCCCCTCACCCAGAAGTCTGAGCCCAGCCTCAGGAGGGGCCAAGAACCAGGGGGCCA
TCAAAAGCATCGGGATTTGGCATTGGTTCCAGATGAGCTTTTAAAGCAAACATAGCAGTTGTTTGCCATTTCTTG
CACTCAGACCTGTGTAATATATGCTCCTGGAAACC

FIGURE 214

GCAAG**<u>ATG</u>**GTGGGTGAAAAAGTTGAGAAGCCAGATGCTAAAGAGAAGAAACCCAAAGCCAAGAAGGCTGATGTTG
GTGGCAAGGTGAAAAAGGGTAACCTCAAGGCTAAAAAGCCCAAGAAGGGAAAGCCCCATTGCAGCCGCAACCCTG
TCCTTGTCAGAGGAATTGGCAGGTATTGCCGATCTGCCATGTATTCCAGAAAGGCCATGTACAAGAGGAAGTACT
CAGCCGCTAAATCTAAGGTTGAAAAGAAAAAGAAGGAGAAGGTTCTTGCAACTGTTACAAAACCAGTTGGTTGTG
ACAAGAATGGCGGTGCCCGGGTGGTTAAACTTCGCAAAATGCCTAGATATTATCCTACTGAAGATGTGCCTCGAA
AGCTGTTGAGCCATGGCAAAAAATCCTTCAGTCAGCACGTGAGGCCA**<u>TAG</u>**GGGCAAGAAGGTGGTTTTCCTGAAG
CAGCTGGCTAGTGGTTTGTTACTTGTGACTGGACCTCTGGTCCTCAATCGAATTCCTCTACGAAGAACATACCAG
AAATTTGTCATTGCCAC

FIGURE 215

MVGEKVEKPDAKEKKPKAKKADVGGKVKKGNLKAKKPKKGKPHCSRNPVLVRGIGRYCRSAMYSRKAMYKRKYSA
AKSKVEKKKKEKVLATVTKPVGCDKNGGARVVKLRKMPRYYPTEDVPRKLLSHGKKSFSQHVRP

FIGURE 216

AATCTGCCATTTTCTGTCCCTGAGTGAGTCTCTGGCGTCCCAAATTGCCTGTTTTTCTCGCAGGCTCTATTCCGT
TCGCTGGTTCGCCACCTCAGGGGAACG**ATG**GCCATGGAGTCCACAGCCACTGCCGCCGTCGCCGCGGAGCTGGTT
TCTGCCGACAAAATTGAAGATGTTCCTGCTCCTTCTACATCTGCAGATAAAGTGGAGAGTCTGGATGTGGATAGT
GAAGCTAAGAAACTATTGGGTTTAGGACAGAAACATCTGGTGATGGGGGATATTCCAGCAGCTGTCAATGCATTC
CAGGAAGCAGCTAGTCTTTTAGGTAAGAAGTATGGAGAGACAGCTAATGAGTGTGGAGAAGCCTTCTTTTTCTAT
GGGAAATCACTTCTGGAGTTGGCAAGAATGGAGAATGGTGTGTTGGGAAACGCCTTGGAAGGTGTGCATGTGGAA
GAGGAAGAAGGAGAAAAAACAGAAGATGAATCTCTGGTAGAAAATAATGATAACATAGATGAGGAAGCAAGGGAA
GAGTTGAGAGAACAGGTTTATGACGCCATGGGAGAAAAAGAAGAAGCCAAAAAAACAGAAGACAAGTCTTTGGCA
AAGCCTGAAACTGATAAAGAACAGGACAGTGAAATGGAGAAGGGTGGAAGAGAAGATATGGATATAAGTAAATCT
GCAGAGGAGCCACAGGAAAAAGTTGACTTGACTCTAGATTGGTTAACTGAAACCTCTGAAGAGGCAAAAGGAGGA
GCAGCACCAGAAGGACCGAATGAAGCTGAGGTCACTTCTGGGAAGCCAGAACAGGAAGTACCAGATGCTGAGGAA
GAAAAATCAGTTTCTGGAACTGATGTCCAAGAAGAGTGCAGAGAAAAAGGAGGTCAGGAGAAGCAGGGAGAGGTA
ATTGTGAGCATAGAGGAGAAGCCAAAAGAAGTTTCAGAAGAGCAGCCTGTGGTGACTCTAGAAAAGCAGGGCACT
GCAGTGGAGGTAGAAGCAGAGTCTTTAGACCCGACAGTCAAGCCAGTGGATGTGGGTGGGACGAGCCAGAGGAG
AAGGTAGTTACCTCTGAAAACGAGGCAGGAAAGGCGGTTCTTGAACAACTGGTAGGTCAAGAAGTACCACCTGCT
GAAGAGTCACCAGAGGTGACAACAGAGGCTGCAGAGGCCTCAGCTGTAGAGGCTGGATCAGAAGTCTCTGAAAAG
CCTGGGCAGGAGGCTCCAGTTCTCCCTAAGGATGGTGCAGTCAATGGACCGTCAGTTGTAGGAGATCAGACTCCT
ATTGAACCACAGACTTCTATAGAAAGACTGACAGAAACAAAAGATGGCTCAGGACTAGAGGAGAAGGTCAGGGCA
AAGCTGGTTCCTAGTCAGGAGGAGACTAAGCTGTCTGTAGAAGAGTCTGAGGCAGCTGGAGATGGGGTTGATACC
AAGGTAGCCCAGGGAGCTACTGAGAAATCACCTGAAGACAAAGTTCAGATAGCTGCTAATGAAGAGACACAAGAG
AGAGAAGAACAGATGAAAGAGGGTGAAGAAACTGAAGGCTCAGAAGAGGATGATAAAGAAAATGATAAGACCGAA
GAAATGCCAAATGATTCAGTCCTTGAAAACAAGTCTCTTCAAGAAAATGAGGAGGAGGAGATTGGGAACCTAGAG
CTTGCCTGGGATATGCTGGATTTAGCAAAGATCATTTTTAAAAGGCAAGAAACAAAAGAAGCACAGCTTTATGCT
GCCCAGGCACATCTTAAACTCGGAGAAGTTAGTGTTGAATCTGAAAACTATGTGCAAGCTGTGGAGGAGTTCCAG
TCCTGCCTTAACCTGCAGGAACAGTACCTGGAAGCCCACGACCGTCTCCTTGCAGAGACCCACTACCAGCTGGGC
TTGGCTTATGGGTACAACTCTCAGTATGATGAGGCAGTGGCACAGTTCAGCAAATCTATTGAAGTCATTGAGAAC
AGAATGGCTGTACTAAACGAGCAGGTGAAGGAGGCTGAAGGATCGTCTGCTGAATACAAGAAAGAAATTGAGGAA
CTAAAGGAACTGCTACCCGAAATTAGAGAGAAGATAGAAGATGCAAAGGAGTCTCAGCGTAGTGGGAATGTAGCT
GAACTGGCTCTGAAAGCTACTCTGGTGGAGAGTTCTACTTCAGGTTTCACTCCTGGTGGAGGAGGCTCTTCAGTC
TCCATGATTGCCAGTAGAAAGCCAACAGACGGTGCTTCCTCATCAAATTGTGTGACTGATATTTCCCACCTTGTC
AGAAAGAAGAGGAAACCAGAGGAAGAGAGTCCCCGGAAAGATGATGCAAAGAAAGCCAAACAAGAGCCGGAGGTG
AACGGAGGCAGTGGGGATGCTGTCCCCAGTGGAAATGAAGTTTCGGAAAACATGGAGGAGGAGGCTGAGAATCAG
GCTGAAAGCCGGGCAGCAGTGGAGGGGACAGTGGAGGCTGGAGCTACAGTTGAAAGCACTGCATGT**TAA**GAGGGG
GCACAGCCCTCCTCCCAAGGGAAAGTGTTTTGTATATAATGTATTTTTTCACTTTTGGAGGATTCTTTTTGTAT
AACTTCAATAAAGATTGTAAGCAAAGGTTGAGGCTTTGATGGTTTTTTTCTTAATTATTGGCTGAATCTGCCTTG
GAGCACTGCTGGTTTTATATATTAGCCAAAGGTTTTGTTCTGGCCTTCTGTACTGATCTGTGTTCCTGATCCTAA
TTCCTATCTGTCTAACGTGGAGGTGATCAAGTGTGGCTGTAGGCCTTTGTTTTCCAATGGTGCTATATTCTGTTT
TCAAACACTTCACTGAACCCAGCTGTCTTGCAAACTTTCAGTGGTGCTGTCCCTGGATGGGGGCTACAAAAACAA
GAATTGGTGAAGATCTTGCTCTTCAGTGCTGAAAATGGATGATGGACTTTGGCTGTGAGCCAGGCCTAGGATGGT
TCTTGTCCTATATCCACCTAGTCTTCACCTGGGGCTATAATTCTGTCCTGGAAAAAGAACTCTGAAAACCTGGGT
CAGGGGAATGATTCCTAAGGAAAACGGTCTGCATTTGAGCTCTGGTTTGAAAGTAGCCAAGGGGACTGATGGTGG
ACACTCCAGATGTGGTTGGAAGCATATGTGGGGAGGCTGGCTGGTTGAGTTTTGTTATTTTCTGTATAGAAAGGT
TGAGATATATCAACACTTGGAATTGTTACCCATCTGCAGAATTGACTTCTCAAATAAAGATGCTAAAAATCT

FIGURE 217

MAMESTATAAVAAELVSADKIEDVPAPSTSADKVESLDVDSEAKKLLGLGQKHLVMGDIPAAVNAFQEAASLLGK
KYGETANECGEAFFFYGKSLLELARMENGVLGNALEGVHVEEEEGEKTEDESLVENNDNIDEEAREELREQVYDA
MGEKEEAKKTEDKSLAKPETDKEQDSEMEKGGREDMDISKSAEEPQEKVDLTLDWLTETSEEAKGGAAPEGPNEA
EVTSGKPEQEVPDAEEEKSVSGTDVQEECREKGGQEKQGEVIVSIEEKPKEVSEEQPVVTLEKQGTAVEVEAESL
DPTVKPVDVGGDEPEEKVVTSENEAGKAVLEQLVGQEVPPAEESPEVTTEAAEASAVEAGSEVSEKPGQEAPVLP
KDGAVNGPSVVGDQTPIEPQTSIERLTETKDGSGLEEKVRAKLVPSQEETKLSVEESEAAGDGVDTKVAQGATEK
SPEDKVQIAANEETQEREEQMKEGEETEGSEEDDKENDKTEEMPNDSVLENKSLQENEEEEIGNLELAWDMLDLA
KIIFKRQETKEAQLYAAQAHLKLGEVSVESENYVQAVEEFQSCLNLQEQYLEAHDRLLAETHYQLGLAYGYNSQY
DEAVAQFSKSIEVIENRMAVLNEQVKEAEGSSAEYKKEIEELKELLPEIREKIEDAKESQRSGNVAELALKATLV
ESSTSGFTPGGGGSSVSMIASRKPTDGASSSNCVTDISHLVRKKRKPEEESPRKDDAKKAKQEPEVNGGSGDAVP
SGNEVSENMEEEAENQAESRAAVEGTVEAGATVESTAC

FIGURE 218

AGCCAGAAATGTGAAGTGCTAGCTGAAGGATGAGCAGCAGCTAGCCAGGCAAAGGGGGCA**ATG**GCGGCTTCCTGT
GTTCTACTGCACACTGGGCAGAAGATGCCTCTGATTGGTCTGGGTACCTGGAAGAGTGAGCCTGGTCAGGTAAAA
GCAGCTGTTAAGTATGCCCTTAGCGTAGGCTACCGCCACATTGATTGTGCTGCTATCTACGGCAATGAGCCTGAG
ATTGGGGAGGCCCTGAAGGAGGACGTGGGACCAGGCAAGGCGGTGCCTCGGGAGGAGCTGTTTGTGACATCCAAG
CTGTGGAACACCAAGCACCACCCCGAGGATGTGGAGCCTGCCCTCCGGAAGACTCTGGCTGACCTCCAGCTGGAG
TATCTGGACCTGTACCTGATGCACTGGCCTTATGCCTTTGAGCGGGGAGACAACCCCTTCCCCAAGAATGCTGAT
GGGACTATATGCTACGACTCCACCCACTACAAGGAGACTTGGAAGGCTCTGGAGGCACTGGTGGCTAAGGGGCTG
GTGCAGGCGCTGGGCCTGTCCAACTTCAACAGTCGGCAGATTGATGACATACTCAGTGTGGCCTCCGTGCGTCCA
GCTGTCTTGCAGGTGGAATGCCACCCATACTTGGCTCAAAATGAGCTAATTGCCCACTGCCAAGCACGTGGCTTG
GAGGTAACTGCTTATAGCCCTTTGGGCTCCTCTGATCGTGCATGGCGTGATCCTGATGAGCCTGTCCTGCTGGAG
GAACCAGTAGTCCTGGCATTGGCTGAAAAGTATGGCCGATCTCCAGCTCAGATCTTGCTCAGGTGGCAGGTCCAG
CGGAAAGTGATCTGCATCCCCAAAAGTATCACTCCTTCTCGAATCCTTCAGAACATCAAGGTGTTTGACTTCACC
TTTAGCCCAGAAGAGATGAAGCAGCTAAATGCCCTGAACAAAAATTGGAGATATATTGTGCCTATGCTTACGGTG
GATGGGAAGAGAGTCCCAAGGGATGCAGGGCATCCTCTGTACCCCTTTAATGACCCGTAC**TGA**GACCACAGCTTC
TTGGCCTCCCTTCCAGCTCTGCAGCTAATGAGGTCCTGCCACAACGGAAAGAGGGAGTTAATAAAGCCATTGGAG
CATCCAT

FIGURE 219

MAASCVLLHTGQKMPLIGLGTWKSEPGQVKAAVKYALSVGYRHIDCAAIYGNEPEIGEALKEDVGPGKAVPREEL
FVTSKLWNTKHHPEDVEPALRKTLADLQLEYLDLYLMHWPYAFERGDNPFPKNADGTICYDSTHYKETWKALEAL
VAKGLVQALGLSNFNSRQIDDILSVASVRPAVLQVECHPYLAQNELIAHCQARGLEVTAYSPLGSSDRAWRDPDE
PVLLEEPVVLALAEKYGRSPAQILLRWQVQRKVICIPKSITPSRILQNIKVFDFTFSPEEMKQLNALNKNWRYIV
PMLTVDGKRVPRDAGHPLYPFNDPY

FIGURE 220

GTTCTTGCCTGGTGTCGGTGGTTAGTTTCTGCGACTTGTGTTGGGACTGCTGATAGGAAG**ATG**TCTTCAGGAAAT
GCTAAAATTGGGCACCCTGCCCCCAACTTCAAAGCCACAGCTGTTATGCCAGATGGTCAGTTTAAAGATATCAGC
CTGTCTGACTACAAAGGAAAATATGTTGTGTTCTTCTTTTACCCTCTTGACTTCACCTTTGTGTGCCCCACGGAG
ATCATTGCTTTCAGTGATAGGGCAGAAGAATTTAAGAAACTCAACTGCCAAGTGATTGGTGCTTCTGTGGATTCT
CACTTCTGTCATCTAGCATGGGTCAATACACCTAAGAAACAAGGAGGACTGGGACCCATGAACATTCCTTTGGTA
TCAGACCCGAAGCGCACCATTGCTCAGGATTATGGGGTCTTAAAGGCTGATGAAGGCATCTCGTTCAGGGGCCTT
TTTATCATTGATGATAAGGGTATTCTTCGGCAGATCACTGTAAATGACCTCCCTGTTGGCCGCTCTGTGGATGAG
ACTTTGAGACTAGTTCAGGCCTTCCAGTTCACTGACAAACATGGGGAAGTGTGCCCAGCTGGCTGGAAACCTGGC
AGTGATACCATCAAGCCTGATGTCCAAAAGAGCAAAGAATATTTCTCCAAGCAGAAG**TGA**GCGCTGGGCTGTTTT
AGTGCCAGGCTGCGGTGGGCAGCCATGAGAACAAAACCTCTTCTGTATTTTTTTTTTCCATTAGTAAAACACAAG
ACTTCAGATTCAGCCGAATTGTGGTGTCTTACAAGGCAGGCCTTTCCTACAGGGGGTGGAGAGACCAGCCTTTCT
TCCTTTGGTAGGAATGGCCTGAGTTGGCGTTGTGGGCAGGCTACTGGTTTGTATGATGTATTAGTAGAGCAACCC
ATTAATCTTTTGTAGTTTGTATTAAACTTGAACTGAG

FIGURE 221

MSSGNAKIGHPAPNFKATAVMPDGQFKDISLSDYKGKYVVFFFYPLDFTFVCPTEIIAFSDRAEEFKKLNCQVIG
ASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGVLKADEGISFRGLFIIDDKGILRQITVNDLPVG
RSVDETLRLVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQKSKEYFSKQK

FIGURE 222

GCTCGGCTCACTGAGACCCGGTGGTCCAGACGCTGCTCCTGGCTGGGGTGGCGCTGCAGGGAGAACCGCGAGCTC
TCAGGGGTCGGCGGGTGACTTCTTTCCGGAAGAAAGCGAGGAACGCGCTCTGCGGGGTGAGCCGGACTCCCCAAC
TCCGGACGATCAGCCCAGGACTGAGAGCCCCGAAGTCCCCAACCACAAGTAAGCGGCCCCAGAAGGACAAGTCTA
GGTCGCCGTCCAGAGCGCC**ATG**GCCGCGCCCGCCCTTCGTTTGTGCCACATCGCCTTCCACGTGCCCGCCGGGCA
GCCCCTAGCCCGGAACCTGCAGCGCCTCTTCGGCTTCCAGCCCCTGGCTTCGCGGGAGGTGGACGGCTGGCGGCA
GCTAGCCCTGCGCAGCGGCGACGCGGTCTTTTTGGTGAACGAGGGCGCAGGGTCTGGAGAGCCGCTGTACGGCCT
GGATCCGCGTCACGCCGTGCCCAGCGCCACAAACCTGTGCTTCGACGTGGCGGACGCCGGCGCTGCAACCCGGGA
GCTGGCAGCGCTGGGCTGCAGCGTGCCTGTCCCTCCCGTTCGCGTGCGGGACGCGCAGGGTGCCGCCACTTACGC
CGTGGTCAGCTCGCCTGCCGGCATCCTCAGCCTGACCTTGCTGGAGCGCGCTGGCTACCGCGGACCCTTCCTACC
CGGCTTCAGGCCCGTGTCCTCTGCGCCTGGCCCCGGGTGGGTCAGCCGCGTGGACCACCTGACCTTGGCCTGCAC
CCCCGGCAGCTCCCCCACACTTTTGCGCTGGTTCCACGACTGCCTGGGCTTTTGCCACTTGCCGCTGAGCCCAGG
TGAGGATCCCGAGCTGGGCCTCGAAATGACAGCAGGGTTTGGGCTTGGGGGACTGAGGCTTACAGCCCTGCAGGC
CCAGCCGGGCAGCATTGTCCCCACTCTTGTTCTGGCTGAGTCCCTTCCGGGGGCGACGACACGACAGGACCAGGT
GGAGCAGTTCCTGGCCCGGCACAAGGGGCCAGGCCTGCAGCACGTGGGGCTGTATACGCCTAACATTGTGGAGGC
CACTGAGGGGGTGGCAACTGCTGGAGGCCAGTTCCTGGCTCCCCCTGGGGCATACTACCAGCAGCCAGGAAAGGA
GAGGCAGATCCGAGCTGCAGGGCACGAGCCTCATCTGCTTGCTCGACAGGGGATCCTGCTAGATGGTGATAAAGG
CAAGTTTCTGCTTCAGGTCTTCACCAAGTCCCTTTTTACTGAGGACACTTTCTTCCTGGAGCTGATTCAGAGGCA
GGGGGCCACTGGCTTTGGTCAGGGCAACATCAGAGCTCTGTGGCAGTCCGTACAGGAGCAATCTGCCAGGAGCCA
GGAAGCC**TAA**GGATGCCCAGGGCTGGGTGCAGCCAGCTGTCCTGCAGCTCTGGGGAGACCAGCACAGAACTGAGG
AACATCTGCAGGAGGCCCAACTAGTGAAAGGCTTTGCCTCCGGGGGGCAGGTGTGACTTCCATTTCATCAGTGCC
TGCCAGAAGCTGTGTCTCTCATTGGGCTCCAAAGAGGTGGGATTTTTTAAAACTAAAACATTTCTTATATACAGT
CTATAATAAATATGTAAGATACAAAGAACAATAAAAGAATTACACACTAGGAAAAAAAAAAAAAAAAAAA

FIGURE 223

MAAPALRLCHIAFHVPAGQPLARNLQRLFGFQPLASREVDGWRQLALRSGDAVFLVNEGAGSGEPLYGLDPRHAV
PSATNLCFDVADAGAATRELAALGCSVPVPPVRVRDAQGAATYAVVSSPAGILSLTLLERAGYRGPFLPGFRPVS
SAPGPGWVSRVDHLTLACTPGSSPTLLRWFHDCLGFCHLPLSPGEDPELGLEMTAGFGLGGLRLTALQAQPGSIV
PTLVLAESLPGATTRQDQVEQFLARHKGPGLQHVGLYTPNIVEATEGVATAGGQFLAPPGAYYQQPGKERQIRAA
GHEPHLLARQGILLDGDKGKFLLQVFTKSLFTEDTFFLELIQRQGATGFGQGNIRALWQSVQEQSARSQEA

FIGURE 224

GACCACGATGAGTGTGCCGCACTTCCGGCCAGATCGCCGGATTTCCGCTGAGTGACCCTTACAAGTCCTTCTTGA
TCCTGAACTGGGTTAGGTGCCGCTGTTGCTGCTCGTGTTGAATCTAGAACCGTAGCCAGAC**ATG**GGACTGGAGGA
CGAGCAAAAGATGCTTACCGAATCCGGAGATCCTGAGGAGGAGGAAGAGGAAGAGGAGGAATTAGTGGATCCCCT
AACAACAGTGAGAGAGCAATGCGAGCAGTTGGAGAAATGTGTAAAGGCCCGGGAGCGGCTAGAGCTCTGTGATGA
GCGTGTATCCTCTCGATCACATACAGAAGAGGATTGCACGGAGGAGCTCTTTGACTTCTTGCATGCGAGGGACCA
TTGCGTGGCCCACAAACTCTTTAACAACTTGAAA**TAA**ATGTGTGGACTTAATTCACCCCAGTCTTCATCATCTGG
GCATCAGAATATTTCCTTATGGTTTTGGATGTACCATTTGTTTCTTATTTGTGTAACTGTAAGTTCACATGAACC
TCATGGGTTTGGCTTAGGCTGGTAGCTTCTATGTAATTCGCAATGATTCCATCTAAATAAAAGTTCTATGATCTG
C

FIGURE 225

MGLEDEQKMLTESGDPEEEEEEEEELVDPLTTVREQCEQLEKCVKARERLELCDERVSSRSHTEEDCTEELFDFL
HARDHCVAHKLFNNLK

FIGURE 226

CGCGCCTGAGGAGGAGGAGGAGGCGGGGGCGGCCATGGCTGCTGTGGTGGTGGCGGCTGCGGGTGGCGCGGGACC
GGCGGTCCTGCAGGTGGCCGGTCTCTACCGGGGCCTGTGCGCGGTGCGCAGCCGCGCCCTGGGCCTGGGGCTCGT
GTCACCCGCGCAGCTGCGCGTCTTCCCAGTGCGCCCCGGCTCGGGCCGGCCCGAGGGGGGCGCCGACAGCAGCGG
GGTCGGGGCCGAGGCCGAGCTCCAGGCCAACCCTTTCTACGACCGCTACCGCGACAAGATCCAGCTGCTGCGCAG
GTCAGACCCAGCTGCTTTTGAGTCCCGCCTGGAGAAACGCAGTGAATTTCGGAAGCAGCCAGTGGGGCATTCCAG
GCAAGGTGATTTTATCAAATGTGTGGAACAGAAGACAGATGCCTTGGGGAAACAGTCTGTGAACAGAGGATTCAC
TAAGGACAAGACTCTCAGTTCAATCTTTAACATTGAGATGGTAAAAGAAAAAACTGCAGAAGAAATAAAACAGAT
TTGGCAGCAATATTTTGCAGCAAAAGATACAGTCTACGCAGTTATTCCTGCAGAAAAGTTTGATTTGATCTGGAA
CCGGGCTCAGTCCTGTCCAACATTTCTATGTGCTCTGCCAAGAAGGGAAGGTTATGAGTTTTTGTAGGACAATG
GACAGGTACTGAACTCCACTTCACTGCACTTATAAATATTCAGACCCGAGGGGAAGCTGCAGCCAGCCAGCTGAT
TTTATATCACTATCCTGAACTTAAGGAAGAAAAGGGCATAGTGCTGATGACTGCAGAAATGGATTCCACATTTCT
GAATGTTGCTGAGGCACAGTGCATCGCCAACCAAGTTCAGCTCTTCTACGCTACTGATCGGAAAGAGACCTACGG
GTTAGTGGAGACCTTTAACCTCAGACCAAATGAGTTCAAATATATGTCTGTCATCGCTGAATTGGAGCAAAGCGG
ACTTGGAGCAGAACTGAAATGTGCCCAGAACCAAAATAAGACTTAGAACTGTACAGGTTGGCCCTTCACCTAGTT
GACTCAGCCCTCGATAGTCTAGAGCCCACCCCCTCCTCAGGAACTCAAGAGCTCAGCATTTATAATGAGCAGTTG
GTAATGAGTTGCCCTATGTGCTTGTCGCAAGCAGTCACAGAGATGAGCCCTATTACTTGATATTCAGGAACAAAG
GTACCTGAACATTCTGATAATTATCTCAGCATACTTGAGGTTTCCTTTTTTAAGTGTTCGAGGTTATAACAAGAG
ACAGCCAAGGACCTACAAGACAGTTGACTTGATTTTGCACAGTGTAACAGCGCAGTTGCATTCTGGCCACTTTGA
CCTTATAGCTCCCAAATGATGAGTTTGTCATCTTTATGAACTCATGACAGGATAATAAGCTTGAAGACCTGCTGT
AGTTAGATATGGGCTTTAATCCTTCCCAGGCACCAGTCAGCTGAACAAAAGCATAAGCCAAACATCCTGTTTAAA
CTGTAGAATAACCAGATATTCCCATCAGGTTAAAGACTTCATCTAGATGATGCCCCCCAGAGATGCCTTTAGTGT
AAGTAGCTGGCTTGGGGTATCAGCAAATTTCAGGTATAGTTAGATAAACAGGTACAGGGCCTGCATACTATTAAA
CCATAGTTTGTGGCACCCGCTTTTCTAACTCCACCTGTTAGAAGCTATGTGTTTGAAGGAATGAATCAGTGCAGT
ATAAATAAAATTCTTTTGTAAGGAG

FIGURE 227

MAAVVVAAAGGAGPAVLQVAGLYRGLCAVRSRALGLGLVSPAQLRVFPVRPGSGRPEGGADSSGVGAEAELQANP
FYDRYRDKIQLLRRSDPAAFESRLEKRSEFRKQPVGHSRQGDFIKCVEQKTDALGKQSVNRGFTKDKTLSSIFNI
EMVKEKTAEEIKQIWQQYFAAKDTVYAVIPAEKFDLIWNRAQSCPTFLCALPRREGYEFFVGQWTGTELHFTALI
NIQTRGEAAASQLILYHYPELKEEKGIVLMTAEMDSTFLNVAEAQCIANQVQLFYATDRKETYGLVETFNLRPNE
FKYMSVIAELEQSGLGAELKCAQNQNKT

FIGURE 228

ACCTGCCCTCATCCTGGCCCGCGACTGTAAGACCGGACCCACATCCAGACCAATCTTCCTGTCCGGCTGCTGCGA
CGCGGTCCGCAGGTTGCAGGCGGGCGGCCGGGGCGCCTGAAGGTTACCGAGTGCATGACGGCCTCAGTTCCCGCG
CTGCCCCGCCCGCTGGCCCGCCGACCTCCCCGCCGCTCGCCCGCCAGCCCCTCGGGCCCGGCGGCGGCGGCGGCG
GTGGCGGCGACGGTCGCAGGAGGTGCCGTCTGCCTCCCAGGTGCGCGCTTCGCTCCCGGAGCCGCGGAACTCGGT
CGCGCCATGGCGTCCAACATGGACCGGGAGATGATCCTGGCGGATTTTCAGGCATGTACTGGCATTGAAAACATT
GACGAAGCTATTACATTGCTTGAACAAAATAATTGGGACTTAGTGGCAGCTATCAATGGTGTAATACCACAGGAA
AATGGCATTCTACAAAGTGAATATGGAGGTGAGACCATACCAGGACCTGCATTTAATCCAGCAAGTCATCCAGCT
TCAGCTCCTACTTCCTCTTCTTCTTCAGCGTTTCGACCTGTAATGCCATCCAGGCAGATTGTAGAAAGGCAACCT
CGGATGCTGGACTTCAGGGTTGAATACAGAGACAGAAATGTTGATGTGGTACTTGAAGACACCTGTACTGTTGGA
GAGATTAAACAGATTCTAGAAAATGAACTTCAGATACCTGTGTCCAAAATGCTGTTAAAAGGCTGGAAGACGGGA
GATGTGGAAGACAGTACGGTCCTAAAATCTCTACACTTGCCAAAAAACAACAGTCTTTATGTCCTTACACCAGAT
TTGCCACCACCTTCATCATCTAGTCATGCTGGTGCCCTGCAGGAGTCATTAAATCAAAACTTCATGCTGATCATC
ACCCACCGAGAAGTCCAGCGGGAGTACAACCTGAACTTCTCAGGAAGCAGTACTATTCAAGAGGTAAAGAGAAAT
GTGTATGACCTTACAAGTATCCCCGTTCGCCACCAATTATGGGAGGGCTGGCCAACTTCTGCTACAGACGACTCA
ATGTGTCTTGCTGAATCAGGGCTCTCTTATCCCTGCCATCGACTTACAGTGGGAAGAAGATCTTCACCTGCACAG
ACCCGGGAACAGTCGGAAGAACAAATCACCGATGTTCATATGGTTAGTGATAGCGATGGAGATGACTTTGAAGAT
GCTACAGAATTTGGGGTGGATGATGGAGAAGTATTTGGCATGGCGTCATCTGCCTTGAGAAAATCTCCAATGATG
CCAGAAAACGCAGAAAATGAAGGAGATGCCTTATTACAATTTACAGCAGAGTTTTCTTCAAGATATGGTGATTGC
CATCCTGTATTTTTTATTGGCTCATTAGAAGCTGCTTTTCAAGAGGCCTTCTATGTGAAAGCCCGAGATAGAAAG
CTTCTTGCTATCTACCTCCACCATGATGAAAGTGTGTTAACCAACGTGTTCTGCTCACAAATGCTTTGTGCTGAA
TCCATTGTTTCTTATCTGAGTCAAAATTTTATAACCTGGGCTTGGGATCTGACAAAGGACTCCAACAGAGCAAGA
TTTCTCACTATGTGCAATAGACACTTTGGCAGTGTTGTGGCACAAACCATTCGGACTCAAAAAACGGATCAGTTT
CCGCTTTTCCTGATTATTATGGGAAAGCGATCATCTAATGAAGTGTTGAATGTGATACAAGGGAACACAACAGTA
GATGAGTTAATGATGAGACTCATGGCTGCAATGGAGATCTTCACAGCCCAACAACAGGAAGATATAAAGGACGAG
GATGAACGTGAAGCCAGAGAAAATGTGAAGAGAGAGCAAGATGAGGCCTATCGCCTTTCACTTGAGGCTGACAGA
GCAAAGAGGGAAGCTCACGAGAGAGAGATGGCAGAACAGTTTCGTTTGGAGCAGATTCGCAAAGAACAAGAAGAG
GAACGTGAGGCCATCCGGCTGTCCTTAGAGCAAGCCCTGCCTCCTGAGCCAAAGGAAGAAAATGCTGAGCCTGTG
AGCAAACTGCGGATCCGGACCCCCAGTGGCGAGTTCTTGGAGCGGCGTTTCCTGGCCAGCAACAAGCTCCAGATT
GTCTTTGATTTTGTAGCTTCCAAAGGATTTCCATGGGATGAGTACAAGTTACTGAGCACCTTTCCTAGGAGAGAC
GTAACTCAACTGGACCCAAATAAATCATTATTGGAGGTAAAGTTGTTCCCTCAAGAAACCCTTTTCCTTGAAGCA
AAAGAGTAAACACGGCCCAGCGGTGGAACCAGCCATTCCTTGACAAGCCAGCAGCCTGCGTCAGGAGAAGGGCTC
CTCGCCAACCCACCCACACGCTCGTCTCACTCAATTCAATGTCACACTTCTGCCTCTTGCAAAATTGCTGGAAAA
AGTAATAATAAATATAGCTACTTAAAAAAAAAAAAA

FIGURE 229

CTCTGCCGAGCCTCCTTAAAACTCTGCCGTTAAAATGGGGGCGGGTTTTTCAACTCAAAAAGCGCTCAATTTTTT
TCTTTTCAAAAAAAGCTGATGAGGTCGGAAAAAAGGGAGAAGAAACCGGCACCCTCTCTGAGAGGCAACAGAAGC
AGCAATTGTTTCAGCGAAAAAAGCAGCAAGGGAGGGAGTGAAGGAAAAAAGCAAAAAAGGGGGCGACACGCAAGT
GCCTGTAGGGGTGAAAGGAGCAGGGACCGGCGATCTAGGGGGGGATCAGCTACAAAAGAAACTGTCACTGGGAGC
GGTGCGGCCAAGGAGGAAGCAGTGCTGCCAGGCTCTGCTCCAGGGCACAGCTGGCTGGCGGCTGCCCTGTCCGCA
GCAAAGGGGCACAGGCCGGGGACCGCGAGAGGTGGCAAAGTGGCACCGGGCGCCGAGGCTGCTGAGCGCTCGCCG
AGACGGCGACCGGACTGGCTGCCCCGGAACTGCGGCGACTCTCCCTACTCAGAACTTGGCCTACGTTTCCCAGGA
CTCTCCCCATCTCCAGAGGCCCCCACAAAACCGGGAAAGGAAGGAAAGGACAGCGGCGGCAGCAGCTCAATGAGT
GCCTACAGCAGAAAGCCTGAACGAGCTCGGTCGTAGGCGGGAAGTTCCCGGGGGGGCTGCCCAGTGCAGCCGCAA
TGCTGCCGCGAGCTGCCCCAGCAGTCCGGGCTCCGTAGACGCTTTCCGCATCACTCTCCTTCCTCGGGCTGCCGG
GAGTCCCGGGACCTGGCGGGGCCGGCATGACGGGCTTCTCGGGGGCCCGCCGCACGCCCGGCAGCCTCCGGAGAC
GCGCGCCGAGCCCGGCTCCCACGGCCTCTGAGGCTCGGCGGGGCTGCGGCTGCCTGGCGGCGGGCTCCGGAGCT
TTCCTGAGCGGCATTAGCCCACGGCTTGGCCCGGACGCGACCAAAGGCTCTTCTGGAGAAGCCCAGAGCACTGGG
CAATCGTTACGACCTGTAACTTGAGGGCCACCGAACTGCTACTCCCGTTCGCCTTTGGCGATCATCTTTTAACCC
TCCGGAGCACGTCAGCATCCAGCCACCGCGGCGCTCTCCCAGCAGCGGAGGACCCAGGACTATCCCTTCGGCGAG
ACGGATGGAAACCGAGCCCCCTGGAGGACCTGCCCCTGCAGTTCTGCCTCACACGGCTCAAGTCACCACCGTGAA
CAAGGGACCCTAAAGA**ATG**GCCGAGCCTTGGGGGAACGAGTTGGCGTCCGCAGCTGCCAGGGGGGACCTAGAGCA
ACTTACTAGTTTGTTGCAAAATAATGTAAACGTCAATGCACAAAATGGATTTGGAAGGACTGCGCTGCAGGTTAT
GAAACTTGGAAATCCCGAGATTGCCAGGAGACTGCTACTTAGAGGTGCTAATCCCGATTTGAAAGACCGAACTGG
TTTCGCTGTCATTCATGATGCGGCCAGAGCAGGTTTCCTGGACACTTTACAGACTTTGCTGGAGTTTCAAGCTGA
TGTTAACATCGAGGATAATGAAGGGAACCTGCCCTTGCACTTGGCTGCCAAAGAAGGCCACCTCCGGGTGGTGGA
GTTCCTGGTGAAGCACACGGCCAGCAATGTGGGGCATCGGAACCATAAGGGGGACACCGCCTGTGATTTGGCCAG
GCTCTATGGGAGGAATGAGGTTGTTAGCCTGATGCAGGCAAACGGGGCTGGGGGAGCCACAAATCTTCAA**TAA**AC
GTGGGGAGGGCTCCCCCACGTTGCCTCTACTTTATCAATTAACTGAGTAGCTCTCCTGACTTTTAATGTCATTTG
TTAAAATACAGTTCTGTCATATGTTAAGCAGCTAAATTTTCTGAAACTGCATAAGTGAAAATCTTACAACAGGCT
TATGAATATATTTAAGCAACATCTTTTTAACCTGCAAAATCTGTTCTAACATGTAATTGCAGATAACTTTGACTT
TCTTCTGAATATTTTATCTTTCCTTGGCTTTTCCCTTGCTTCCCCTTTTGCCAATCTCAACACCCAAGTTGAAGA
CTTTGTTTTTAAAATGGTTTGTCCTGATGCTTTTGTCTAATTAAAACACTTTCAAAACAGGAAAAAAAAAAAAAA
AAAA

FIGURE 230

MAEPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGANPDLKDRTGFAVIH
DAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFLVKHTASNVGHRNHKGDTACDLARLYGRN
EVVSLMQANGAGGATNLQ

FIGURE 231

AAAACACCAAATGGTGGATGACACCAGTGCAGCGGGGGGGGGCCCGGAGGCCCTGGG**<u>ATG</u>**GGAACTGCGGTGGC
TTCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCAGCCGTAGACGGGGCCGGGGCCGAGGCCGCGGA
GCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCCGTCACCAAGCTGGGCTGCTTGGTGAAGGACATGAAG
ATCAAGTCCCTGGAGGAGATCTATCTCTTCTCCCTGCCCATTAAGGAATCAGAGATCATTGACTTTTTCCTGGGG
GCCTCTCTCAAGGATGAGGTTTTGAAGATTATGCCAGTGCAGACGCAGACCCGTGCTGGCCAGCGCACCAGGTTC
AAGGCGTTTGTTGCTATCGGGGACTACAATGGCCACGTCGGTCTGGGTGTTAAGTGCTCCAAGGAGGTGGCCACC
GCCATCCATGGGGCCATCATCCTGGCCAAGCTCTCCATTGTCCCCGTGCGCAGAGGCTACTGGGGGAACAAGATT
GGCAAGCCCCACACCGTCCCTTGCAAGGTGACAGGCCGCTGCGGCTCTGCACTGGTGCACCTCATCCCTGTACCC
AGGGGCACTGGCATTGTCTCCGCACCTGTGCCCAAGAAGCTGCTCATGATGGCTGGTATCGATGACTGCTGCACC
TCAGCCTGGGGCTGCACTGCCACCCTGGGCAACTTCGCCAAGGCCACCTTTGATGCCATTTCTAAGACCTACAGC
TACCTGACCCCCGACCTCTGGAAGGAGACTGTATTTACCAAGTCTCCCGATCAGGAATTCACTGACCACCTCATC
AAGGCCCACGCCAGAGTCTCCGTGCAGCGGACCCAGGCTCCAGCTGTGGCTACAACA**<u>TAG</u>**GGTTTTTAGACAAGG
AAAATAAAGCGAATTAAGCGT

FIGURE 232

MGNCGGFRGGFGSGIRGRGRSRRRGRGRGRGARGGKAEDKEWMPVTKLGCLVKDMKIKSLEEIYLFSLPIKESEI
IDFFLGASLKDEVLKIMPVQTQTRAGQRTRFKAFVAIGDYNGHVGLGVKCSKEVATAIHGAIILAKLSIVPVRRG
YWGNKIGKPHTVPCKVTGRCGSALVHLIPVPRGTGIVSAPVPKKLLMMAGIDDCCTSAWGCTATLGNFAKATFDA
ISKTYSYLTPDLWKETVFTKSPDQEFTDHLIKAHARVSVQRTQAPAVATT

FIGURE 233

ATGTCTAAGTCAGAATCTCTTAAAGAGCCCGAACAGCTGCAGAAACTCCTCACTGGAGGGTTGAGCATTGAAGCA
ACCAATGAGAGCCTGAGGAGCCATTTTGAGCAATGGGGAACGCTCACGGACTGTGTGGTCCTGAGAGATCCAAAC
ACTAAGTGCTCCAGGGGCTTTGGGTTTGTCACATATGCCACTGTGGAGGAGGTGGATGCAGCCACAAATGCAAGG
CCACACAAGGTGGATGGAAGAGTTGTGGAAACAAAGAGAGCTGTCTCAAGAGAAGATTCCCAAAGACCAGGTGCT
CACTTAACTGTGAAAAAGTTTGGAAAAATGGAAGTGATTGAAATCATGACTGACCATGGCAGTGGCAAGAAAAGG
GACTTTGCCTTTGTAACCTTTGATGACCATGACTCCGTGGATAAGACTGTCATTCAGAAATACCATATTGTGAAT
GGCCACAACTGTGAAGTTAGGAAAGCCCTGTCAAAGCAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAGGTCGA
ACAGGCTCCTTGATGCCTAAAGCCCAATGTCTGGCATTCGAGCCCTCCATGACAGGTTCCCAGCTTTCCTGCAAG
GCCATGCTCCTCACGGCCTATGACTGCCTCCTGTTCTGCGCCTGTCAGGTCTTCCACCTCACCCCTCTTCTCAGC
CTATCCAAGCCCATTCAGTCTTCAGGCGAGCTC**TAG**

FIGURE 234

MSKSESLKEPEQLQKLLTGGLSIEATNESLRSHFEQWGTLTDCVVLRDPNTKCSRGFGFVTYATVEEVDAATNAR
PHKVDGRVVETKRAVSREDSQRPGAHLTVKKFGKMEVIEIMTDHGSGKKRDFAFVTFDDHDSVDKTVIQKYHIVN
GHNCEVRKALSKQEMASASSSQRGRTGSLMPKAQCLAFEPSMTGSQLSCKAMLLTAYDCLLFCACQVFHLTPLLS
LSKPIQSSGEL

FIGURE 235

CGGTCCCGCACTGGTGCAGCC**ATG**TCCTCTTCCCCGTGGGAGCCTGCGACCCTGCGCCGGGTGTTCGTGGTGGGG
GTTGGCATGACCAAGTTTGTGAAGCCTGGAGCTGAGAATTCAAGAGACTACCCTGACTTGGCAGAAGAAGCAGGC
AAGAAGGCTTTAGCTGATGCACAGATCCCTTATTCAGCAGTGGACCAGGCATGTGTTGGCTATGTTTTTGGTGAC
TCTACCTGTGGGCAGAGGGCTATCTATCACAGTTTGGGAATGACTGGAATTCCTATAATCAATGTCAACAATAAC
TGTGCTACTGGTTCTACTGCTTTGTTTATGGCCCGCCAGCTGATTCAGGGTGGTGTGGCAGAATGTGTCTTGGCT
CTTGGGTTTGAGAAGATGAGTAAGGGAAGCCTTGGAATAAAATTTTCAGATAGAACCATTCCCACTGATAAGCAT
GTTGACCTCCTGATCAATAAGTATGGATTGTCTGCTCACCCAGTTGCTCCTCAGATGTTTGGGTATGCTGGAAAA
GAACATATGGAAAAATATGGAACAAAAATTGAACACTTTGCAAAAATTGGATGGAAAAATCATAAACATTCAGTT
AATAACCCGTATTCCCAGTTCCAAGATGAATACAGTTTAGATGAAGTGATGGCATCTAAAGAAGTTTTTGATTTT
TTGACTATCTTACAATGTTGTCCCACTTCAGATGGTGCTGCAGCAGCAATTTTGGCCAGTGAAGCATTTGTACAG
AAGTATGGCCTGCAATCCAAAGCTGTGGAAATTTTGGCACAAGAAATGATGACTGATTTGCCAAGCTCGTTTGAA
GAAAAAAGCATTATTAAAATGGTTGGCTTTGATATGAGTAAAGAAGCTGCAAGAAAATGCTATGAGAAATCTGGC
CTGACACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTCTACCAACGAACTCCTGACTTATGAAGCA
CTCGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGAGGAGATAATACATATGGAGGAAAGTGGGTC
ATAAATCCTAGTGGTGGACTGATTTCAAAGGGACACCCACTAGGCGCTACAGGTCTTGCTCAGTGTGCAGAACTC
TGCTGGCAGCTGAGAGGGGAAGCCGGAAAGAGGCAAGTTCCTGGTGCAAAGGTGGCTCTGCAGCATAATTTAGGC
ATTGGAGGAGCTGTGGTTGTAACACTCTACAAGATGGGTTTTCCGGAAGCCGCCAGTTCTTTTAGAACTCATCAA
ATTGAAGCTGTTCCAACCAGCTCTGCAAGTGATGGATTTAAGGCAAATCTTGTTTTTAAGGAGATTGAGAAGAAA
CTTGAAGAGGAAGGGGAACAGTTTGTGAAGAAAATCGGTGGTATTTTTGCCTTCAAGGTGAAAGATGGCCCTGGG
GGTAAAGAGGCCACCTGGGTGGTGGATGTGAAGAATGGCAAAGGATCAGTGCTTCCTAACTCAGATAAGAAGGCT
GACTGCACAATCACAATGGCTGACTCAGACTTCCTGGCTTTAATGACTGGTAAAATGAATCCTCAGTCGGCCTTC
TTTCAAGGCAAATTGAAAATCACTGGCAACATGGGTCTCGCTATGAAGTTACAAAATCTTCAGCTTCAGCCAGGC
AACGCTAAGCTC**TGA**AGAACTCCCTTTGGCTACTTTTGAAAATCAAGATGAGATATATAGATATATATCCATACA
TTTTATTGTCAGAATTTAGACTGAAACTACACATTGGCAAATAGCGTGGATAGGATTTGTTTCTTAATGGGTGTG
ACCAATCCTGTTTTTCCTATGCTCTGGGTGAATAGAGCCTGATGGTATACTACTGCTTTGCGGAATTGCATACAA
CTGTGCATTACAAAGTTAATATGGTAATTATGGTCTGGGGTAAAATTGAGTTTCAGAATAAAATTAGGAACAGTA
AAATCCAAAGAACTATGTAAACAAAAAAGCTTTTGTTTTGCTTACAAAGTATATTTAAGGATTATTCTGCTGAAG
ATTCAGTTTAAGAGTTTTCCTTGGGAGAACTAAGTAAGAAACACAATGCCAACAGCTGGCCAGTAATTAGTGTTG
TGCACTTCATGTCATTAATCAATTTCTCAATAGTTCTTAAAATTAGTGAGATTAAAAATCTAAAAATTTTGCATT
TCATGCTATCAGAAACAGTATTTTCTTCCCAAATCAAAATAAAAGAAATATGATCAGAGCTTGAACACAGGCTTA
TTTTTAAAATAAAAATATTTTTAACATGGGTTTCCTTATTGAAAAATCAGTGTATTAGTCATAAAACACCATCAT
TAAGAATAATTGAACAATAAAGTTTGCTTTCAGATGCAGTTTTCAAATTATAATCTCATTTCAATTTATAACGTT
CTCAGTCCTTTGTTATAATTTTCCTTTTTCATGTAAGTTTAATTATCTGCATTTATCTTTTTTCCTAGTTTTTCT
AATACTAATGTTATTTCTTAAAATTCAGTGAGATATAGGATAAAATAATGCTTTGAGAAGAATGTTTAATAGAAA
ATTAAAATAACTTTTTCTGGCA

FIGURE 236

MSSSPWEPATLRRVFVVGVGMTKFVKPGAENSRDYPDLAEEAGKKALADAQIPYSAVDQACVGYVFGDSTCGQRA
IYHSLGMTGIPIINVNNNCATGSTALFMARQLIQGGVAECVLALGFEKMSKGSLGIKFSDRTIPTDKHVDLLINK
YGLSAHPVAPQMFGYAGKEHMEKYGTKIEHFAKIGWKNHKHSVNNPYSQFQDEYSLDEVMASKEVFDFLTILQCC
PTSDGAAAAILASEAFVQKYGLQSKAVEILAQEMMTDLPSSFEEKSIIKMVGFDMSKEAARKCYEKSGLTPNDID
VIELHDCFSTNELLTYEALGLCPEGQGATLVDRGDNTYGGKWVINPSGGLISKGHPLGATGLAQCAELCWQLRGE
AGKRQVPGAKVALQHNLGIGGAVVVTLYKMGFPEAASSFRTHQIEAVPTSSASDGFKANLVFKEIEKKLEEEGEQ
FVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDKKADCTITMADSDFLALMTGKMNPQSAFFQGKLKI
TGNMGLAMKLQNLQLQPGNAKL

FIGURE 237

GGCCCTGCGCGCGGCAACATGGCGGGGTCCAGGTGGAGGTCTTGAGGCTATCAGATCGGT<u>ATG</u>GCATTGGCGTCC
GGGCCCGCAAGGCGGGCGCTAGCTGGCTCCGGGCAGCTCGGCCTTGGGGGCTTCGGGGCCCCGAGACGCGGGGCG
TATGAGTGGGGCGTGCGCTCCACGCGGAAGTCGGAGCCTCCTCCCCTGGATAGGGTGTACGAGATCCCTGGACTG
GAGCCCATCACCTTTGCGGGGAAGATGCACTTCGTGCCCTGGCTGGCGCGGCCGATCTTTCCGCCCTGGGACCGC
GGCTACAAGGACCCAAGGTTCTACCGCTCGCCCCCTCTTCACGAGCATCCGCTGTACAAAGACCAGGCCTGCTAT
ATCTTTCACCACCGTTGCCGCCTTCTCGAGGGTGTAAAGCAGGCCCTCTGGCTCACCAAGACCAAGTTAATAGAA
GGCCTTCCCGAGAAAGTGCTTAGCCTTGTTGATGATCCAAGGAACCACATAGAGAACCAAGACGAGTGCGTTCTG
AATGTGATCTCTCACGCCCGTCTCTGGCAGACCACTGAGGAAATCCCCAAGAGAGAGACCTACTGCCCGGTCATC
GTGGACAACCTAATACAGCTGTGTAAATCTCAGATTCTCAAGCATCCTTCTCTGGCCAGGAGGATCTGTGTCCAA
AACTCCACGTTTTCTGCTACCTGGAACCGAGAGTCTCTTCTCCTTCAAGTCCGTGGTTCTGGTGGAGCCCGACTG
AGCACTAAGGATCCTCTGCCCACCATCGCCTCCAGAGAGGAGATTGAAGCTACTAAGAATCATGTTCTAGAGACC
TTCTACCCCATATCACCCATCATCGATCTTCATGAATGCAATATTTATGATGTGAAAAATGACACAGGATTCCAG
GAAGGCTATCCTTACCCCTATCCCCATACCCTGTACTTACTGGACAAAGCCAATTTACGACCACACCGCCTTCAA
CCAGATCAGCTGCGGGCCAAGATGATCCTGTTTGCTTTTGGCAGTGCCCTGGCTCAGGCCCGGCTCCTCTATGGG
AATGATGCCAAGGTCTTGGAGCAGCCCGTGGTGGTGCAGAGCGTGGGCACGGATGGACGTGTCTTCCATTTCCTA
GTGTTTCAACTGAATACCACAGACCTGGACTGTAACGAGGGTGTCAAGAATTTGGCCTGGGTGGACTCAGACCAG
CTCCTCTATCAGCATTTTTGGTGTCTCCCAGTGATCAAAAAGAGAGTGGTTGTGGAACCTGTTGGGCCAGTTGGT
TTCAAGCCAGAGACATTCAGAAAGTTTTTAGCTCTATATTTGCATGGTGCTGCG<u>TGA</u>GCGGAGGACCCCTCTGAA
TCCTGAAACCCCTCTTGCCTCTCTTCCACGGAAGAGGGCCTGGGCCCCGTGGAGCCTCAGTGCCCGTTTGGCCTG
CTGCTCTCGCTGACAATAAAGAGCCCTTGCGTTGC

FIGURE 238

MALASGPARRALAGSGQLGLGGFGAPRRGAYEWGVRSTRKSEPPPLDRVYEIPGLEPITFAGKMHFVPWLARPIF
PPWDRGYKDPRFYRSPPLHEHPLYKDQACYIFHHRCRLLEGVKQALWLTKTKLIEGLPEKVLSLVDDPRNHIENQ
DECVLNVISHARLWQTTEEIPKRETYCPVIVDNLIQLCKSQILKHPSLARRICVQNSTFSATWNRESLLLQVRGS
GGARLSTKDPLPTIASREEIEATKNHVLETFYPISPIIDLHECNIYDVKNDTGFQEGYPYPYPHTLYLLDKANLR
PHRLQPDQLRAKMILFAFGSALAQARLLYGNDAKVLEQPVVVQSVGTDGRVFHFLVFQLNTTDLDCNEGVKNLAW
VDSDQLLYQHFWCLPVIKKRVVVEPVGPVGFKPETFRKFLALYLHGAA

FIGURE 239

CCGCGGCCGGGGCTGACGCTTTGACAGCTGGAAAGAGCGCGGAGCCAGCGCCTGGGGGGGAGGGAGGGGAGCGCG
GCGAGGAGAGCGCCAGCGAGCGAGAGAGCGAGCGAGCGCCGGGGAGGGGGCCGGGAGCGAGGGGCAGCTCGGGAG
AGCCGGAGCGGTAGCGGCGGCGGCGGCGGCGGCGGCGAGGCTCGGCGCCCTCTTCCCTGCAAACC**ATG**TTTGCCA
AAGGCAAAGGCTCGGCGGTGCCCTCGGATGGGCAGGCTCGGGAAAAGTTAGCTTTATACGTCTACGAATATTTAC
TGCACGTAGGAGCACAGAAATCTGCACAGACCTTCTTATCGGAGATTCGATGGGAAAAAAACATCACGTTGGGAG
AACCGCCTGGGTTTTTGCACTCGTGGTGGTGTGTATTTTGGGACCTTTACTGTGCAGCTCCTGAAAGGAGAGACA
CTTGTGAACATTCAAGTGAAGCAAAAGCCTTTCATGATTATAGTGCAGCAGCTGCCCCGAGCCCCGTGCTTGGCA
ACATTCCCCCCAACGATGGGATGCCGGGAGGCCCCATCCCGCCAGGTTTCTTTCAGGGTCCTCCGGGGTCACAGC
CCTCGCCGCACGCACAGCCTCCACCTCACAATCCTAGCAGCATGATGGGACCCCACAGTCAGCCTCCGGGAGGAG
TTCCTGGGACACAGCCATTGCTGCCCAATTCTATGGATCCCACACGACAACAAGGCCACCCCAACATGGGAGGAT
CAATGCAGAGAATGAACCCTCCCCGAGGCATGGGGCCCATGGGTCCCGGCCCACAGAATTACGGCAGCGGCATGA
GACCACCACCCAACTCCCTCGGCCCCGCCATGCCCGGGATTAACATGGGCCCGGGAGCTGGCAGACCCTGGCCCA
ATCCTAACAGTGCTAACTCAATTCCATACTCCTCCTCATCACCTGGTACCTATGTGGGACCCCCTGGTGGTGGCG
GTCCTCCAGGAACACCCATTATGCCCAGTCCCGCAGATTCAACAAATTCCAGTGACAACATCTACACAATGATTA
ATCCAGTGCCGCCTGGAGGCAGCCGGTCCAACTTCCCGATGGGTCCCGGCTCGGACGGTCCGATGGGCGGCATGG
GTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGACTTCCAAAAAATTCTCCTA
ACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAGCTAGGAGGGAACTTCCTCCACT
CCTTTCAGAACGACAATTATTCTCCAAGCATGACGATGAGTGTG**TGA**TCCCCCCTTCTCCGAGACGCTGAGAGAG
CAGGCATTGCAGGCGGGAAGATGCCAGAAATTATGCAAGAAGTGAGGTGTCATTATCCAGGAGCTGGTGGGGAGG
GCATCTCCCTGCTCCCCTCAACCCCCTCCCACCCCATCCACGCCCCCTACCTTTCCCAATTTTAGTTTCATGCAA
TAAAAAGGCCAAACTTTTTATTCCATAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA.

FIGURE 240

MFAKGKGSAVPSDGQAREKLALYVYEYLLHVGAQKSAQTFLSEIRWEKNITLGEPPGFLHSWWCVFWDLYCAAPE
RRDTCEHSSEAKAFHDYSAAAAPSPVLGNIPPNDGMPGGPIPPGFFQGPPGSQPSPHAQPPPHNPSSMMGPHSQP
PGGVPGTQPLLPNSMDPTRQQGHPNMGGSMQRMNPPRGMGPMGPGPQNYGSGMRPPPNSLGPAMPGINMGPGAGR
PWPNPNSANSIPYSSSSPGTYVGPPGGGGPPGTPIMPSPADSTNSSDNIYTMINPVPPGGSRSNFPMGPGSDGPM
GGMGGMEPHHMNGSLGSGDIDGLPKNSPNNISGISNPPGTPRDDGELGGNFLHSFQNDNYSPSMTMSV

FIGURE 241

ATGTACGCCTTTGTGCGGTTCCTGGAGGACAACGTCTGCTACGCGCTGCCCGTGTCGTGCGTGCGCGACTTCAGC
CCCCGCTCGCGGCTGGATTTTGACAACCAGAAGGTGTACGCCGTGTACCGGGGCCCGGAGGAATTGGGCGCCGGG
CCCGAGAGCCCCCCGCGCGCCCCCCGCGACTGGGGCGCGCTGTTGCTCCACAAGGCCCAGATCCTGGCGCTGGCA
GAAGACAAATCTGACCTTGAAAACAGTGTGATGCAGAAGAAAATAAAAATCCCCAAGCTTTCTCTTAATCATGTA
GAAGAAGATGGAGAGGTTAAAGATTATGGGGAAGAAGATTTACAGCTTAGACACATCAAGGATTGTCTGGGGAAA
TATTGATCTGCAGTCCAAGAAAATCCCAGCTGCCCTTGCCTGAACTGATTCTCGTTGTCCTACACAGAGACCTGA
GGGGCGGAAGCCGAGCGAAGTGGCGCACAAGAGCATCGAGGCAGTGGTGGCTCGGCTAGAGAAGCAGAACGGCCT
GAGCCTGGGCCATAGCACGTGTCCGGAAGAGGTCTTCGTGGAGGCCTCGCCAGGCACAGAGGAC**ATG**GACAGTCT
AGAAGATGCTGTGGTGCCCCGGGCTCTGTATGAGGAGCTGCTGCGCAACTACCAGCAGCAACAGGAAGAGATGCG
CCACCTCCAGCAGGAGCTGGAGCGGACTCGGAGGCAGCTGGTACAACAGGCCAAGAAGCTCAAGGAGTACGGGGC
ACTTGTGTCTGAAATGAAGGAGCTCCGTGACCTTAACCGGAGGCTCCAGGACGTGCTGCTCCTGAGGCTTGGCAG
CGGTCCCGCCATTGATCTGGAAAAAGTAAAGTCAGAATGTCTCGAGCCCGAGCCGGAGTTACGGAGCACTTTCAG
TGAGGAAGCAAATACGTCGTCCTATTACCCCGCTCCTGCGCCTGTCATGGACAAGTATATCCTAGACAATGGCAA
GGTCCATCTGGGAAGCGGGATTTGGGTTGATGAGGAGAAATGGCACCAGCTACAAGTAACCCAAGGAGATTCCAA
GTACACGAAGAACTTGGCAGTTATGATTTGGGGAACAGATGTTCTGAAAAACAGAAGCGTCACAGGCGTCGCCAC
AAAAAAAAAGAAAGATGCAGTCCCTAAACCACCCCTCTCGCCTCGCAAACTAAGCATCGTCAGAGAGTGTTTGTA
TGACAGAATAGCACAAGAAACTGTGGATGAAACTGAAATTGCACAGAGACTCTCCAAAGTCAACAAGTACATCTG
TGAAAAAATCATGGATATCAATAAATCCTGTAAAAATGAAGAACGAAGGGAAGCAAAATACAATTTGCAA**TAA**AC
TTTGGATTTTTCAT

FIGURE 242

MDSLEDAVVPRALYEELLRNYQQQQEEMRHLQQELERTRRQLVQQAKKLKEYGALVSEMKELRDLNRRLQDVLLL
RLGSGPAIDLEKVKSECLEPEPELRSTFSEEANTSSYYPAPAPVMDKYILDNGKVHLGSGIWVDEEKWHQLQVTQ
GDSKYTKNLAVMIWGTDVLKNRSVTGVATKKKKDAVPKPPLSPRKLSIVRECLYDRIAQETVDETEIAQRLSKVN
KYICEKIMDINKSCKNEERREAKYNLQ

FIGURE 243

CCTTTCGTTGCCTGATCGCCGCCATCATGGGTCGTATGCGTGCTCCTGAGAAGGGCCTGTCCCAGTCGGCTTTAC
CCTATCGACGCAGCTTCCCCACTTGGTTGAAGTTGACATCTGACGACGTGAAGGAGCAGATTTACAAACTGGCCA
AGAAGGGCCTTACTCCTTCACAGATCGGTGTAATCGTGAGAGAATCACATGGTGTTGCACAAGTACGTTTTGTGA
CAGGCAATCTCTACCATTTAATTAAGAAAGCAGTTGCTGTTCAAAGCATCTTGAGAGGAACAGAAAGGATAAGGA
TGCTAAATTCCATCTGATTCTGATAGAGAGCCAGATTCACCGTTTG

FIGURE 244

CGCCGCCATCATGGGTCGTATGCGTGCTCCTGAGAAGGGCCTGTCCCAGTCGGCTTTACCCTATCGACGCAGCTT
CCCCACTTGGTTGAAGTTGACATCTGACGACGTGAAGGAGCAGATTTACAAACTGGCCAAGAAGGGCCTTACTCC
TTCACAGATCGGTGTAATCGTGAGAGAATCACATGGTGTTGCACAAGTACGTTTTGTGACAGGCAATAAAATTTT
AAGAATTCTTAAGTCTAAGGGACTTGCTCCTGATCTTCCTGAAGATCTCTACCATTTAATTAAGAAAGCAGTTGC
TGTTCAAAGCATCTTGAGAGGAACAGAAAGGATAAGGATGCTAAATTCCATCTGATTCTGATAGAGAGCCAGATT
CACCGTTTGGCTCAATATTATAAGACCAAGCGAGTCCTCCCTCCCAGTTGGAAATATGAATCATCTACAGCCTCT
GCCCTGGTCGCATAAATTTGTCTGTGTACTCAAGCAATAAAATGATTGTTTAACTAAAATAAAACAAAAACAAAA
ACAAAAAAA

FIGURE 245

AGAAG<u>ATG</u>CTTCAAATTCAACCCGAGAAGGATATCATTGTAGAGTTTATCAAAAATGGAGATTTCAAGTATGTCC
GCATGCTGGGGGCACTTTACATGAGGCTGACAGGCACTGCAATTGATTGCTACAAGTACTTGGAACCTTTGTACA
ATGACTATCGAAAAATCAAGAGCCAGAACCGAAATGGGGAGTTTGAATTGATGCATGTTGATGAGTTTATTGATG
AACTATTGCACAGTGAGAGAGTCTGTGATATCATTCTGCCCCGACTACAGAAACGCTATGTATTAGAGGAAGCTG
AGCAACTGGAGCCTCGAGTTAGTGCTCTGGAAGAGGACATGGATGATGTGGAGTCCAGTGAAGAGGAAGAAGAGG
AGGATGAGAAGTTGGAAAGAGTGCCATCACCTGATCACCGCCGGAGAAGCTACCGAGACTTGGACAAGCCCCGTC
GCTCTCCCACACTGCGCTACAGGAGGAGTAGGAGCCGGTCTCCCAGAAGGCGGAGTCGATCTCCCAAAAGGAGAA
GCCCCTCCCCTCGCCGAGAAAGGCATCGGAGCAAGAGTCCAAGACGTCACCGCAGCAGGTCCCGAGATCGGCGGC
ACAGATCCCGTTCCAAGTCCCCAGGTCATCACCGTAGTCACAGACACAGGAGCCACTCAAAGTCTCCCGAAAGGT
CTAAGAAGAGCCACAAGAAGAGCCGGAGAGGGAATGAG<u>TAA</u>TGGACTCAGTTTGGTTTTAGTCCACATGGCCTCC
TGTGGATATAAGGATATCTGTATGTGGAAGGATTAAGATCTCCCCCAGGCAGCTATAAGAATATTTTAGTTTTTT
TCTTATCAAGTTTCTCAACCTTTATTTTTAATGAAGGAGGTGCTGAGTTTTGTATCTTTTTAATCATAATCAACA
TCAGTTTTTGACCCAACTAACCTTGACTGTATTCAAACTTATGAGAGTATAAAGGATCTGGAGGTTGGGGATATG
ACTGACAAGGAAAGGCTGTGGCCACCTGATGACCCTTTCCCTTTTTATTAAACCGGACACACCTGTTTCCCATTT
CGCTGTAGTTTAGTTTTTGGTTTGTTGTGGTTGGAACTGCTTTGAGAATCCTGGGATTTGTGCTGCTGCTGTTAT
TCAAAGATCAAAGGAGTAAAACATAGTTGCTCCTAACTTTTTTCCAGCAGCAGCAAGTGGTAATAAACATGAAAA
CTGGTTTGTAGCAGTTTTGAAAGAATAGAATGCATTCAAATGTAAGGCTGCTTCTGGATCATTAAAGCCAGTTTC
ATCAAACAGTTCAACAGAGAGCAGCACTTAATACCCTTTATACAGCCCATTTTTTCATAGTTTCATTTGTTCTTG
CCCACAAGCTTGAAATCCAGGTTAAGGTATCCAGCCTTTATCATATAAGCATTGACATTATCCAGGCCTAGTCAG
TAGCAGTAGGGTAACGGGATTGAAAAAGATTTGATGGAGAGGAAAGTATCTAATATTAGTCATGGTTTTGACCTA
AATTGCTAGACAGTCGTGCCATTCACAAAGTCAGAAAATACAGCAGGAAGAGACAGCTTTTAGAGGGGCAGAGAA
TTAGAGGATGGTGGTAGTAATGAAAAAGATGCATTCAGTTTAACAAGTTTAATTTGAGACAGCTATGGTATAGCT
AAAAACAAAAGCCCATAAAGTTGGAGATAGGGACCAGAGTTTAACATAGCGATCTAGGCCAGAATTGACAATGTT
TAAGTAATGGTGGAATCTGTCAATAAGACTTCCCAGAGTGTTAATATATATCAGAAATGCACACAACAGAACCAT
AGGCAACACCAACACAGGAAGAAATAGAAGTCACCTATTGAAAACTGGAATGGCCCATTCAGAAAGACAGGAGAA
TTAGGAGAGAGTGAGTGAAAGAAGCCAAGGGTCAAGAATGCAGAAGCAAAGGAAGGACTAAAAAGCCTCCACGGA
CATCGATAATCAAGAGATTATTAAGATCTTTGCTAGAAGAGTTCCTTTACCTGTACTTAACTCCCTTAAAAAGAG
AAAAGTGATGGAATGACTTCTGCAACTGTAGTCCCAGCAGGAACTGTGAAGACCAGCTGCCCTGCAGGATCCAGT
TTTTCTTGGGAGGTTGTATCTGGTCATAAGGTAAACATTCTATATATTCTATGCCTGCTCTAGAATTGAAAGACT
TCAGCAGTATTAAAGCATTTTTTAATCTT

FIGURE 246

MLQIQPEKDIIVEFIKNGDFKYVRMLGALYMRLTGTAIDCYKYLEPLYNDYRKIKSQNRNGEFELMHVDEFIDEL
LHSERVCDIILPRLQKRYVLEEAEQLEPRVSALEEDMDDVESSEEEEEEDEKLERVPSPDHRRRSYRDLDKPRRS
PTLRYRRSRSRSPRRRSRSPKRRSPSPRRERHRSKSPRRHRSRSRDRRHRSRSKSPGHHRSHRHRSHSKSPERSK
KSHKKSRRGNE

FIGURE 247

GTTCGGGCCAG**ATG**GCGTCCATCATGGAAGGGCCGCTGAGCAAATGGACTAACGTGATGAAGGGCTGGCAGTACC
GTTGGTTCGTGCTGGACTACAATGCAGGACTGCTCTCCTACTACACGTCCAAGGACAAAATGATGAGAGGCTCTC
GCAGAGGATGTGTTAGACTCAGAGGAGCTGTGATTGGTATAGACGATGAGGACGACAGCACCTTCACAATAACTG
TTGATCAGAAAACCTTCCATTTCCAGGCCCGTGATGCTGATGAGCGAGAGAAGTGGATCCATGCCTTAGAAGAAA
CAATTCTTCGACATACTCTCCAGCTTCAAGGTTTGGATTCAGGATTTGTTCCTAGTGTCCAAGATTTTGATAAGA
AACTTACAGAAGCTGATGCTTACCTACAAATCTTGATTGAACAATTAAAGCTTTTTGATGACAAGCTTCAAAACT
GCAAAGAAGATGAACAGAGAAAGAAAATTGAAACTCTCAAAGAGACAACAAATAGCATGGTAGAATCAATTAAAC
ACTGCATTGTGTTGCTGCAGATTGCCAAAGACCAGAGTAATGCGGAGAAGCACGCAGATGGAATGATAAGTACTA
TTAATCCCGTAGATGCAATATATCAACCTAGTCCTTTGGAACCTGTGATCAGCACAATGCCTTCCCAGACTGTGT
TACCTCCAGAACCTGTTCAGTTGTGTAAGTCAGAGCAGCGTCCATCTTCCCTACCAGTTGGACCTGTGTTGGCTA
CCTTGGGACATCATCAGACTCCTACACCAAATAGTACAGGCAGTGGCCATTCACCACCGAGTAGCAGTCTCACTT
CTCCAAGCCACGTGAACTTGTCTCCAAATACAGTCCCAGAGTTCTCTTACTCCAGCAGTGAAGATGAATTTTATG
ATGCTGATGAATTCCATCAAAGTGGCTCATCCCCAAAGCGCTTAATAGATTCTTCTGGATCTGCCTCAGTCCTGA
CACACAGCAGCTCGGGAAATAGTCTAAAACGCCCAGATACCACAGAATCACTTAATTCTTCCTTGTCCAATGGAA
CAAGTGATGCTGACCTGTTTGATTCACATGATGACAGAGATGATGATGCGGAGGCAGGGTCTGTGGAGGAGCACA
AGAGCGTTATCATGCATCTCTTGTCGCAGGTTAGACTTGGAATGGATCTTACTAAGGTAGTTCTTCCAACGTTTA
TTCTTGAAAGAAGATCTCTTTTAGAAATGTATGCAGACTTTTTTGCACATCCGGACCTGTTTGTGAGCATTAGTG
ACCAGAAGGATCCCAAGGATCGAATGGTTCAGGTTGTGAAATGGTACCTCTCAGCCTTTCATGCGGGAAGGAAAG
GATCAGTTGCCAAAAAGCCATACAATCCCATTTTGGGCGAGATTTTTCAGTGTCATTGGACATTACCAAATGATA
CTGAAGAGAACACAGAACTAGTTTCAGAAGGACCAGTTCCCTGGGTTTCCAAAAACAGTGTAACATTTGTGGCTG
AGCAGGTTTCCCATCATCCACCCATTTCAGCCTTTTATGCTGAGTGTTTTAACAAGAAGATACAATTCAATGCTC
ATATCTGGACCAAATCAAAATTCCTTGGGATGTCAATTGGGGTGCACAACATAGGGCAGGGCTGTGTCTCATGTC
TAGACTATGATGAACATTACATTCTCACATTCCCCAATGGCTATGGAAGGTCTATCCTCACAGTGCCCTGGGTGG
AATTAGGAGGAGAATGCAATATTAATTGTTCCAAAACAGGCTATAGTGCAAATATCATCTTCCACACTAAACCCT
TCTATGGGGGCAAGAAGCACAGAATTACTGCCGAGATTTTTTCTCCAAATGACAAGAAGTCTTTTTGCTCAATTG
AAGGGGAATGGAATGGTGTGATGTATGCAAAATATGCAACAGGGGAAAATACAGTCTTTGTAGATACCAAGAAGT
TGCCTATAATCAAGAAGAAAGTGAGGAAGTTGGAAGATCAGAACGAGTATGAATCCCGCAGCCTTTGGAAGGATG
TCACTTTCAACTTAAAAATCAGAGACATTGATGCAGCAACTGAAGCAAAGCACAGGCTTGAAGAAAGACAAAGAG
CAGAAGCCCGAGAAAGGAAGGAGAAGGAAATTCAGTGGGAGACAAGGTTATTTCATGAAGATGGAGAATGCTGGG
TTTATGATGAACCATTACTGAAACGTCTTGGTGCTGCCAAGCAT**TAG**GTTGGAAGATGCAAAGTTTATACCTGAT
GATCAGGGCAGTAGGCATAATTCAGCAACAAACAATCTTCCTTTGGGAGAAACCTGTTCATTCCAATCTTCTAAT
TACAGTGGTTCCTATCTCAGGGATACTGGACTTTCTGACGCAGATGAACAATTAAGGGGAAAAGCTTCCCTTTTC
CCTCTGTGGCAGTTACGATTTTGACTTCAGTCCTGAGAAAAACTTCAGGTTTTGAAAATCAGATGATGTCTTCTC
CTTTTCCAAACACCACACGTTGAAAGCATTTATAAATCCAAGTCTGAAACTCTGCGCTCTAGTACTGCTGTTAAG
ATACACAACTTGTTTCTTAGTTCATATAATCTCGGGATACACACACACACACACATATATATACACACACATACG
TATACACACACATACATATATATAAATATACCTGATGCCAGATTTTTTCATAAATATTCTGCCTACTGTAAATA
TGGGTTCCTCTGAGTTGTTTTAGAAAATTAGCGCAATGTATTAAAATCAAGTGTTAGGAAATTTCATGGTCTTAC
CTACAATAACTTTTATTTTGGAATTGAACTATTATTAAATTGTATCTAATCCTGGATTACAGTTTAATTAATTAT
TCTTAGTGCTTAAGGCTTCATAAAGTAATTTTTCCAACCTTTTTTTAAAAAAAAAAAAAA

FIGURE 248

MASIMEGPLSKWTNVMKGWQYRWFVLDYNAGLLSYYTSKDKMMRGSRRGCVRLRGAVIGIDDEDDSTFTITVDQK
TFHFQARDADEREKWIHALEETILRHTLQLQGLDSGFVPSVQDFDKKLTEADAYLQILIEQLKLFDDKLQNCKED
EQRKKIETLKETTNSMVESIKHCIVLLQIAKDQSNAEKHADGMISTINPVDAIYQPSPLEPVISTMPSQTVLPPE
PVQLCKSEQRPSSLPVGPVLATLGHHQTPTPNSTGSGHSPPSSSLTSPSHVNLSPNTVPEFSYSSSEDEFYDADE
FHQSGSSPKRLIDSSGSASVLTHSSSGNSLKRPDTTESLNSSLSNGTSDADLFDSHDDRDDDAEAGSVEEHKSVI
MHLLSQVRLGMDLTKVVLPTFILERRSLLEMYADFFAHPDLFVSISDQKDPKDRMVQVVKWYLSAFHAGRKGSVA
KKPYNPILGEIFQCHWTLPNDTEENTELVSEGPVPWVSKNSVTFVAEQVSHHPPISAFYAECFNKKIQFNAHIWT
KSKFLGMSIGVHNIGQGCVSCLDYDEHYILTFPNGYGRSILTVPWVELGGECNINCSKTGYSANIIFHTKPFYGG
KKHRITAEIFSPNDKKSFCSIEGEWNGVMYAKYATGENTVFVDTKKLPIIKKKVRKLEDQNEYESRSLWKDVTFN
LKIRDIDAATEAKHRLEERQRAEARERKEKEIQWETRLFHEDGECWVYDEPLLKRLGAAKH

FIGURE 249A

CCCGGGCTGTGGGCTACAGGCGCAGAGCGGGCCAGGCGCGGAGCTGGCGGCAGTGACAGGAGGCGCGAACCCGCA
GCGCTTACCGCGCGGCGCCGCACCATGGAGCCCGCCGTGTCGCTGGCCGTGTGCGCGCTGCTCTTCCTGCTGTGG
GTGCGCCTGAAGGGGCTGGAGTTCGTGCTCATCCACCAGCGCTGGGTGTTCGTGTGCCTCTTCCTCCTGCCGCTC
TCGCTTATCTTCGATATCTACTACTACGTGCGCGCCTGGGTGGTGTTCAAGCTCAGCAGCGCTCCGCGCCTGCAC
GAGCAGCGCGTGCGGGACATCCAGAAGCAGGTGCGGGAATGGAAGGAGCAGGGTAGCAAGACCTTCATGTGCACG
GGGCGCCCTGGCTGGCTCACTGTCTCACTACGTGTCGGGAAGTACAAGAAGACACACAAAAACATCATGATCAAC
CTGATGGACATTCTGGAAGTGGACACCAAGAAACAGATTGTCCGTGTGGAGCCCTTGGTGACCATGGCCAGGTG
ACTGCCCTGCTGACCTCCATTGGCTGGACTCTCCCCGTGTTGCCTGAGCTTGATGACCTCACAGTGGGGGGCTTG
ATCATGGGCACAGGCATCGAGTCATCATCCCACAAGTACGGCCTGTTCCAACACATCTGCACTGCTTACGAGCTG
GTCCTGGCTGATGGCAGCTTTGTGCGATGCACTCCGTCCGAAAACTCAGACCTGTTCTATGCCGTACCCTGGTCC
TGTGGGACGCTGGGTTTCCTGGTGGCCGCTGAGATCCGCATCATCCCTGCCAAGAAGTACGTCAAGCTGCGTTTC
GAGCCAGTGCGGGGCCTGGAGGCTATCTGTGCCAAGTTCACCCACGAGTCCCAGCGGCAGGAGAACCACTTCGTG
GAAGGGCTGCTCTACTCCCTGGATGAGGCTGTCATTATGACAGGGGTCATGACAGATGAGGCAGAGCCCAGCAAG
CTGAATAGCATTGGCAATTACTACAAGCCGTGGTTCTTTAAGCATGTGGAGAACTATCTGAAGACAAACCGAGAG
GGCCTGGAGTACATTCCCTTGAGACACTACTACCACCGCCACACGCGCAGCATCTTCTGGGAGCTCCAGGACATT
ATCCCCTTTGGCAACAACCCCATCTTCCGCTACCTCTTTGGCTGGATGGTGCCTCCCAAGATCTCCCTCCTGAAG
CTGACCCAGGGTGAGACCCTGCGCAAGCTGTACGAGCAGCACCACGTGGTGCAGGACATGCTGGTGCCCATGAAG
TGCCTGCAGCAGGCCCTGCACACCTTCCAAAACGACATCCACGTCTACCCCATCTGGCTGTGTCCGTTCATCCTG
CCCAGCCAGCCAGGCCTAGTGCACCCCAAAGGAAATGAGGCAGAGCTCTACATCGACATTGGAGCATATGGGGAG
CCGCGTGTGAAACACTTTGAAGCCAGGTCCTGCATGAGGCAGCTGGAGAAGTTTGTCCGCAGCGTGCATGGCTTC
CAGATGCTGTATGCCGACTGCTACATGAACCGGGAGGAGTTCTGGGAGATGTTTGATGGCTCCTTGTACCACAAG
CTGCGAGAGAAGCTGGGTTGCCAGGACGCCTTCCCCGAGGTGTACGACAAGATCTGCAAGGCCGCCAGGCACTGA
GCTGGAGCCCGCCTGGAGAGACAGACACGTGTGAGTGGTCAGGCATCTTCCCTTCACTCAAGCTTGGCTGCTTTC
CTAGATCCACACTTTCAAAGAGAAACCCCTCCAGAACTCCCACCCTGACAGCCCAACACCACCTTCCTCCTGGCT
TCCAGGGGGCAGCCCAGTGGAATGGAAAGAATGTGGGATTTGGAGTCAGACAAGCCTGAGTCCAGTTCCCCGTTT
AGAACTCATTAGCTGTGTGACTCTGGGTGAGTCCCTTAACCCCTCTGAGCCCGGGTCTCTTCATTAGTTGAAAGG
GATAGTAATACCTACTTGCAGGTTGTTGTCATCTGAGTTGAGCACTGGTCACATTGAAGGTGCTGGGTAAGTGGT
AGCTCTTGTTGCTTCCCGTTCAGCGTCACATCTGCAGTGGAGCCTGAAAAGGCTCCACATTAGGTCACCTGTGCA
CAGCCATGGCTGGAATGATGAAGGGGATACGCTGGAGTTGCCCTGCCATCGCCTCCATCAGCCAGACGAGGTCCT
CACAGGAGAAGGACAGCTCTTCCCCACCCTGGGATCTCAGGAGGGCAGCCACGGAGTGGGGAGGCCCCAGATGCG
CTGTGCCAAAGCCAGGTCCGAGGCCAAAGTTCTCCCTGCCATCCTTGGTGCCGTCCTGCCCCTTCCTCCTTCATG
CCTGGGCCTGCAGGCCCACCCCAGCCACCACTGAGTCCACTCGGAGTGCCCTGTGTTCCTGGAGAAGGCATTCCA
GGGTTGAATCTTGTCCCAGCCTCAGCCTGGGACACCTAGGTGGAGAGAGTGGTCTCCGCTCTGAATTGGATCCAG
GGGACCTGGGCTCATTCTTCTTGGCTCACCAACCCTGCAGGCCTCATCTTTCCCAAAACCCACTTTGTCTTGGTG
GGAGTGGGTCCGCGCTGCTCTGCAGCAGGGGCTGGGGAGTGGACAGCATCAGGTGGGAAAGTGGAGTCCACCCTC
ATGTTTCTGTAGGATTCTCACCGTGGGGCTGGAAGAAAAGAGCATCGACTTGATTTCTCCAACCACTCATCCCTC
TTTTTCTTTCTTCCACCACTCCCCACCCCAGCTGTAGTTAATTTCAGTGCCTTACAAATCCTAAGCTCAGAGAAA
GTTCCATTTCCGTTCCAGAGGGAAGGGAACCTCCCTAGGTCCTTCCCTGGCTTGTTATAACGCAAAGCTTGGTTG
TTTATGCAACTCTATCTTAAGAACTGCCCAGCCTCAGCTGAAAACCCGAATCTGAGAAGGAATTGCGTCATGTAA
GGGAAGCTGGAATTAAGGGAGCTGAGCCAGTCATGGTTGTGGCGTGTGAGTCAGGAGACCTAGGTTTCAGCCCCT
CTCTACTGTCAGCGAGCTGTGCAACGTGGGCAAGTCATTGTCCTCTGAGCTGCAGTTTCCTCATCTGTCACATCG
CTACAGACAAGACCTCCCTGGAACCCTTCTGATTGTCTTAGACACTGTGGTTGCAAAACCCACGGAAAGCCTCAT
TTGTGTGGAAAGTCAGAGGAAAAATGATCCAGTGGACACTTGGGGATTATCTGTCATTCAAGATCCTTCCTTCAA
CCCCAAGGTCAGCTCCCATCTCATTTCCAGAAAGGCTCATACCTGGCTTGCAGGGAAGCATCTGTCTTGTCATTC
CAGGTGCCAGAATCCTCTCAGAGTCATTGAAGGGTGTTCACCCATCCCACCCAAGGCTTGGCACACTGCCAGTGT
CTTAGCAGGGTCTTGTGAGGGCTGGGGGCATCCAGGCACTCAGAAGGCAAAGGAACCACCCTACCCATTTGGCCT
CTGGAGGGGGCAGAAGAAAGAAATAAACCTCATCCTATATTTACAAAGCATGTGAATTCTGGCATTAGCTCTCA
TAGGAGACCCATGTGCTTCCTTGCTCAGTGCAAAACTGATGATTCTACTTGCTGTAGATGAATGGTTAACACGAG

FIGURE 249B

CTAGTTAAACAGTGCCATTGTTTTGCCAGTGAAGCCTCCAACCCTAAGCCACTGGGACGGTGGCCAGAGATGCCA
GCAGCCTCTGTCGCCCTTAGTCATATAACCAAAATCCAGACCTTATCCACAACCCGGGGCTTGGAAAGGAAGGTA
TTTTGGAATCACACCCTCCGGTTATGTTGCTCCAGTAAAATCTTGCCTGGAAAGAGGCAGTCTTCTTAGCATGGT
GAGCTGAGTTCATGGCTTTTTTTTGTAGCCAGTCCTGTCCCTGGCCATCCATGTGATGGTTTTGGATGGAGTTAA
ACTTGATGCCAGTGGGCAGTGCATGTGGAAAGTATCAGAGTAAGGCTCTCCCCTCCAGAGCCCTGAGTTTCTTGG
CTGCATGAAGGTTTTCTTTAGAATCAGAATTGTAGCCAGTTTCTTTGGCCAGAAGGATGAATACTTGGATATTAC
TGAAAGGGAGGGGTGGAGATGGGTGTGGCAGTGTATGGTGTGTGATTTTTATTTTCTTCTTTGGTCATGGGGGCC
AAGGAGAAAGGCATGAATCTTCCCTGTCAGGCTCTTACAGCCACAGGCACTGTGTCTACTGTCTGGAAGACATGT
CCCCATGGCTGTGGGGCCGCTGCTTCTGTTTAAATAAAAGTGGCCTGG

FIGURE 250

GACATCATGGGCTATTTTTAGGGGTTGACTGGTAGCAGATAAGTGTTGAGCTCGGGCTGGATAAGGGCTCAGAGT
TGCACTGAGTGTGGCTGAAGCAGCGAGGCGGGAGTGGAGGTGCGCGGAGTCAGGCAGACAGACAGACACAGCCAG
CCAGCCAGGTCGGCAGTATAGTCCGAACTGCAAATCTTATTTTCTTTTCACCTTCTCTCTAACTGCCCAGAGCTA
GCGCCTGTGGCTCCCGGGCTGGTGTTTCGGGAGTGTCCAGAGAGCCTGGTCTCCAGCCGCCCCCGGGAGGAGAGC
CCTGCTGCCCAGGCGCTGTTGACAGCGGCGGAAAGCAGCGGTACCCACGCGCCCGCCGGGGGAAGTCGGCGAGCG
GCTGCAGCAGCAAAGAACTTTCCCGGCTGGGAGGACCGGAGACAAGTGGCAGAGTCCCGGAGCCAACTTTTGCAA
GCCTTTCCTGCGTCTTAGGCTTCTCCACGGCGGTAAAGACCAGAAGGCGGCGGAGAGCCACGCAAGAGAAGAAGG
ACGTGCGCTCAGCTTCGCTCGCACCGGTTGTTGAACTTGGGCGAGCGCGAGCCGCGGCTGCCGGGCGCCCCCTCC
CCCTAGCAGCGGAGGAGGGGACAAGTCGTCGGAGTCCGGGCGGCCAAGACCCGCCGCCGGCCGGCCACTGCAGGG
TCCGCACTGATCCGCTCCGCGGGGAGAGCCGCTGCTCTGGGAAGTGAGTTCGCCTGCGGACTCCGAGGAACCGCT
GCGCACGAAGAGCGCTCAGTGAGTGACCGCGACTTTTCAAAGCCGGGTAGCGCGCGCGAGTCGACAAGTAAGAGT
GCGGGAGGCATCTTAATTAACCCTGCGCTCCCTGGAGCGAGCTGGTGAGGAGGGCGCAGCGGGGACGACAGCCAG
CGGGTGCGTGCGCTCTTAGAGAAACTTTCCCTGTCAAAGGCTCCGGGGGGCGCGGGTGTCCCCCGCTTGCCACAG
CCCTGTTGCGGCCCCGAAACTTGTGCGCGCAGCCCAAACTAACCTCACGTGAAGTGACGGACTGTTCTATGACTG
CAAAGATGGAAACGACCTTCTATGACGATGCCCTCAACGCCTCGTTCCTCCCGTCCGAGAGCGGACCTTATGGCT
ACAGTAACCCCAAGATCCTGAAACAGAGCATGACCCTGAACCTGGCCGACCCAGTGGGGAGCCTGAAGCCGCACC
TCCGCGCCAAGAACTCGGACCTCCTCACCTCGCCCGACGTGGGGCTGCTCAAGCTGGCGTCGCCCGAGCTGGAGC
GCCTGATAATCCAGTCCAGCAACGGGCACATCACCACCACGCCGACCCCCACCCAGTTCCTGTGCCCCAAGAACG
TGACAGATGAGCAGGAGGGCTTCGCCGAGGGCTTCGTGCGCGCCCTGGCCGAACTGCACAGCCAGAACACGCTGC
CCAGCGTCACGTCGGCGGCGCAGCCGGTCAACGGGGCAGGCATGGTGGCTCCCGCGGTAGCCTCGGTGGCAGGGG
GCAGCGGCAGCGGCGGCTTCAGCGCCAGCCTGCACAGCGAGCCGCCGGTCTACGCAAACCTCAGCAACTTCAACC
CAGGCGCGCTGAGCAGCGGCGGCGGGGCGCCCTCCTACGGCGCGGCCGGCCTGGCCTTTCCCGCGCAACCCCAGC
AGCAGCAGCAGCCGCCGCACCACCTGCCCCAGCAGATGCCCGTGCAGCACCCGCGGCTGCAGGCCCTGAAGGAGG
AGCCTCAGACAGTGCCCGAGATGCCCGGCGAGACACCGCCCCTGTCCCCCATCGACATGGAGTCCCAGGAGCGGA
TCAAGGCGGAGAGGAAGCGCATGAGGAACCGCATCGCTGCCTCCAAGTGCCGAAAAAGGAAGCTGGAGAGAATCG
CCCGGCTGGAGGAAAAAGTGAAAACCTTGAAAGCTCAGAACTCGGAGCTGGCGTCCACGGCCAACATGCTCAGGG
AACAGGTGGCACAGCTTAAACAGAAAGTCATGAACCACGTTAACAGTGGGTGCCAACTCATGCTAACGCAGCAGT
TGCAAACATTTTGAAGAGAGACCGTCGGGGGCTGAGGGGCAACGAAGAAAAAAAATAACACAGAGAGACAGACTT
GAGAACTTGACAAGTTGCGACGGAGAGAAAAAAGAAGTGTCCGAGAACTAAAGCCAAGGGTATCCAAGTTGGACT
GGGTTGCGTCCTGACGGCGCCCCCAGTGTGCACGAGTGGGAAGGACTTGGCGCGCCCTCCCTTGGCGTGGAGCCA
GGGAGCGGCCGCCTGCGGGCTGCCCCGCTTTGCGGACGGGCTGTCCCCGCGCGAACGGAACGTTGGACTTTTCGT
TAACATTGACCAAGAACTGCATGGACCTAACATTCGATCTCATTCAGTATTAAAGGGGGGAGGGGGAGGGGGTTA
CAAACTGCAATAGAGACTGTAGATTGCTTCTGTAGTACTCCTTAAGAACACAAAGCGGGGGGAGGGTTGGGGAGG
GGCGGCAGGAGGGAGGTTTGTGAGAGCGAGGCTGAGCCTACAGATGAACTCTTTCTGGCCTGCCTTCGTTAACTG
TGTATGTACATATATATATTTTTTAATTTGATGAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAG
TTATTTCTTGTTTGTTTGTTTGGGTATCCTGCCCAGTGTTGTTTGTAAATAAGAGATTTGGAGCACTCTGAGTTT
ACCATTTGTAATAAAGTATATAATTTTTTTATGTTTTGTTTCTGAAAATTCCAGAAAGGATATTTAAGAAAATAC
AATAAACTATTGGAAAGTACTCCCCTAACCTCTTTTCTGCATCATCTGTAGATACTAGCTATCTAGGTGGAGTTG
AAAGAGTTAAGAATGTCGATTAAAATCACTCTCAGTGCTTCTTACTATTAAGCAGTAAAAACTGTTCTCTATTAG
ACTTTAGAAATAAATGTACCTGATGTACCTGATGCTATGGTCAGGTTATACTCCTCCTCCCCCAGCTATCTATAT
GGAATTGCTTACCAAAGGATAGTGCGATGTTTCAGGAGGCTGGAGGAAGGGGGGTTGCAGTGGAGAGGGACAGCC
CACTGAGAAGTCAAACATTTCAAAGTTTGGATTGTATCAAGTGGCATGTGCTGTGACCATTTATAATGTTAGTAG
AAATTTTACAATAGGTGCTTATTCTCAAAGCAGGAATTGGTGGCAGATTTTACAAAAGATGTATCCTTCCAATTT
GGAATCTTCTCTTTGACAATTCCTAGATAAAAAGATGGCCTTTGCTTATGAATATTTATAACAGCATTCTTGTCA
CAATAAATGTATTCAAATACC

FIGURE 251A

GTTAACAAAAGGATTAATGGGTTGCTTAAATTAGTGAGCTTCATCAGTTTTATTTTAATTCCTTGAGATAATGA
ATTTTAAAAGCAATAAATACAATGCTGTAGTTTTTGACTTCTTTTCTAAATATTTACATGGATTTACATGAAAGA
ACTAAAGAGATAGTATTTGTGGAACCAATTTAAACTCTTACATGCCTTTCAGGATTTGGGAATGTATTAACACCT
GCTGCTTTGTATCCAGTCTAAGGGAGCCTATTTGTTTGTTATCACATTGACTTCCTTTGATGTCTTTTAGTGTTA
CCCTCACTCAGACCCAAGGATTATGTCTTTTGGGGCTCCCATCATCCTGAGCTAGAGACACGTGACAGGGGTACA
CTCTCCTACAAAACCAGCCAGTTACTCAGTAAAGTGGACGATAGAAGAAAAAGAGCTGTTTGAACAAGGGCTGGC
TAAATTTGGCCGAAGATGGACCAAAATTTCAAAGCTAATTGGAAGCCGCACTGTTTTACAAGTGAAGAGTTATGC
AAGACAGTATTTTAAAAATAAGGTCAAATGCGGTCTGGATAAAGAAACACCAAATCAGAAGACCGGCCATAATCT
TCAAGTTAAAAATGAAGATAAAGGGACAAAGGCATGGACACCATCATGTTTAAGGGGACGTGCTGATCCCAACTT
GAATGCTGTAAAAATTGAAAAGTTATCTGATGATGAAGAAGTAGACATCACAGATGAGGTGGACGAGTTGTCTTC
TCAAACACCCCAGAAGAATTCTAGCAGTGATCTCTTGTTAGACTTTCCTAATAGTAAA<u>ATG</u>CATGAAACCAATCA
AGGAGAATTCATTACTTCTGACAGCCAGGAAGCTCTCTTTTCTAAGTCTTCCAGGGGCTGTCTTCAAAATGAAAA
GCAAGATGAAACACTTTCAAGCTCAGAAATTACACTGTGGACTGAGAAACAGAGCAATGGTGACAAAAAAATCAAT
TGAATTAAATGACCAGAAATTTAATGAATTGATTAAAAACTGCAACAAGCATGATGGAAGGGGAATAATAGTTGA
TGCCAGGCAGTTGCCTTCTCCAGAGCCTTGTGAAATTCAGAAAAATTTGAATGATAATGAAATGCTTTTTCATTC
TTGCCAAATGGTAGAGGAAAGCCATGAGGAAGAAGAGCTTAAGCCACCAGAACAGGAAATAGAAATAGATAGAAA
TATCATTCAAGAAGAAGAAAAACAAGCAATTCCTGAGTTTTTTGAGGGGCGCCAAGCTAAAACACCAGAACGCTA
TTTGAAAATTAGAAATTATATTTTGGATCAATGGGAGATATGCAAACCAAAATACTTAAATAAGACCTCAGTACG
TCCTGGCCTGAAGAACTGTGGAGATGTTAATTGTATTGGACGGATTCATACATACCTCGAATTGATAGGAGCAAT
CAATTTTGGATGTGAACAGGCTGTGTATAATAGGCCACAAACAGTTGACAAAGTACGAATCAGAGACAGAAAAGA
TGCAGTAGAAGCATACCAACTTGCCCAGCGTCTGCAGTCTATGCGTACAAGGAGACGTAGGGTCCGAGACCCATG
GGGAAACTGGTGTGATGCAAAGGACTTAGAAGGACAAACGTTTGAGCATCTCTCTGCTGAGGAGTTGGCAAAAAG
AAGAGAAGAGGAAAAAGGCAGACCTGTTAAATCTTTAAAAGTGCCAAGACCAACAAAAAGCTCGTTTGATCCCTT
CCAACTGATACCTTGTAATTTTTTTAGTGAAGAAAAGCAGGAGCCATTTCAGGTGAAAGTGGCTTCAGAAGCACT
TTTAATAATGGATTTGCATGCTCATGTTTCTATGGCAGAAGTGATTGGTCTGTTAGGAGGAAGATACTCAGAAGT
TGATAAAGTAGTTGAAGTCTGTGCAGCAGAACCATGTAACAGTCTGAGTACAGGACTACAGTGTGAGATGGATCC
TGTATCACAAACACAGGCCTCAGAAACCTTGGCTGTTAGAGGCTTCAGTGTTATTGGATGGTATCATTCTCATCC
TGCTTTTGATCCTAATCCTTCCTTACGAGATATTGACACACAAGCTAAATACCAGAGTTACTTCTCCAGAGGAGG
TGCAAAGTTCATTGGGATGATTGTTAGTCCCTATAATCGAAATAATCCCTTACCATATTCTCAGATTACCTGCCT
GGTTATAAGTGAGGAAATTAGCCCAGATGGCTCTTATCGCTTACCTTACAAATTTGAAGTACAGCAGATGTTAGA
AGAACCTCAGTGGGGATTAGTATTTGAAAAGACAAGATGGATAATAGAAAAATACAGGCTCTCCCATAGCAGCGT
CCCCATGGATAAAATCTTTCGCCGGGATTCTGACCTGACTTGTTTGCAGAAACTTTTGGAGTGTATGAGGAAGAC
TCTGAGCAAAGTGACCAATTGCTTTATGGCTGAAGAATTCTTGACTGAAATAGAAAATTTGTTCCTTTCCAATTA
TAAAAGCAACCAAGAGAATGGAGTAACCGAAGAGAACTGTACAAAGGAATTGTTAATG<u>TGA</u>TTATTTTAAAGTTA
AGACATTTTAATCTTGACACAGTAGATCTTACTTTCAAAGTTATAAACTTGAAGTGATTGTAGTTAACATTGGCA
CAGCTTTGGTATTTTTTCTCTATTTCACAAAATCCAAACTTTGCCACATAAATCATGTGAAAAGGAAGAGATACA
AATTTGTTTTCATATAGTGATTATCAGAGTGTTCTGCAAACCAGGGTCCACCACGGTGTTCTAGTCCTTTACTGA
GCAATGCTGTAGGCTGTGAAACTAAGCAACCTGGTCGGCTTTACTGTTGTGTTCAGCTTGGGATTTGGACTATGT
CTCTAAGTCATTTCTTCCCTGAACTAGTCATTTATGTTCCATTGTGGTATCTCCTATTTCATTTAAAAGCACTTC
CATTCTTTCCATATATTCTGCTGAGATTTGTTTATGGCTATAAATGAGATATGGATGGGTGGTCACTGAGATAAT
TAATATGGTTTAGAACTACTGATTAATAAATCTAACAGGAGACCAGGAGAGGCATGACAAGAAAATCTTAAAAAC
AGGAAAAACCCAAAGGAGAGAACTAAATTACCAGTTTCTAATCATAGATACTATCTTCCATTTCATTGTATAGCA
GTAGTATCATAAGATATGCCATTTTCTCAGCTATCTGAAAATTTTTAACCAATTTTACACACATAAAATAATTAG
CTTCAATTGTGAGTCCACTTACATTAGTAGGTGTGATAAAACCTCATTTAACTGGAACATAGGTAATCATAACTC
AAACTTTTTTTCTACTGCCTACTACTAGGAGAAAGAGGCAAATGATAATAAAGCTGGAATAAATCAGAGATTTAA
TTTTTAAAACAAGCCTTTCAGGACATGTTACATATTCAGCCCAGTTTCATATGCTTTCTGAATCTATAATGGAGG
TCAGTGAACTTTTTTTAATGTAAAGGGCCAGTTTGTAAATAATTTTGGCTTTTCAGGCCACATATGATGTCTATGA
GACATTCTTCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTTTACAGCCCTTTAAAATGATAAAAA

FIGURE 251B

CCATTGTTAACTCACAGGCCTCATAAAACATAGGCTGTTGGCTATTATTCTCCAACCCTTGATCTAGAGAATTTT
AAACATTAGAATTTTGTTTTACATTTGTTAAGCTTTACGTCATCTTCAAATGACACCAAAACTCAGAATTATGAT
CTGCATTTAAGCCAATTTTAAAATAAAATAAGCAGTCAATGCTGCCTCATTTATTGAAATTCAGTAGATTTTAGT
TTATTTCTTAGTAGTCAGAGAATTGATTTATAGCTATTCACCAAACATTCTTACTAACGTTTCCTTATATCTAAA
TCAGATTGATTCTATATTTTGCTTTGTTTGTAATCAATAGCCAATGAAGAATAAGGAGTATTGGAAGAAGCAGTG
AGTCAGCTTTAGGTGACCTGGTTCTTGTCTCAACTTTGTGATTTGGGGAGATACAGTTTACTTTCCCTGAGCCTT
AATTCTTGTGTAACTGAAGTCTAACTTAACTTCTTAATGTCCTTCCAGAACTAAAATTTTATTGTTCATTCTAAT
CGTTGGACTACTCTTGTGAAGTTTATATTTTGAGTTAATACAGTTTCCAAATTAACATACATTTAAAAAAAAAAG
GGTAGTATTTTTCCATTTCTCTGTGTGCACTTAGGATAAACAGTGAAGTATAGCTTATAAAACAATTAGTTTGAG
GGCTGAGAGTGTAAGAGGAACTATACCAAAAGTCAGGAAACCTGAGCTCTTACCCTAACTCTGTTACCAACTTTG
CTGTGTGACCTTAATCAAAACACATAACCTGGACCCCATGCTCCTCACCAGTAAATCAAGGGCCTGAATTTTATG
GCTTAGTATTCCCTTCCAAGCTCCGAAGTTGCGTGATTCTGTGAAAGGCAGTGATTGATTCCTTTGTACTCATCT
TCCTTTTGACCTGTTTCCTCATGATATATTGGGGAACAAATACTAAAAAGTGTTTTATACTAGCTTTCTTGATTG
ACATTTCCCTATAATACTGATGAATTTGGGTGATGGAAAGTAATGGAAATTGTTAAAAGTTCTGCTCTCAAATCT
GAGTCTCCTTGCCCTGTGTGCCAATGTTTAACCATATTTGCTAATCTAAGCCATATTGCGAGGATCTCAAGGATG
ATACTTGTCAAGAGTTTGGGGCCTTGAGAGCACAGTTTTCAAAATAATACTTAGTATTTTCTGACTATAGAGTAC
ATTTGTCTTGTAAAGTATATTTTAAAATACAGAGAAGTGTGAAGTACAAATATCTCAGTGCTACTATTTAAAAAA
ACACAATTAGTATATAAATCCTTCCCCATTTTTTTGACAGTATAATTTTAGTATGTTAAACTTGGTTACTTCTTT
CTCTCTTCCTCCATCATTTTCCCTGCTTCCTTTTTCTTTTGTCATATTCTTAAAACAATTTTGCAACCACAGGTA
CCCACATTGCTGGCACTACCAGCCTTGGGCTACTACCGAGGATAATGGAGCCAGGGCCTTGTAGAAGCACAGAGG
AAGTCTAGAACTGAGGGGGCCTATGATACAGGAAGTTCAGGAGGCAGAGTCTCAAAGGAACACCTGCCTTTAATA
ATGTTTACAGAAGTGGAGAAAGGACTAAAGGACTTAAAGACATGCAGGTGTCTTCATCCTGATTCTGTCTTTGTT
ATTGCACAATGACTATAAAATAATGACCTAATTTTTTTTTTTTTCTGGCTTGGCTAATGGAAATCGACACTAGCG
CTTCCCCAGTATTAGACTTAATCTAATTCCAAAGTAACATTCAAGAAAAGAAAAACCAGTGGAACAGGATCAGTA
AGCTCAGACTCTCCATCTCCATTATTTTAGCCTTGACCATTCTTCTCTAATCCTTTTAAATTATCTTCAGTTTCC
AGTTCAAGTTACATTGCTTCAGTTACAGTTTGTTTGACCCTGTATTCAGAGCTGCATTATGATTCTTGTGGGCCC
TAGATAGTTTTGCCATCTTAGACCCCTTCTTCCATACAAAATTAAAAGTGATATTTTACAATTGTATCTGTATGA
AATGAATGTATTAATATTTTAGATTAAAACATTTTGTTTAGAAGTTCAGTTTTTTCTTATGAGGCTAAAAAAAAT
TAAAACATTTTTGTGGGCTTCTAAAAAACTGTGGGCCTTAGGTACTGTGCCTAATGGATAAGTTGGCATTGCCTG
TATTCTGAAGGGCATCATTGGAAAAATAGCAGTCATTATTCTGTCCCCTTCTCCCACCACCACAGTCCTTGGAGA
AGCCTTTGCCACTCCATCCAGGAGCACTGCAGTTTCCACGGTTATAGATCTATAGACTTGAACTTACTTCCTTCC
CAACCTAACGAAAACTCACAAGGATTACTTGGGACCATTCATCCTCAAAAAAGATAGGAGGCAGTGGTTTGTTTT
AGTCTTCAGATATTTTTGTTTTGGTCAGTCCCTAATCTGTAGTTTTGAAACTCGTGCCACACTTGAAAGGGAAAC
ATCCTACTACCTTTCTTTCCTCTCCATTTCCCACAAACCCTTTCCTTCATCATCACTCCCTGCATTCTTACTTCT
CAGCATATAAATACAAGACCCTTCTTTCTATTATTTGTTGAAAGCTAGGCCTGTAAAATAGAGATGGACAGACCA
TGCATGTTTCCATGAAGCTATTTAATGCTGCTCCCAGTCTTCTGTCCATACCATTCCTTCCCTGCCCCTAGGAGT
GGGGTTGAGGTCTGTGACATGCAGACTGTAAGCACAGTCAGAACCTCTGCAGCTCTCAACCCAACAGAGGAGACT
GTGGCTTCAACATGCCAACCTGAGCAGGTCTCCTCTGCATTACCTTCCTCCCATTTCTCTTCCTGGGTCCTGATG
AGGTGAGCTGGAGGAACCAATAGTCAGGATGCCCTGGAATTGATGTTGCTCTGTTTTGTGCTCACAAAACAGCCA
TGTAACACATGAGCACCTGAGTTGAAGCCATCCAGTCGCAAGTCAGCAGACAGCAGTTGATGGAATTCTCAGTAG
AAATTCAGTAAGGGTGCCCAAATTTTATTTTTTTTTTCACCTATACTCTACCAATATATGGTATTTAGGAAAACT
TCTTTTATCCAAGCACAAAGAAAAGCACACACATTTTTATAATCATCTGCTTCATCAGGGTAAATAAATAATTTA
ACAAATTTGATCAGCATCTCTAGTTTACCAGTACTTTAATATTAGTTTTCTTACAAATTAATGTATTTTGCAATA
TTTCCAGAAAATCACTGTGGGAGAATAATGTAATATACTTTAGGATATATTTCCTGACCTTTTCTTAAATGGCTT
CATGTGCTATTCCCCCAAATTCTGCTTTCTCTATTTTCTTTTTTATTTAACCTATAATTATACTTTCTAGTATAT
TCTGAGTCTATCTTCTAAGCCACCTTACATTTTTCCTGGAACAAGGGAGGGAATAAATAGTTGCCTCCACTAAAT
CAGGAAAAAATAAAAATATCCCAGGGGAGCTGTGATTATGCCAAGAGCTCTAAACAGAAGTTTGAGAAGGTAAAA
ATTAAGTTGTAGTATCTGAGTTGTTTTTATTTTCTTCCTTTGGTGTTTATGAAGGTATTCATAAGAACTTTAATT

FIGURE 251C

TCAGGGGAAAAAAATGCCTGATTTGCTATTTTTGACATTTCCTCGTCTCTTAAGAAGTCAGTTAAATATGTTTTC
ATAGTTTATATTCCTGTTTCATAGATTACTGTGAAACATGTATTTAAACCTATGAATTATAAAATAGTATTTAGA
TTCTAGCGTGAGTTAAATAGATTAGTCATATATCTTTTAGATTTGTGGATTTGACATGTAAATTATGTGTTGTGT
ATAAGTAAGTTAGTTACTAAACATATGGCATGGTTATTGATAAACTTGTTGCTATTTTTTTCCAAATGCTATCAG
TGTTTGTGGACTTTTAAAAATTAGTTTGAATTTTGGAATGTTCTGTGATAAAATGTAATTTCAACTATTTTGTAC
ATTTAAATATGCCATGTTGTATATGTCTGTATTTAAAAATGTTGTAAATACCTGCATTTTAAGAATTATGAAAGA
TTTTCCTCAAAAATGACAGAACTCTCCATACTTAATTGTGACACATTATAAGATATCTGATTTTAAGCTTTTGGA
TTTTGTTCTAAAAATTAAGTTTAAACATGCTGAAAATTCCATAAAAATAAAATTTTGAAAATAAA

FIGURE 252

MHETNQGEFITSDSQEALFSKSSRGCLQNEKQDETLSSSEITLWTEKQSNGDKKSIELNDQKFNELIKNCNKHDG
RGIIVDARQLPSPEPCEIQKNLNDNEMLFHSCQMVEESHEEEELKPPEQEIEIDRNIIQEEEKQAIPEFFEGRQA
KTPERYLKIRNYILDQWEICKPKYLNKTSVRPGLKNCGDVNCIGRIHTYLELIGAINFGCEQAVYNRPQTVDKVR
IRDRKDAVEAYQLAQRLQSMRTRRRRVRDPWGNWCDAKDLEGQTFEHLSAEELAKRREEEKGRPVKSLKVPRPTK
SSFDPFQLIPCNFFSEEKQEPFQVKVASEALLIMDLHAHVSMAEVIGLLGGRYSEVDKVVEVCAAEPCNSLSTGL
QCEMDPVSQTQASETLAVRGFSVIGWYHSHPAFDPNPSLRDIDTQAKYQSYFSRGGAKFIGMIVSPYNRNNPLPY
SQITCLVISEEISPDGSYRLPYKFEVQQMLEEPQWGLVFEKTRWIIEKYRLSHSSVPMDKIFRRDSDLTCLQKLL
ECMRKTLSKVTNCFMAEEFLTEIENLFLSNYKSNQENGVTEENCTKELLM

FIGURE 253

CTCTCTCTGGTCCGTGCCTCCAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGGCCAC
GTGCAGCCTATTCGCTGCACTAACTGTGCCCGATGCGTGCCCAAGGACAAGGCCATTAAGACATTCGTCATTCGA
AACATAGTGAAGGCCGCAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTTCGATGCCTATGTGCTTCCCAAGCTG
TATGTGAAGCTACATTACTGTGTGAGTTGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGC
AAGGACCGAACACCCCCATCCCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCCACCAAAGCCCATGTAAGGA
GCTGAGTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTT

FIGURE 254A

ATGGCACAACCGGGCAAATGCTCTGAAAAACGGATAAATAAAATGCTGGTCACAGATGAGAACATCAGTCTAGCA
GAGCTTGCGAAGGCAGCAGGGAGGAGAAAACCTCTGAGCTGTGTTTTGCCCAGTGTCCACAGAGGGTTAGGAGGA
CCCAATGAAGGAATGACCCTGAAATGTGAACAGGGCGAAGAACTAGGCCCCAGCTCCCTGCAGAGAAGATACATC
AAAGCCCCACATGAGGATTTTTATAGCTCCACATTGGACAAGCTTCCTCTTCCTGAGATAGAGCCTACAGGGAAG
GGACAGATTTGGGGCAAGGAGAGGAGTCTGAAAGAGATGGGGTACGCCGTAGTGAAAGCTGGAGTGAGAGCCTTC
GTATTCGAAGGCGGGGACTCGGGCGCTGTTGGCAGCTGGCGACGCGGGGCGAAGCCGCGGCTGGCGGCGCCTGGC
CAGTCCCGCATCCGCCGCGTGCACCCGGAGGTTGCGTGCGCTCCGAAGCCGGGGTGTGCGCCTAGCTGCCCCGGC
CCCGTGCACCGCGGGCCGCCTCGCGCAGGACTTCCGCAGCTCGCCAAGCCTGGGGTCTGCGACAGAAAAGGAGCG
GGGCTGCTCGGGCTGCCCAAAGGGTCATGGTATTAAGGAAGAAAACACAGAATGGGCCCTTGTATGGACTCTAT
TACCAAGTGCCATTGGACACGCAGGCAGTGTACTGGGAGACAGTCGTGGTGTGCTCAGAGGTATTGCCACGGCCT
GAAGTTCCTCTCTTGGCCGCAGCTGCCCCCACTCTGCTGCAATCTTCTGGGGAGGGCTTCACCTGCCACTGCCTC
CTGCATGCCAGCATCGCCTGCTGCAGACTGCAGAGCTGGGGTGCCAAAGACCAGTCCTCTCAGGGGGATGAAGAG
AAAGACCCTCCGAAGAGCCACCCTTATTCTGTGGAGACCCCATATGGCTTTCATTTAGACCTGGACTTCCTCAAG
TATGTGGATGACATCGAGAAGGGAAACACTATCAAAAGAATTCCTATCCACAGAAGGGCCAAGCAGGCCAAATTT
AGCACTCTGCCCCGAAACTTCAGCCTTCCTGACAGTGGGGCTCGCCCCCCTGCAGCCCCGCCCCTCCAAAACTGG
TCTCCCGTGGTGCCAAGGGAGGCATCACTTGGGACACAGGAGCAAAACCAGTCACCACCGCTTGGTAATGCCCCC
CAGGCCTCAACAAGCAGGAGTGAGGTGAGCTACCACAGGAAGGCTCTGTTGGCAGAGGCCACCAGACAGTTGGAA
GCTGCTGAGCCAGAGGATGCCGAGCTCACTTTTGGGAGTGGACGGCCCCAGCTCTTGAGAGCATCCAGCATGCCT
GCCACGCTGCTGCACAGCAGGGCTTCTGAGGAGCCAGGCCTGAGCCTGGGGCCCCCTGCCCCTCCTGCCCTCCCT
CCCCTTCAGGGTGAAGGCAGTGTCTGTGATGGCACCTTTGAACCTGCAGAAGGATTGGCAGGTTTCCACAGCTCC
AGCCCACGAGCATCAACTCGGATTCCAGAGCTGGTCCAGGAGGGAGCTGAGCCTCCAGAGGGTGTGGTGAAGGTT
CCAAATCACCTCCCTCTCCCAGGCCCTCCTTTCTCATTCCAGAATGTGCTTGTAGTTCTAGAGGACAAGGAAGAT
GAACACAATGCCAGAGAAGCAGAGGTGTTGTTCACCCCTGGCTCCCCTACGCCAAGCCCGCCACCTCTGCCATCA
CCCATCCCTGAGAATGAGCTCCTCCTGGAAGAAATCGAGCTCAACATCAGCGAGATTCCACCCCCGCCACCTGTA
GAGGTGGACATGAGAAGCATTGGCATCAGGGTAACTGAGGAAAGCCTGGGCCTTGCCAGGGTGGATCCAGGCAGC
ATCTCCAGCCTGAAACAGCAGGTCTCGGCCCTGGAGGGAGAGTTGTCTGGAAGAACCGAGGAACTGGCACAGGTC
AGAACTGCTCTCCAGCAGCAGGAAGAGGAAATCAAAGCTAGGGAGCAAAGAATTCGAGAGCTGGAGTTCACTGTA
GCCCAACTGGAAGGACAGTTTCACCAAGAGAACGCCAAAGACACTCAGGGCCAGACGGACGTGATGGTGAACACT
GACCCTGTCCATGGACTCTTGACCAGGGAGTCGTGTGATAAGGGCATTGAAGTCAACCTTCTAGGCAGCATGGAG
TCTGAAAGCTGGGGGCACCGAGGAGAGGAGAATGGCCTCCTATGGGGGCCAGATGGTCATAAACAAGGGAATCAG
AGCCCAGCAGAACGTGTGCTTCTGCCCCAGCTGTCACTGCCACAGGGACCCGAGCAGGTCCTTACCTCCTCTGTA
CATAGCTTCCTCTCCACTGAACTCAGGATTGAAGAAGCAGGCACTGAACAGGAAGGAGGCCCTCAGGGAGGAACC
AGGGGAGCAGGAGGCTTTCTGTGGGGCAGCGACAGAAAGACTCCCCCAGCAGGGAGGGAGGAGACCAGTTCCAAT
CTCCCAGGGAAGGAGCACCCGGGAAGGCCACCAAGCTCGCCAACGGATGCCACTATTGGGCAGTATGTGAAGAAG
ATCCAGGAGCTCCTGCAGGAGCAGTGGAACTGCCTGGAGCATGGGTACCCGGAGCTGGCCAGCGCCATCAAGCAG
CCAGCCTCCAAGCTCAGCAGCATCCAGAGCCAGCTGCTGAGCTCCCTCAACCTGCTGCTGTCGGCCTACTCGGCC
CAGGCTCACCCACCCAAGGAGCCACCGGCCTCCTCCTCCTCCCCGCCAGTGGAGATCTCCCCATCGACCAGCCTT
AAATCCATAATGAAAAAGAAAGACTATGGCTTCCGTGCAGGAGGTAATGGGACCAAAAAGAACCTTCAGTTTGTT
GGGGTTAACGGTGGGTATGAGACCACCTCAAGTGAGGAGACCAGCGGTGAGGACAGCACCCCAGAGGACTTGTCT
GACAGCGAGGCAGAGAAGAAGTGTGACGGCCCAGATCACAAGCATGTCAAAGATGCCCATCTCACCTGCGAGGCT
GGGCAGGGCATCCCTGAGGGCACCTGCCATGCTGCCCAGGAAAGTGGGCCTGGGGAAGAAGTCCCCCACTCCAAG
GCCGAGAGCCGGAAGTCGTCTAGCCCCGCCGTGGTGGCCTCCTACCTCCACGAGGTCCAGCCTCACTCCCCACAC
TTCCTGAAACTGCTTGTCAACTTGGCCGATCACAACGGGAACACGGCCCTTCACTACAGCGTGTCCCACTCCAAC
TTCTCCATCGTGAAGCTGCTGCTGGAGACAGGCGTCTGCAATGTGGACCATCAGAACAAAGCTGGCTACACTGCC
GTAATGATCACTCCCTTGGCTTCCGCAGAGACCAATGAAGACATGGCTGTTGTCTGGAAGCTCTTAAGAGAAGGA
AATGTGAACATTCAAGCTACTCAGGGAGGCCAGACTGCGCTGATGCTGGGAGTCAGCCACGACAGGGAGGACATG
GTTCAAGCGCTGCTTAGCTGCCAGGCAGATGTCAATCTGCAGGACCACGATGGATCCTCGGCCCTCATGGTGGCC
TGTCACCATGGCAACGTGGACCTGGTGCGGCTGCTCCTGGCACACCCAGCCTGCGACAGCAGCCTGACTGACAAG

FIGURE 254B

GCTGGCCGCACAGCTTTGTCCATCGCTCTGAAGTCACCCACCCATATGGAAATTGCTGGGCTTCTGAGAGCCCAC
GCGGAGCAGGGCAGGTCCCTGGGGCTGTAG

FIGURE 255

MASVQEVMGPKRTFSLLGLTVGMRPPQVRRPAVRTAPQRTCLTARQRRSVTAQITSMSKMPISPARLGRASLRAP
AMLPRKVGLGKKSPTPRPRDINPQKNFLMHAGH

FIGURE 256A

GCGGCGGCCGCGGAGTATCCTGGAGCTGCAGACAGTGCGGGCCTGCGCCCAGTCCCGGCTGTCCTCGCCGCGACC
CCTCCTCAGCCCTGGGCGCGCGCACGCTGGGGCCCCGCGGGGCTGGCCGCCTAGCGAGCCTGCCGGTCGACCCCA
GCCAGCGCAGCGACGGGGCGCTGCCTGGCCCAGGCGCACACGGAAGTGCGCTTCTCTGAAGTAGCTTTGGAAAGT
AGAGAAGAAAATCCAGTTTGCTTCTTGGAGAACACTGGACAGCTGAATAAATGCAGTATCTAAATATAAAAGAGG
ACTGCAATGCCATGGCTTTCTGTGCTAAAATGAGGAGCTCCAAGAAGACTGAGGTGAACCTGGAGGCCCCTGAGC
CAGGGGTGGAAGTGATCTTCTATCTGTCGGACAGGGAGCCCCTCCGGCTGGGCAGTGGAGAGTACACAGCAGAGG
AACTGTGCATCAGGGCTGCACAGGCATGCCGTATCTCTCCTCTTTGTCACAACCTCTTTGCCCTGTATGACGAGA
ACACCAAGCTCTGGTATGCTCCAAATCGCACCATCACCGTTGATGACAAGATGTCCCTCCGGCTCCACTACCGGA
TGAGGTTCTATTTCACCAATTGGCATGGAACCAACGACAATGAGCAGTCAGTGTGGCGTCATTCTCCAAAGAAGC
AGAAAAATGGCTACGAGAAAAAAAAGATTCCAGATGCAACCCCTCTCCTTGATGCCAGCTCACTGGAGTATCTGT
TTGCTCAGGGACAGTATGATTTGGTGAAATGCCTGGCTCCTATTCGAGACCCCAAGACCGAGCAGGATGGACATG
ATATTGAGAACGAGTGTCTAGGGATGGCTGTCCTGGCCATCTCACACTATGCCATGATGAAGAAGATGCAGTTGC
CAGAACTGCCCAAGGACATCAGCTACAAGCGATATATTCCAGAAACATTGAATAAGTCCATCAGACAGAGGAACC
TTCTCACCAGGATGCGGATAAATAATGTTTTCAAGGATTTCCTAAAGGAATTTAACAACAAGACCATTTGTGACA
GCAGCGTGTCCACGCATGACCTGAAGGTGAAATACTTGGCTACCTTGGAAACTTTGACAAAACATTACGGTGCTG
AAATATTTGAGACTTCCATGTTACTGATTTCATCAGAAAATGAGATGAATTGGTTTCATTCGAATGACGGTGGAA
ACGTTCTCTACTACGAAGTGATGGTGACTGGGAATCTTGGAATCCAGTGGAGGCATAAACCAAATGTTGTTTCTG
TTGAAAAGGAAAAAAATAAACTGAAGCGGAAAAAACTGGAAAATAAACACAAGAAGGATGAGGAGAAAAACAAGA
TCCGGGAAGAGTGGAACAATTTTTCTTACTTCCCTGAAATCACTCACATTGTAATAAAGGAGTCTGTGGTCAGCA
TTAACAAGCAGGACAACAAGAAAATGGAACTGAAGCTCTCTTCCCACGAGGAGGCCTTGTCCTTTGTGTCCCTGG
TAGATGGCTACTTCCGGCTCACAGCAGATGCCCATCATTACCTCTGCACCGACGTGGCCCCCCCGTTGATCGTCC
ACAACATACAGAATGGCTGTCATGGTCCAATCTGTACAGAATACGCCATCAATAAATTGCGGCAAGAAGGAAGCG
AGGAGGGGATGTACGTGCTGAGGTGGAGCTGCACCGACTTTGACAACATCCTCATGACCGTCACCTGCTTTGAGA
AGTCTGAGCAGGTGCAGGGTGCCCAGAAGCAGTTCAAGAACTTTCAGATCGAGGTGCAGAAGGGCCGCTACAGTC
TGCACGGTTCGGACCGCAGCTTCCCCAGCTTGGGAGACCTCATGAGCCACCTCAAGAAGCAGATCCTGCGCACGG
ATAACATCAGCTTCATGCTAAAACGCTGCTGCCAGCCCAAGCCCCGAGAAATCTCCAACCTGCTGGTGGCTACTA
AGAAAGCCCAGGAGTGGCAGCCCGTCTACCCCATGAGCCAGCTGAGTTTCGATCGGATCCTCAAGAAGGATCTGG
TGCAGGGCGAGCACCTTGGGAGAGGCACGAGAACACACATCTATTCTGGGACCCTGATGGATTACAAGGATGACG
AAGGAACTTCTGAAGAGAAGAAGATAAAAGTGATCCTCAAAGTCTTAGACCCCAGCCACAGGGATATTTCCCTGG
CCTTCTTCGAGGCAGCCAGCATGATGAGACAGGTCTCCCACAAACACATCGTGTACCTCTATGGCGTCTGTGTCC
GCGACGTGGAGAATATCATGGTGGAAGAGTTTGTGGAAGGGGGTCCTCTGGATCTCTTCATGCACCGGAAAAGCG
ATGTCCTTACCACACCATGGAAATTCAAAGTTGCCAAACAGCTGGCCAGTGCCCTGAGCTACTTGGAGGATAAAG
ACCTGGTCCATGGAAATGTGTGTACTAAAAACCTCCTCCTGGCCCGTGAGGGCATCGACAGTGAGTGTGGCCCAT
TCATCAAGCTCAGTGACCCCGGCATCCCCATTACGGTGCTGTCTAGGCAAGAATGCATTGAACGAATCCCATGGA
TTGCTCCTGAGTGTGTTGAGGACTCCAAGAACCTGAGTGTGGCTGCTGACAAGTGGAGCTTTGGAACCACGCTCT
GGGAAATCTGCTACAATGGCGAGATCCCCTTGAAAGACAAGACGCTGATTGAGAAAGAGAGATTCTATGAAAGCC
GGTGCAGGCCAGTGACACCATCATGTAAGGAGCTGGCTGACCTCATGACCCGCTGCATGAACTATGACCCCAATC
AGAGGCCTTTCTTCCGAGCCATCATGAGAGACATTAATAAGCTTGAAGAGCAGAATCCAGATATTGTTTCAGAAA
AAAAACCAGCAACTGAAGTGGACCCCACACATTTTGAAAAGCGCTTCCTAAAGAGGATCCGTGACTTGGGAGAGG
GCCACTTTGGGAAGGTTGAGCTCTGCAGGTATGACCCCGAAGGGGACAATACAGGGGAGCAGGTGGCTGTTAAAT
CTCTGAAGCCTGAGAGTGGAGGTAACCACATAGCTGATCTGAAAAAGGAAATCGAGATCTTAAGGAACCTCTATC
ATGAGAACATTGTGAAGTACAAAGGAATCTGCACAGAAGACGGAGGAAATGGTATTAAGCTCATCATGGAATTTC
TGCCTTCGGGAAGCCTTAAGGAATATCTTCCAAAGAATAAGAACAAAATAAACCTCAAACAGCAGCTAAAATATG
CCGTTCAGATTTGTAAGGGGATGGACTATTTGGGTTCTCGGCAATACGTTCACCGGGACTTGGCAGCAAGAAATG
TCCTTGTTGAGAGTGAACACCAAGTGAAAATTGGAGACTTCGGTTTAACCAAAGCAATTGAAACCGATAAGGAGT
ATTACACCGTCAAGGATGACCGGGACAGCCCTGTGTTTTGGTATGCTCCAGAATGTTTAATGCAATCTAAATTTT
ATATTGCCTCTGACGTCTGGTCTTTTGGAGTCACTCTGCATGAGCTGCTGACTTACTGTGATTCAGATTCTAGTC
CCATGGCTTTGTTCCTGAAAATGATAGGCCCAACCCATGGCCAGATGACAGTCACAAGACTTGTGAATACGTTAA

FIGURE 256B

AAGAAGGAAAACGCCTGCCGTGCCCACCTAACTGTCCAGATGAGGTTTATCAACTTATGAGGAAATGCTGGGAAT
TCCAACCATCCAATCGGACAAGCTTTCAGAACCTTATTGAAGGATTTGAAGCACTTTTAAAATAAGAAGCATGAA
TAACATTTAAATTCCACAGATTATCAAGTCCTTCTCCTGCAACAAATGCCCAAGTCATTTTTTAAAAATTTCTAA
TGAAAGAAGTTTGTGTTCTGTCCAAAAAGTCACTGAACTCATACTTCAGTACATATACATGTATAAGGCACACTG
TAGTGCTTAATATGTGTAAGGACTTCCTCTTTAAATTTGGTACCAGTAACTTAGTGACACATAATGACAACCAAA
ATATTTGAAAGCACTTAAGCACTCCTCCTTGTGGAAAGAATATACCACCATTTCATCTGGCTAGTTCACCATCAC
AACTGCATTACCAAAAGGGGATTTTTGAAAACGAGGAGTTGACCAAAATAATATCTGAAGATGATTGCTTTTCCC
TGCTGCCAGCTGATCTGAAATGTTTTGCTGGCACATTAATCATAGATAAAGAAAGATTGATGGACTTAGCCCTCA
AATTTCAGTATCTATACAGTACTAGACCATGCATTCTTAAAATATTAGATACCAGGTAGTATATATTGTTTCTGT
ACAAAAATGACTGTATTCTCTCACCAGTAGGACTTAAACTTTGTTTCTCCAGTGGCTTAGCTCCTGTTCCTTTGG
GTGATCACTAGCACCCATTTTTGAGAAAGCTGGTTCTACATGGGGGGATAGCTGTGGAATAGATAATTTGCTGCA
TGTTAATTCTCAAGAACTAAGCCTGTGCCAGTGCTTTCCTAAGCAGTATACCTTTAATCAGAACTCATTCCCAGA
ACCTGGATGCTATTACACATGCTTTTAAGAAACGTCAATGTATATCCTTTTATAACTCTACCACTTTGGGGCAAG
CTATTCCAGCACTGGTTTTGAATGCTGTATGCAACCAGTCTGAATACCACATACGCTGCACTGTTCTTAGAGGGT
TTCCATACTTACCACCGATCTACAAGGGTTGATCCCTGTTTTTACCATCAATCATCACCCTGTGGTGCAACACTT
GAAAGACCCGGCTAGAGGCACTATGGACTTCAGGATCCACTAGACAGTTTTCAGTTTGCTTGGAGGTAGCTGGGT
AATCAAAAATGTTTAGTCATTGATTCAATGTGAACGATTACGGTCTTTATGACCAAGAGTCTGAAAATCTTTTTG
TTATGCTGTTTAGTATTCGTTTGATATTGTTACTTTTCACCTGTTGAGCCCAAATTCAGGATTGGTTCAGTGGCA
GCAATGAAGTTGCCATTTAAATTTGTTCATAGCCTACATCACCAAGGTCTCTGTGTCAAACCTGTGGCCACTCTA
TATGCACTTTGTTTACTCTTTATACAAATAAATATACTAAAGACTTT

FIGURE 257

CTCTTCATAAGCCGGCGCTCGGCGAGTTCTCCCAGGAGAAGGCC**ATG**TTCAGTTCGAGCGCCAAGATCGTGAAAC
CCAACGGCGAGAAGCCGGAGGAGTTCGAGTCCGGCATCTCCCAGGCTCTTCTGGAGCTGGAGATGAACTCAGAAC
TCAAGGCTCAGCTCAGAGAGCTGAATATTACGGCAGCCAAGGAAATTGAAGTTGGTGGTGGTCGGAAAGCTATCA
TAATACTTGTTCCCGTTACTCAACTGAAATCTTTCCAGAAAATCCAAATCCGGCTAGTAAGTGAATTGGAGAAAA
AGTTCAGTGGGAAGCATGTCGTCTTTATCGCTCAGAGGAGAATTCTGCCTAAGCCAACTCGAAAAAGCTGTACAA
AAAATAAGCAAAAGCGTCCCAGGAGCAGCACTGTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCC
CAAGTGAAATTGTGGGCAAGAAAATCCGCGTCAAACTAGATGGCAGCCGGCTCATAAAGGTTCATTTGGACAAAG
CACAACAGAACAATGTGGAACACAAGGTTGAAACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTA
ATTGTGAATTCCCAGAGTTTCAATAG**TAA**ACAAAAATGACTAAATAAAAATATATATATTCATAGT

FIGURE 258

MFSSSAKIVKPNGEKPEEFESGISQALLELEMNSELKAQLRELNITAAKEIEVGGGRKAIIILVPVTQLKSFQKI
QIRLVSELEKKFSGKHVVFIAQRRILPKPTRKSCTKNKQKRPRSSTVTAVHDAILEDLVFPSEIVGKKIRVKLDG
SRLIKVHLDKAQQNNVEHKVETFSGVYKKLMGKDVNCEFPEFQS

FIGURE 259

GGAGAAGGCCATGTTCAGTTCGAGCGCCAAGATCGTGAAACCCAACGGCGAGAAGCCGGAGGAGTTCGAGTCCGG
CATCTCCCAGGAAATTGAAGTTGGTGGTGGTCGGAAAGCTATCATAATACTTGTTCCCGTTACTCAACTGAAATC
TTTCCAGAAAATCCAAATCCGGCTAGTAAGTGAATTGGAGAAAAAGTTCAGTGGGAAGCATGTCGTCTTTATCGC
TCAGAGGAGAATTCTGCCTAAGCCAACTCGAAAAAGCTGTACAAAAAATAAGCAAAAGCGTCCCAGGAGCAGCAC
TGTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCCCAAGTGAAATTGTGGGCAAGAAAATCCGCGT
CAAACTAGATGGCAGCCGGCTCATAAAGGTTCATTTGGACAAAGCACAACAGAACAATGTGGAACACAAGGTTGA
AACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTAATTGTGAATTCCCAGAGTTTCAATAGTAAAC
AAAAATGACTAAATAAAAATATATATATTCATAGTAAAAAAAAAAAAAAAAATCTC

FIGURE 260

GGGGGTGGGAAGAGCTGAAGCAGGCGCTCTTGGCTCGGCGCGGCCCGCTGCAATCCGTGGAGGAACGCGCCGCCG
AGCCACCATC**ATG**CCTGGGCACTTACAGGAAGGCTTCGGCTGCGTGGTCACCAACCGATTCGACCAGTTATTTGA
CGACGAATCGGACCCCTTCGAGGTGCTGAAGGCAGCAGAGAACAAGAAAAAAGAAGCCGGCGGGGGCGGCGTTGG
GGGCCCTGGGGCCAAGAGCGCAGCTCAGGCCGCGGCCCAGACCAACTCCAACGCGGCAGGCAAACAGCTGCGCAA
GGAGTCCCAGAAAGACCGCAAGAACCCGCTGCCCCCCAGCGTTGGCGTGGTTGACAAGAAAGAGGAGACGCAGCC
GCCCGTGGCGCTTAAGAAAGAAGGAATAAGACGAGTTGGAAGAAGACCTGATCAACAACTTCAGGGTGAAGGGAA
AATAATTGATAGAAGACCAGAAAGGCGACCACCTCGTGAACGAAGATTCGAAAAGCCACTTGAAGAAAAGGGTGA
AGGAGGCGAATTTTCAGTTGATAGACCGATTATTGACCGACCTATTCGAGGTCGTGGTGGTCTTGGAAGAGGTCG
AGGGGGCCGTGGACGTGGAATGGGCCGAGGAGATGGATTTGATTCTCGTGGCAAACGTGAATTTGATAGGCATAG
TGGAAGTGATAGATCTGGCCTGAAGCACGAGGACAAACGTGGAGGTAGCGGATCTCACAACTGGGGAACTGTCAA
AGACGAATTAACTGACTTGGATCAATCAAATGTGACTGAGGAAACACCTGAAGGTGAAGAACATCATCCAGTGGC
AGACACTGAAAATAAGGAGAATGAAGTTGAAGAGGTAAAAGAGGAGGGTCCAAAAGAGATGACTTTGGATGAGTG
GAAGGCTATTCAAAATAAGGACCGGGCAAAAGTAGAATTTAATATCCGAAAACCAAATGAAGGTGCTGATGGGCA
GTGGAAGAAGGGATTTGTTCTTCATAAATCAAAGAGTGAAGAGGCTCATGCTGAAGATTCGGTTATGGACCATCA
TTTCCGGAAGCCAGCAAATGATATAACGTCTCAGCTGGAGATCAATTTTGGAGACCTTGGCCGCCCAGGACGTGG
CGGCAGGGGAGGACGAGGTGGACGTGGGCGTGGTGGGCGCCCAAACCGTGGCAGCAGGACCGACAAGTCAAGTGC
TTCTGCTCCTGATGTGGATGACCCAGAGGCATTCCCAGCTCTGGCT**TAA**CTGGATGCCATAAGACAACCCTGGTT
CCTTTGTGAACCCTTCTGTTCAAAGCTTTTGCATGCTTAAGGATTCCAAACGACTAAGAAATTAAAAAAAAAAAG
ACTGTCATTCATACCATTCACACCTAAAGACTGAATTTTATCTGTTTTAAAAATGAACTTCTCCCGCTACACAGA
AGTAACAAATATGGTAGTCAGTTTTGTATTTAGAAATGTATTGGTAGCAGGGATGTTTTCATAATTTTCAGAGAT
TATGCATTCTTCATGAATACTTTTGTATTGCTGCTTGCAAATATGCATTTCCAAACTTGAAATATAGGTGTGAAC
AGTGTGTACCAGTTTAAAGCTTTCACTTCATTTGTGTTTTTTAATTAAGGACTTAGAAGTTCCCCCAATTACAAA
CTGGTTTTAAATATTGGACATACTGGTTTTAATACCTGCTTTGCATATTCACACATGGTCAACTGGGACATGTTA
AACTTTGATTTGTCAAATTTTATGCTGTGTGGAATACTAACTATATGTATTTTAACTTAGTTTTAATATTTTCAT
TTTGGGGGAAAAATCTTTTTTCACTTCTCATGATAGCTGTTATATATATATGCTAAATCTTTATATACAGAAATA
TCAGTACTTGAACAAATTCAAAGCACATTTGGTTTATTAACCCTTGCTCCTTGCATGGCTCATTAGGTTCAAATT
ATAACTAATTTACATTTTCAGCTATATTTACTTTTTAAATGCTTGAGTTTCCCATTTTAAAATCTAAACTAGACA
TCTTAATTGGTGAAAGTTGTTTAAACTACTTATTGTTGGTAGGCACATCGTGTCAAGTGAAGTAGTTTTATAGGT
ATGGGTTTTTTCTCCCCCTTCACCAGGGTGGGTGGAATAAGTTGATTTGGCCAATGTGTAATATTTAAACTGTTC
TGTAAAATAAAAAAAAAAAAAAAAAA

FIGURE 261

MPGHLQEGFGCVVTNRFDQLFDDESDPFEVLKAAENKKKEAGGGGVGGPGAKSAAQAAAQTNSNAAGKQLRKESQ
KDRKNPLPPSVGVVDKKEETQPPVALKKEGIRRVGRRPDQQLQGEGKIIDRRPERRPPRERRFEKPLEEKGEGGE
FSVDRPIIDRPIRGRGGLGRGRGGRGRGMGRGDGFDSRGKREFDRHSGSDRSGLKHEDKRGGSGSHNWGTVKDEL
TDLDQSNVTEETPEGEEHHPVADTENKENEVEEVKEEGPKEMTLDEWKAIQNKDRAKVEFNIRKPNEGADGQWKK
GFVLHKSKSEEAHAEDSVMDHHFRKPANDITSQLEINFGDLGRPGRGGRGGRGGRGRGGRPNRGSRTDKSSASAP
DVDDPEAFPALA

FIGURE 262

ACCTTTAAGCGTCACGGGTGGGGCTGCAGCTTCTGGACCTAGGACTTTGAACATGTCGCGCCTGAAGCGGATAGC
GGGGCAGGATCTCCGCGCTGGTTTCAAAGCAGGTGGAAGAGACTGCGGTACCTCGGTACCCCAAGGGCTGTTGAA
GGCAGCGAGGAAGAGCGGCCAGTTAAACCTGTCGGGTAGAAACCTCAGTGAAGTGCCGCAGTGTGTCTGGAGAAT
AAATGTGGATATCCCTGAGGAAGCTAATCAGAATCTTTCGTTTGGTGCTACTGAAAGATGGTGGGAGCAGACAGA
TTTGACCAAACTAATAATATCAAACAATAAACTTCAGTCACTTACAGATGACCTGCGACTCTTGCCTGCACTGAC
TGTTCTTGATATACATGATAATCAGTTGACATCCCTTCCTTCTGCTATAAGAGAGCTAGAAAATCTTCAGAAACT
TAATGTCAGCCATAATAAACTGAAAATACTCCCTGAAGAAATTACAAACCTAAGAAACCTGAAGTGCCTGTATCT
CCAGCATAATGAATTAACCTGCATATCAGAGGGATTTGAACAACTTTCCAATTTAGAAGATTTAGATCTTTCAAA
CAATCATCTTACAACTGTTCCTGCTAGTTTTTCTTCTCTGTCCAGTCTGGTGCGACTCAATCTTTCTAGTAATGA
ACTGAAGAGTTTGCCAGCAGAAATAAATAGAATGAAAAGGTTGAAGCATTTGGATTGTAATTCAAATCTCTTGGA
AACTATACCTCCTGAATTGGCTGGCATGGAATCACTAGAATTGCTTTATTTGCGGAGGAATAAATTACGTTTTCT
ACCAGAATTTCCTTCTTGTAGTCTATTGAAGGAATTGCACGTAGGTGAAAACCAGATTGAAATGTTAGAGGCAGA
ACATCTTAAACATCTGAATTCAATTCTTGTGCTAGACCTGAGGGATAACAAGTTAAAATCTGTTCCAGATGAAAT
TATACTACTACGGTCCTTGGAAAGGCTTGACCTAAGCAACAATGATATTAGTAGTCTTCCCTATTCATTGGGGAA
CCTTCATTTGAAATTTTTGGCATTAGAAGGAAATCCTTTGAGAACAATTCGAAGAGAAATTATAAGTAAAGGAAC
ACAAGAAGTCCTAAAATATCTACGAAGCAAGATCAAAGATGATGGACCTAGCCAAAGTGAGTCTGCTACTGAGAC
TGCCATGACACTACCAAGTGAATCCAGAGTCAATATACATGCCATCATTACATTAAAAATATTAGACTATAGTGA
TAAACAAGCAACTTTGATTCCTGATGAGGTGTTTGATGCAGTAAAAAGCAACATCGTCACTTCTATTAACTTCAG
TAAGAATCAACTATGTGAAATTCCAAAAAGGATGGTAGAACTGAAGGAAATGGTTTCTGATGTCGATCTCAGTTT
TAATAAACTTTCCTTTATATCCTTGGAGTTATGTGTGCTTCAGAAATTGACTTTTTTAGATCTCAGGAACAATTT
TTTAAATTCTTTGCCAGAAGAAATGGAATCACTGGTAAGACTGCAAACGATCAATCTTTCCTTTAATAGGTTTAA
AATGCTACCTGAAGTTCTATATCGTATCTTCACACTTGAAACAATTCTGATTAGTAATAATCAGGTTGGATCTGT
GGACCCTCAGAAAATGAAGATGATGGAAAATCTGACCACGTTGGACCTTCAAAATAATGACCTCTTACAAATTCC
ACCAGAGCTCGGTAATTGTGTAAACTTAAGAACATTACTATTGGATGGAAATCCATTCCGAGTTCCTCGAGCAGC
CATATTAATGAAAGGAACAGCTGCTATACTTGAATATTTGAGAGACCGAATTCCTACTTAACATGGAGTTGCTTT
ATAACCCTTGTCATGTATTATTAACCCTGGTTAATTCTAAGGAGGATGTAACATTTGTTTTAGTATCATCTTAAA
AGGTGATTATTGTAATTGATCTTGTAGTTTCCCAGTATCACCTACCCGTTGGTATAATTAGCCTGGGCCATATTC
ACTGCCAGTAAATATTTTTACATTTTTATTTAAGATTTTTGTAAGGTGTTGTGTACATTTGTAATGGTGATAACC
ACAATGTGTTCATACATTTGTTCTAAATGTTTTGCTTATGATTTATCCTGCTAACTTTCATTTTCTTATAGCAAG
CAGTTTTTTCAAAAATGAATTTTTATTTAATGTGGTTCAGTATTATAATAACAAAGCATTTTTGTAGAACTGGTT
TTTTTTCTCATTTATTTTTGTATTCCATACAATGTGACCAATTGACTTGAATATGACTAGCCAGTTTCTATGTTT
TTGTTAGATATAAAATTAAATCGAATTTTGTTGAATACTGTTCTTTGGCATTTAAAAAATAAGACCTTCTTATCT
TGGGCCACATGTCAAAAGAAAAAGGAAACAAAAATATATTAAAAATAAGACTTTTCATTACCCATGATAGGACTT
TTGTGATATGGCTAATCTCAGTACACATTTCAACTTAAAACCTTTTTATTTACAGCACCATAATTTTAAAATTTA
CTTGCAATCTTGGTAAGACTAAACTTGCAGTGTTTTTCTAAAAGGGAATTTGATAGGTAAACTTGATTTAATAAA
AATTAAATATCATTTTTGTTTACACCAAAATTATCAGAAGTAGGTTGATTAGTCATTATAACACTTACCATATGA
TTCTATTAAGAAGTCAATTCAGTAGCATGTATATCAATTTATATAGATAGGTAGATAGCTTTTGGATGATTGAGG
CATGCTTATATTATGAAAAAAATTGCTAATAAAGATAAATACTACATGTTCAGAATAAAAGTTACATTTTTC

FIGURE 263

MSRLKRIAGQDLRAGFKAGGRDCGTSVPQGLLKAARKSGQLNLSGRNLSEVPQCVWRINVDIPEEANQNLSFGAT
ERWWEQTDLTKLIISNNKLQSLTDDLRLLPALTVLDIHDNQLTSLPSAIRELENLQKLNVSHNKLKILPEEITNL
RNLKCLYLQHNELTCISEGFEQLSNLEDLDLSNNHLTTVPASFSSLSSLVRLNLSSNELKSLPAEINRMKRLKHL
DCNSNLLETIPPELAGMESLELLYLRRNKLRFLPEFPSCSLLKELHVGENQIEMLEAEHLKHLNSILVLDLRDNK
LKSVPDEIILLRSLERLDLSNNDISSLPYSLGNLHLKFLALEGNPLRTIRREIISKGTQEVLKYLRSKIKDDGPS
QSESATETAMTLPSESRVNIHAIITLKILDYSDKQATLIPDEVFDAVKSNIVTSINFSKNQLCEIPKRMVELKEM
VSDVDLSFNKLSFISLELCVLQKLTFLDLRNNFLNSLPEEMESLVRLQTINLSFNRFKMLPEVLYRIFTLETILI
SNNQVGSVDPQKMKMMENLTTLDLQNNDLLQIPPELGNCVNLRTLLLDGNPFRVPRAAILMKGTAAILEYLRDRI
PT

FIGURE 264

GCTCTTTCCCTAAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTACTCACTTGACCCGGAGAACCCCACGAAA
TCACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACAAAAAGCCACGAAGTATCTGAAAGATGTCACTT
TACAGAAACAGTGTGTACCATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAGTGGGGCT
GGACACAAGGTCGGTGGCCCAAAAAGAGTGCTGAATTTTTGCTGCACATGCTTAAAAACACAGAGAGTAATGCTG
AACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCC
GGACCTACAGAGCTCATGGTCGGATTAACCCATACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAA
AGGAACAGATTGTTCCTAAACCAGAAGAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAAAC
AAAAACTTATGGCACGGGAGTAAATTCAGCATTAAAATAAATGTAATTAAAAGGAAAAATAAAAAATAAAAATAA
ATAAATAAATAAATAAAAAAAAAAAAAAAAAAAAAG

FIGURE 265

GCTCTTTCCCTAAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTACTCACTTGACCCGGAGAACCCCACGAAA
TCATGCAAATCAAGAGGTTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGT
ATGCATATACAAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACCATTCCGACGTTAC
AATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAGTGGGGCTGGACACAAGGTCGGTGGCCCAAAAAGAGTGCT
GAATTTTTGCTGCACATGCTTAAAAACACAGAGAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTC
ATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCCGGACCTACAGAGCTCATGGTCGGATTAACCCA
TACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAAAGGAACAGATTGTTCCTAAACCAGAAGAGGAG
GTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAAACAAAAACTTATGGCACGGGAGTAAATTCAGCAT
TAAAATAAATGTAATTAAAAGG

FIGURE 266

MVRYSLDPENPTKSCKSRGSNLRVHFKNTRETAQAIKGMYIQKGTKYLKDVTLQKQCIPFRHYNGGVGRCAQAKQ
WGWTQGRWPKKSAEFLLHVLKNTESNAELKGRFSGH

FIGURE 267

CGGGAAGGATTGAATACGAGACGCTGTCTGCTTGCTGCCTTAAGACAGCTAGCTGAATTGCTGATTAACTTTTAA
AATACCCAGCTTGGTTTATTTTTCTTAGAATCTGTTGCTAAGACTGGGGACGCTGTTTTCTTTTACAAAGGGAAA
TCTAAGTTAATTTCAAGGCATTCGAA**ATG**GGGAAAGACTATTATTGCATTTTGGGAATTGAGAAAGGAGCTTCAG
ATGAAGATATTAAAAAGGCTTACCGAAAACAAGCCCTCAAATTTCATCCGGACAAGAACAAATCTCCTCAGGCAG
AGGAAAAATTTAAAGAGGTCGCAGAAGCTTATGAAGTATTGAGTGATCCTAAAAAGAGAGAAATATATGATCAGT
TTGGGGAGGAAGGGTTGAAAGGAGGAGCAGGAGGTACTGATGGACAAGGAGGTACCTTCCGGTACACCTTTCATG
GCGATCCTCATGCTACATTTGCTGCATTTTTCGGAGGGTCCAACCCCTTTGAAATTTTCTTTGGAAGACGAATGG
GTGGTGGTAGAGATTCTGAAGAAATGGAAATAGATGGTGATCCTTTTAGTGCCTTTGGTTTCAGCATGAATGGAT
ATCCAAGAGACAGGAATTCTGTGGGGCCATCCCGCCTCAAACAAGATCCTCCAGTTATTCATGAACTTAGAGTAT
CACTTGAAGAGATATATAGTGGTTGTACCAAACGGATGAAGATTTCTCGAAAAAGGCTAAACGCTGATGGAAGGA
GTTACAGATCTGAGGACAAAATTCTTACCATTGAGATTAAAAAAGGGTGGAAAGAAGGCACCAAAATTACTTTTC
CAAGAGAAGGAGATGAAACACCAAATAGTATTCCAGCAGACATTGTTTTTATCATTAAAGACAAAGATCATCCAA
AATTTAAAAGGGATGGATCAAATATAATTTATACTGCTAAAATTAGTTTACGAGAGGCATTGTGTGGCTGCTCAA
TTAATGTACCAACACTGGATGGAAGAAACATACCTATGTCAGTAAATGATATTGTGAAACCCGGAATGAGGAGAA
GAATTATTGGATATGGGCTGCCATTTCCAAAAAATCCTGACCAACGTGGTGACCTTCTAATAGAATTTGAGGTGT
CCTTCCCAGATACTATATCTTCTTCATCCAAAGAAGTACTTAGGAAACATCTTCCTGCCTCA**TAG**AATGAAGAAC
TTTGTTACACATATTTTGATAAGGCACTGAAAATATAAAAGGACTGGTAGTTTACTGATGTAGATGTGAATTCTG
TATAAAGATGTGTAAATTGTTTTGAGGGTTCATTAAATTGCAT

FIGURE 268

MGKDYYCILGIEKGASDEDIKKAYRKQALKFHPDKNKSPQAEEKFKEVAEAYEVLSDPKKREIYDQFGEEGLKGG
AGGTDGQGGTFRYTFHGDPHATFAAFFGGSNPFEIFFGRRMGGGRDSEEMEIDGDPFSAFGFSMNGYPRDRNSVG
PSRLKQDPPVIHELRVSLEEIYSGCTKRMKISRKRLNADGRSYRSEDKILTIEIKKGWKEGTKITFPREGDETPN
SIPADIVFIIKDKDHPKFKRDGSNIIYTAKISLREALCGCSINVPTLDGRNIPMSVNDIVKPGMRRRIIGYGLPF
PKNPDQRGDLLIEFEVSFPDTISSSSKEVLRKHLPAS

FIGURE 269

GCGCACGGCCTGTCCGCTGCACACCAGCTTGTTGGCGTCTTCGTCGCCGCGCTCGCCCCGGGCTACTCCTGCGCG
CCACA**ATG**AGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGGCTGGCGCTCT
CCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCGCCGGGAGTCGGGCTGGTCCGGGACG
GCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCA
AGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGAC
CCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTA
TTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTC
GGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGG
ACCAGGACGGCCTCCTTGGTAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGA
TTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGATCCCTGTTTTTGGAATGGAGCCTCGCATCCGATACAACCCTT
TACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCA
CACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGAC
AGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTA
CTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGCCGATGCTGCA
CGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGA
TGATCCAGTCCTGCAAATGCAACTACAACTGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCA
ATGACATTCACAAATTTAGGGAC**TAA**ATGCTACCTGGGTTTCCAGGGCACACCTAGACAAACAAGGGAGAAGAGT
GTCAGAATCAGAATCATGGAGAAAATGGGCGGGGGTGGTGTGGGTGATGGGACTCATTGTAGAAAGGAAGCCTTG
CTCATTCTTGAGGAGCATTAAGGTATTTCGAAACTGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACG
ATTGGAGAATACTTTGCTTCATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACT
TTCTGTTTTCTGTTTGTAAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCCTTTTGGGGTTCTACAGTCG
TAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTGACAAAAGTAAATGGGAGGGCAT
TCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTGTGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAG
AAATCAGGTGTTTTAAGACTGAATGTTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACT
GGAATAATTTGTAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATAAAG
AAATATTTACCT

FIGURE 270

MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKG
LECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRL
VKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGSSLKRIPVFGMEPRIRYNPLQ
GQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY
AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANEAAFPFYRLFND
IHKFRD

FIGURE 271

GCTCTGTCAGTAACACATGTGTAAGAGCCGCGGAGGGAGCGAGCGAGCCGGCTAGAGGCCAGCGCCGCCGCC
GCCGCCTCCGAGCCGGGCAGCAACAGCCCCGGCAGCGGCGCAGGCTCCAGCGCGCCGGGCCCGGCCGGCCGCAGC
CCCCGACGCCTGGGTGCGCCTGCCTGCCGGCCTCCGCACCGTCCGCCGCCGCTCCCGGGGCTGTTGTGTCTGCGA
CTGCTCCCGGCCGGAGGTGCAGGGAGCTCAGCCGAGCCGCCGCTGCCATCCCGGAGCGAGCAAGCGAGCGAGCGC
GCGGGAGGGAGGAAGGCGGCGGCGGAGGAGGAGGAGGAGCGGGAGGAGCGCGGGCGGGGGCGGGGGCCGCCGGGC
GGGGGAATATACAAAGTGAAGCCACATTGCCAAACTTGCAGCAGCGATTGCAGCAGTTGCTGCCGCTGCGCCGCG
CCTGAAGCCGCGCCGCGCGGGCCGAGGGCTCCTGCAGCTGCTCGCGCGCAGTCGGAGGCGGAGAAGGACGAAGAC
TGAGACTGACACTTCTGCTCCCGGCCGCCCGGCACTTACGCGGGGGCCCCCCAACCCGCCCCAGAGCAACGCGAT
TTAAAAAAAAAAAAAAAGCCGCCCTTAGCCCCTCCTCTCCTTTCCTGCTTCTGCGAGAACTCCCTCCCTCCCTC
CAGCTCCGCCAGCCCAGGCGCCCCTTCCCTGGAAGCCGAGCGGCTTCGCTCGCATTTCACCGCCGCCGCCTCTCG
CAATATTGCAATATAGGGGAAAAGCAGACC**ATG**GTGAATCCGGGCAGCAGCTCGCAGCCGCCCCCGGTGACGGCC
GGCTCCCTCTCCTGGAAGCGGTGCGCAGGCTGCGGGGGCAAGATTGCGGACCGCTTTCTGCTCTATGCCATGGAC
AGCTATTGGCACAGCCGGTGCCTCAAGTGCTCCTGCTGCCAGGCGCAGCTGGGCGACATCGGCACGTCCTGTTAC
ACCAAAAGTGGCATGATCCTTTGCAGAAATGACTACATTAGGTTATTTGGAAATAGCGGTGCTTGCAGCGCTTGC
GGACAGTCGATTCCTGCGAGTGAACTCGTCATGAGGGCGCAAGGCAATGTGTATCATCTTAAGTGTTTTACATGC
TCTACCTGCCGGAATCGCCTGGTCCCGGGAGATCGGTTTCACTACATCAATGGCAGTTTATTTTGTGAACATGAT
AGACCTACAGCTCTCATCAATGGCCATTTGAATTCACTTCAGAGCAATCCACTACTGCCAGACCAGAAGGTCTGC
TAAAAGGTCAGAGTAATGCAGAATGCGTGCCTTCATCTCAGATTTGTTCATCACAGGTGGATCCCATGTGTCTTC
AGTAGACAAGTCACCTTTGTAGCTAGCACCAGTGCCAGCTCCATGCCATTGCACCTTCTTTAGTCTTGATTGCCC
TTCCCGCATTTATTGGTGTATTAAAATGACTGAATATGAACATTAAGGACTCCATGAACCTGGGCTAATGGAGA
CTGTAGAGAAAATGAAAAAAGATCCACCAGAGGACATCTTGGGGAGGGGGAGGGAGCTGGGGGGGAGGGAAATGA
CTAATGAAGCTAATTAAAAGAAGCATTCAAATCTGCTTTCTACCCTCATTAACAATTAGCAGGGCACTGGCCAGA
GTTTGTACCCTGTGTTTTACCTTAACAACATTCTATTTGCTCTTTGTATATTTAAGTGTTGTAAGGAAACGTGTT
TCAATCAAAACTGACCATGAGATAAAGGAAAGAGATGTGGCTTTTGTGATATTCTATCACAAACACTTATTGTAT
CTCTGTAAAATACAATGTATGTATGCATGTAAGTGTTTTTGTCCTAATGTTGCTACTCCCATGGCAAAGAAAAAA
AAAAGAATGAAAAAAAGAAAAAAAAATTTGGAAAAAAAATCAGGCTCATAGCAGCTACTGTGTAGAAAATTCCCC
CTACTTCTAATTTGCTGAATGAAGAAAAAAAAAAAATCTTTTATTTGTGATATTTTCAGAGACATTTGCTCTAGTA
TGGTGTATTTAAATAATAAAAACTTAAAAGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 272

MVNPGSSSQPPPVTAGSLSWKRCAGCGGKIADRFLLYAMDSYWHSRCLKCSCCQAQLGDIGTSCYTKSGMILCRN
DYIRLFGNSGACSACGQSIPASELVMRAQGNVYHLKCFTCSTCRNRLVPGDRFHYINGSLFCEHDRPTALINGHL
NSLQSNPLLPDQKVC

FIGURE 273

AGCGATGGCGGCTGGGCCGAGTGGGTGTCTGGTGCCGGCGTTTGGGCTACGGTTGTTGTTGGCGACTGTGCTTCA
AGCGGTGTCTGCTTTTGGGGCAGAGTTTTCATCGGAGGCATGCAGAGAGTTAGGCTTTTCTAGCAACTTGCTTTG
CAGCTCTTGTGATCTTCTCGGACAGTTCAACCTGCTTCAGCTGGATCCTGATTGCAGAGGATGCTGTCAGGAGGA
AGCACAATTTGAAACCAAAAAGCTGTATGCAGGAGCTATTCTTGAAGTTTGTGGATGAAAATTGGGAAGGTTCCC
TCAAGTCCAAGCTTTTGTTAGGAGTGATAAACCCAAACTGTTCAGAGGACTGCAAATCAAGTATGTCCGTGGTTC
AGACCCTGTATTAAAGCTTTTGGACGACAATGGGAACATTGCTGAAGAACTGAGCATTCTCAAATGGAACACAGA
CAGTGTAGAAGAATTCCTGAGTGAAAAGTTGGAACGCATATAAATCTTGCTTAAATTTTGTCCTATCCTTTTGTT
ACCTTATCAAATGAAATATTACAGCACCTAGAAAATAATTTAGTTTTGCTTGCTTCCATTGATCAGTCTTTTACT
TGAGGCATTAAATATCTAATTAAATCGTGAAATGGCAGTATAGTCCATGATATCTAAGGAGTTGGCAAGCTTAAC
AAAACCCATTTTTTATAAATGTCCATCCTCCTGCATTTGTTGATACCACTAACAAAATGCTTTGTAACAGACTTG
CGGTTAATTATGCAAATGATAGTTTGTGATAATTGGTCCAGTTTTACGAACAACAGATTTCTAAATTAGAGAGGT
TAACAAGACAGATGATTACTATGCCTCATGTGCTGTGTGCTCTTTGAAAGGAATGACAGCAGACTACAAAGCAAA
TAAGATATACTGAGCCTCAACAGATTGCCTGCTCCTCAGAGTCTCTCCTATTTTTGTATTACCCAGCTTTCTTTT
TAATACAAATGTTATTTATAGTTTACAATGAATGCACTGCATAAAAACTTTGTAGCTTCATTATTGTAAAACATA
TTCAAGATCCTACAGTAAGAGTGAAACATTCACAAAGATTTGCGTTAATGAAGACTACACAGAAAACCTTTCTAG
GGATTTGTGTGGATCAGATACATACTTGGCAAATTTTTGAGTTTTACATTCTTACAGAAAAGTCCATTTAAAAGT
GATCATTTGTAAGACCAAAATATAAATAAAAAGTTTCAAAAATCTATCTGAATTTGGAATTCTTCTGGTTTGTTC
TTTCATGTTTAAAAATGATGTTTTTCAATGCATTTTTTTCATGTAAGCCCTTTTTTTAGCCAAAATGTAAAAAATG
GCTGTAATATTTAAAACTTATAACATCTTATTGTTGGTAATAGTGCTTTATATTTGTCTGATTTTATTTTTCAAA
GTTTTTTCATTTATGAACACATTTTCATTGGTATATTATTTAAGGAATATCTCTTGATATAGAATTTTTATATTA
AAAATGATTTTTCTTTGGC

FIGURE 274

MAAGPSGCLVPAFGLRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNLLQLDPDCRGCCQEEA
QFETKKLYAGAILEVCGENWEGSLKSKLLLGVINPNCSEDCKSSMSVVQTLYLKLLDDNGNIAEELSILKWNTDS
VEEFLSEKLERI

FIGURE 275

GCTCTTTCCCTAAGCAGCCTGAAGTAATCTGTGAAAATGGTTCGCTATTCACTTGACCCGGAGAACCCCATGAAA
TCACACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACGAAAAGCCACGAAGTATCTTAAAGATGTCAC
TTTACAGAAACAGTGCATACCATTCCGACGTTACAATGGTGGAGTTGGCAAGTGTGCGCAGGCCAAGCAGTGGGG
CTGGACACAAGGTCGGTGGCCCAAAAAGAGTGCTGAATTTTTGCTGCACATGTTTAAAAACGCAGAGGGTAATAC
TGAACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGTATATCCAAGTGAACAAAGCACCTAAGATGCTCCG
CCGGACCTACAGAGCTCATGGTCGGATTAACTCATACATGAGCTCTCCCTGGCACATTGAGATGATCCTTACTGA
AAAGGAACAGATTGTTCCTAAACCAGAAAAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAA
ACAAAAACTTATGGCCCGGAAGTAAATTCAGCATTAAAATAAATGTAATTAAAAGGAAAAAAAAAAAAAAAAAAA
AAAAAAAAAG

FIGURE 276

GCTCTTTCCCTAAGCAGCCTGAAGTAATCTGTGAAAATGGTTCGCTATTCACTTGACCCGGAGAACCCCATGAAA
TCATGCAAATCAAGAGGTTCCAATCTTCGTGTTCACTTTAAGGACACTCGTGAAACTGCTCAGGCCATCAAGGGT
ATGCATATACGAAAAGCCACGAAGTATCTTAAAGATGTCACTTTACAGAAACAGTGCATACCATTCCGACGTTAC
AATGGTGGAGTTGGCAAGTGTGCGCAGGCCAAGCAGTGGGGCTGGACACAAGGTCGGTGGCCCAAAAAGAGTGCT
GAATTTTTGCTGCACATGTTTAAAAACGCAGAGGGTAATACTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTC
ATTGAGTATATCCAAGTGAACAAAGCACCTAAGATGCTCCGCCGGACCTACAGAGCTCATGGTCGGATTAACTCA
TACATGAGCTCTCCCTGGCACATTGAGATGATCCTTACTGAAAAGGAACAGATTGTTCCTAAACCAGAAAAGGAG
GTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAAACAAAAACTTATGGCCCGGAAGTAAATTCAGCAT
TAAAATAAATGTAATTAAAAGG

FIGURE 277

CTTTTTCACAACGGGTTTGCTGCCAGAACACAGGTGTCGTGAAAACTACCCCTAAAAGCCAAAATGGGAAAAGAA
AAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTCGGGCAAGTCCACCACTTCTGGCCATCTGATCTAC
AAATGCGGTGGCATCGACAAAAGAACAATTGAAAAATTGCAGAAAGAGGCTGCTGAGATGGGAAAGGGCTCCTTC
AAGTATGCCTGAGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAA
TTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTCATCAAAAACATGATTACA
GGGACATCTCAGGCTGGTTGTGCTGTCCTAATTGTTGCTGCTGGTGTTGGTGAATTTGAAGCTGGTATCTCCAAG
AATGGGCAGACCCGAGAGCATGCCCTTCTGGCATATACACTGGGTGTGAAACAACTAATTGTTGATGTTAACAAA
ATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAATCAGCACTTACATTAAG
AAAATTGGCTACAACCCCAACACAGTAGCATTTGTGCCAATTTCTGGTTAGAATGGTGACAAC**ATG**CTGGAGCCA
AGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCATAAGGATGGCAATGCCAGTGGAACCATGCTGCTT
GAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACTGACAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTAC
AAAATTGGTGGTATTGGTACTGTTCTTGTTGGCCGAGTGGAGACTGGTATTCTCAAACCTGGTATGGTGGTCACC
TTTGCTCCAGTCAGCGTTACAACAGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTTGAATGAAGCTCTTCCT
GGGGACAATATGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCATCGTGGCAACGTTGCTGGTGACAGC
AAAAATGACCCACCAATGGAAGCAGCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGT
CGCTTTACTGTTCATGATATGAGACAGACACTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGA
GCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAA**TGA**ATATTATCCCTAATACCTGCCACCCCA
CTCTTAATCAGTGGTGGAAGAACGGTCTCAGAACTGTTTGTTTCAATTGGCCATTTAAGTTTAGTAGTAAAAGAC
TGGTTAATGATAATAATGCAACATAAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGGACCACTTTGGTTTTCTT
TTTCGCATGCAGCAGTTTTAAGTTATTAGTTTTTAAAATCAGTACTTTTTAAATGGAAACAACTTGACCAAAAAT
TTGTCACAGAATTTTGAGACCCATTAAAAAAGTTTAATGAG

FIGURE 278

MLEPSANMPWFKGWKVTHKDGNASGTMLLEALDCILPPTRPTDKPLRLPLQDVYKIGGIGTVLVGRVETGILKPG
MVVTFAPVSVTTEVKSVEMHHEALNEALPGDNMGFNVKNVSVKDVHRGNVAGDSKNDPPMEAAGKPMCVESFSDY
PPLGRFTVHDMRQTLAVGVIKAVDKKAAGAGKVTKSAQKAQKAK

FIGURE 279

CACAGGTGTCGTGAAAACTACCCCTAAAAGCCAAAATGGGAAAAGAAAAGACTCATATCAACATTGTCGTCATTG
GACACGTAGATTCGGGCAAGTCCACCACTTCTGGCCATCTGATCTACAAATGCGGTGGCATCGACAAAAGAACAA
TTGAAAAATTGCAGAAAGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGAGTCTTGGATAAACTGA
AAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTA
TCATTGATGCCCTTCTGGCATATACACTGGGTGTGAAACAACTAATTGTTGATGTTAACAAAATGGATTCCACTG
AGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAATCAGCACTTACATTAAGGGTGACAACATGC
TGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCATAAGGATGGCAATGCCAGTGGAACCA
TGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACTGACAAGCCGGCCAAATAAGCTCTGGCTA
TGCACCTGTATTGGATTGCCACACAGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCG
TTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGCTGATATGGTTCCTGG
CAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTACTGTTCATGATATGAGACAGAC
ACTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAA
AGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGG

FIGURE 280

GCCAAAATGGGAAAAGAAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTCGGGCAAGTCCACCACT
TCTGGCCATCTGATCTACAAATGCGGTGGCATCGACAAAAGAACAATTGAAAAATTGCAGAAAGAGGCTGCTGAG
ATGGGAAAGGGCTCCTTCAAGTATGCCTGAGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATT
GATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTC
ATCAAAAACATGATTACAGGGACATCTCAGGCTGGTTGTGCTGTCCTAATTGTTGCTGCTGGTGTTGGTGAATTT
GAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCATATACACTGGGTGTGAAACAACTA
ATTGTTGATGTTAACAAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAA
ATCAGCACTTACATTAAGAAAATTGGCTACAACCCCAACACAGTAGCATTTGTGCCAAATTCTTGAAGTCTGGTG
ATGCTGCCATTGCTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTC
GCTTTACTGTTCATGATATGAGACAGACACTTGCGGTGGGTG

FIGURE 281

GTGGAGACTGGTATTCTCAAACCTGGTATGGTGGTCACCTTTGCTCCAGTCAGCGTTACAACAGAAGTAAAATCT
GTCGAAATGCACCATGAAGCTTTGAATGAAGCTCTTCCTGGGGACAATATGGGCTTCAATGTCAAGAATGTGTCT
GTCAAGGATGTTCATCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACT
GCTCAGGTGATTATCCTGAACCATCCGGGCCAAATAAGCTCTGGCTATGCACCTGTATTGGATTGCCACACAGCT
CACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCT
AAATTCTTGAAGTCTGGTGATGCTGCCATTGCTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCA
GACTATCCACCTTTGGGTCGCTTTACTGTTCATGATATGAGACAGACACTTGCGGTGGGTGTCATCAAAGCAGTG
GACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCC
CTAATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGAACGGTCTCAGAACTGTTTGTTTCAATTGGCCATTTA
AGTTTAGTAGTAAATTTTGTGGACCACTTTGGTT

FIGURE 282

GTTACTCAAAGACTACCTACTGCGTGGTGCTCCAAGTGAAATTCGTGAAGAATTAGAAAAGCAGCTTTATTCTTG
TATTGCTCTCAAAGTCACAGCAAATCAAATGGAAATGGAACATTCTTTGATACTAAATAACCTAAAAACATTATT
GTGGAAGAAAATTTCCTACACTAATGACTCTTAGTTCATTTGGACATAATTACCATTTTAAGAAACCTGCCACTT
TTAAAGAACAATTTTGAGCATTAAAAAAAAATGGCTTCAAATTCCGGCCAGTTACACAAAACTCCTTCCCCCCAG
GCCTGAGAAGCCATCAGTATGTGATCACTGAAGTAATGGCAGGTGTAGGATCAACAGGTCCCCAAGATGTCATTC
CTGCCCTTTTAGAAGCCCTGTTACATCTCCGAAGTACATTCATTGTGTAACTATTTTGACTGACTTTAAAAACCA
ATGCTGTGAAAAGCTTCATTCCATAAACATCAACAGTGAGTGATTTGTAGATTTACCTTAGCCAAAATACCAATG
CTGGAAGCATTGTGTTTGCATTGAAGCTGCTGTTCAACAAGAAAATTTATAAATTTACTAATGTCTTAGCATGGT
AAAGTTTGCACATTAACAGAAATTAAGACTGCAAAGCAGGTTAAACTTGCTTCTTTATAAAACAGATGTTGGGTT
AATAGCATGGTTTACTGTATTAAAGACTTATACACCCATTTTTAACCTCATTCAGACATCAAGTTATGTGTAGCT
TCACAATGGTTCAAGTGGCTTACTTCAAGAAATCTTATACTTGACAGTACACCAATTTTATTGACTAAAAATGGA
TGAACTTTCCTAAAGATTCAAAGGGCCCATCTTAGTATCACGCAGCTGACTGAGCCCTTCAAAACTGACATCTTA
AGGCCCAATCAAGATCCACATATCCTGATTTTGAACTATGTGAAAGTGGGACTGTAAGTGCAAGACTAAAATAAA
TTATAGCAGACTTTTTAGTAATAACTTTCCATTTTCAAACAGTATATCCTGTGGGCCAAAGGGCTATTTCTTAAA
GAGGCATGTAAATGTATTTATTTATCTA**ATG**TTTTTTTCCCCATGTAAACTTGATATACAAGGTTTAGTATTTGC
TCCTCTTTCATATTATTTTCACACGTATACTCAGATTTGGCATGTACCTTTCAACATCTCCATAAAATTAAACAC
CTTTTGGAGAAAAGAACCACTATTTTCTGCTCAAAGGTTTCGCCTACCTAAAGTGGAACATGTTAAAAATCTATG
TGACCATCACTGGACAGCTTTCTCTCAAAACTTTCCTTCAACGCCATGGATTAGCACCAGTTTGTTTACTTTAA
GGTACTTTTCCCATTCATCATCTGGTTA**TAA**TAAATGGATGGAAGAAATATTTCCCACTGATGGTTGGTCTGTTG
CTTGCCAAATTTTTAGGGAGAGCTGTTCATCATACAACATAAGGGATAATGACTCCTGTCAGGTAAAACAGAAGC
CCAAGAAATAACAACTTTTTTTCTTAAAAAGTTAGTTACACTTGTTTCTTGGAGAAAAAAACCTGTCAACTCCT
TTGCTTTTCCAAAATATTTCAGGGTATTTCCTATAAGGTTCATAAGAATAAGAGCTTAACACAGAAATAGTTGCT
GTTCATAAGTTTATTATCTATATCTGAAAAAATCATAGAAAATTGCTGGGTTTAGCTCTCAGCAGCCCGCTCCTG
AGCTCTGAGGAAGCTTGCCTTCTTTTGAGCTACCCGATCCTTCTTCTGAGCAAGGGACATTTTGGGACGGTTCCA
CCTACAAAAGATAGGAATATATATTTTTTAAACTATAACTGAAGAGAATAGAATATTTAATTTAAAATTTTAATA
AAATTTAATTTTGATAGAGAATATTTAAGACTTTGCAATCAGAAGGTTAAATAATCCAAGTTCAAATACATTTAC
TTATGTATGATCTTAAGCTAACTTTCCCAAACCCCAACTTCTGTGATGTCCTACTACCATAGGGCCAAAAGTCAA
ATAGAAGACATGTTAGATTCAGTAATACCACTTCTAGGTATTTGCCCAAATGTTTTGAAATCAGTTTGTCCAAGA
GAGTGGCACTCCCATGTTCATTGCAGCACTATATATTAATAGCAACAGATAAATGGATAAAGGAAATGTGGTATA
CATATACATAATGGATTATTACCCAGTCTTTAAAAATGATGGAAATTCTGTCATTTGCAACATGAATGAAGTGGA
GAATATTGTGCTCAGTGAAATAAGCCAGGCACAAAAAGACAAATACTTCATATTCATATAGAATCTAAAACAATG
GAACTCACAGAAGCAGAGAGCAGAATGGTGGTTACAGAGGCTGGTGGGTGCAAAGAATGGGCAGATGATAGTCAA
GTATAAAATCTCCAACAGGAGGAGTATGATTTGTTTTAGTTCTATTGCACAGCATGATGAATATAGAATATCG
TACATTTCACAATTAAGAGAATAAATTTCAAATGTTGTTGCCACAAAGTGTTAAGTATTTGAGGTGAATATGTTA
AATACATTGATTTAATTACTATACATTGTATTTGTGGGCCATCACATCACTTTATGCTTACATGTTCATTAAGTA
TTACTTTCTATTCCATTTAAAGATCAAAACATGAAAGATCAACAAAAAGCAACTTGTCAGCCAATAAAAAAATGC
AGTAACCAGTACTTAGACTGTACTAGGATAGAAAGAACCACCTCAGTAGTGTCTGAGGCTAACACATTTCCATCA
CCACAGTTACTTTGCAAACCTGGTTCCCTTCGCTTCTGCCACATCACGCAGAGCTAGTGATCGAGTTTGCACAA
TTACACCAACAGTCTGCCCCACGTGGGAACCATTCCCAACCTGTTTTCTTGAAAAGACAAAAAAAAAGACGACAT
ACCTCTTCTTTTTAACTTCTTTCTTGGGCTTCTTTTCATAGACTGGATTCTCTCGTATAGCAGCATGAGCTTTCT
TATACATCTCCTCCATCTGAAACAAAGGAAAGCAAACAGTACTTGGTTTCATTTCATGTGCCCTACTATATTAAT
GCAACCATAACTTATCTTGTCCTTCTAAGCCAGATTCTCAAAAGGAACTAAACTAAATCAATGTTGGTAAACACT
TTAACTTCTAAATGTAACTCACCTTTTCCTAACAAATTCCCAATTTTCACCTTATGCAATGTGAATTATCACTAC
AGAACTCCATCTTACTCAAGAAAAAAATCAGGCCAGGTGTGGTGGTTCATGCCTGTAATCTCAAGCACTTTGGGA
GTCTGAAGTGGGAGGATCACTTCAGCCCAGGAGTTTGAGACCAGCTAAGGCAACACAGTGAGACCTGTCTCCATA
AAAAAACTAATTAGCCAGGTGGCAATTATTAATGGTGGCATGCACCTGTAGTCCCAGCTACAGGACTACACGTGA
GTCCAGGAGGTCAAGGCTGCAGTGGCACAATCACAGCTCACTGGACCCCAGCCTAGATGACAGAATGAGACCTCA
TCTCTACCAAAAATTAAAAAAAAAAAAAAAAAATTAGCAGGG

FIGURE 283

MFFSPCKLDIQGLVFAPLSYYFHTYTQIWHVPFNISIKLNTFWRKEPLFSAQRFRLPKVEHVKNLCDHHWTAFSQ
NFPSTPWISTSFVYFKVLFPFIIWL

FIGURE 284

CCTAGCGCCGCTGGGCCTGCAGGTCTCTGTCGAGCAGCGGACGCCGGTCTCTGTTCCGCAGG**<u>ATG</u>**GGGTTTGTTA
AAGTTGTTAAGAATAAGGCCTACTTTAAGAGATACCAAGTGAAATTTAGAAGACGACGAGAGGGTAAAACTGATT
ATTATGCTCGGAAACGCTTGGTGATACAAGATAAAAATAAATACAACACACCCAAATACAGGATGATAGTTCGTG
TGACAAACAGAGATATCATTTGTCAGATTGCTTATGCCCGTATAGAGGGGGATATGATAGTCTGCGCAGCGTATG
CACACGAACTGCCAAAATATGGTGTGAAGGTTGGCCTGACAAATTATGCTGCAGCATATTGTACTGGCCTGCTGC
TGGCCCGCAGGCTTCTCAATAGGTTTGGCATGGACAAGATCTATGAAGGCCAAGTGGAGGTGACTGGTGATGAAT
ACAATGTGGAAAGCATTGATGGTCAGCCAGGTGCCTTCACCTGCTATTTGGATGCAGGCCTTGCCAGAACTACCA
CTGGCAATAAAGTTTTTGGTGCCCTGAAGGGAGCTGTGGATGGAGGCTTGTCTATCCCTCACAGTACCAAACGAT
TCCCTGGTTATGATTCTGAAAGCAAGGAATTTAATGCAGAAGTACATCGGAAGCACATCATGGGCCAGAATGTTG
CAGATTACATGCGCTACTTAATGGAAGAAGATGAAGATGCTTACAAGAAACAGTTCTCTCAATACATAAAGAACA
GCGTAACTCCAGACATGATGGAGGAGATGTATAAGAAAGCTCATGCTGCTATACGAGAGAATCCAGTCTATGAAA
AGAAGCCCAAGAAAGAAGTTAAAAAGAAGAGGTGGAACCGTCCCAAAATGTCCCTTGCTCAGAAGAAGGATCGGG
TAGCTCAAAAGAAGGCAAGCTTCCTCAGAGCTCAGGAGCGGGCTGCTGAGAGC**<u>TAA</u>**ACCCAGCAATTTTCTATGA
TTTTTTCAGATATAGATAATAAACTTATGAACAGCAACTAAAAAAAAAAAAAAAAAAA

FIGURE 285

MGFVKVVKNKAYFKRYQVKFRRRREGKTDYYARKRLVIQDKNKYNTPKYRMIVRVTNRDIICQIAYARIEGDMIV
CAAYAHELPKYGVKVGLTNYAAAYCTGLLLARRLLNRFGMDKIYEGQVEVTGDEYNVESIDGQPGAFTCYLDAGL
ARTTTGNKVFGALKGAVDGGLSIPHSTKRFPGYDSESKEFNAEVHRKHIMGQNVADYMRYLMEEDEDAYKKQFSQ
YIKNSVTPDMMEEMYKKAHAAIRENPVYEKKPKKEVKKKRWNRPKMSLAQKKDRVAQKKASFLRAQERAAES

FIGURE 286

ATGGTAAATGTTAAGACAAATCTTGGGAGAAACATTTATCAATTCCAATACCTCTCTCCACCCCAATACTGTATG
CTCTTGGAAGAAGATGAAGATGCTTACAAGAAACAGTTCTCTCAATACATAAAGAACAGTGTAACTCCAGACATG
ATGGAGGAGATGTATAAGAAAGCTCATGCTGCTGTACCAGAGAATCCGGTCTATGAAAAGAAGCCCAAGAAAGAA
GTTAAAAAGAAGAGGTGGAACCGTTCCAAAATGTCCCTTGCTCAGAAGAAGGATTGGGTAGCTCAAAAGAAGGCA
AGCTTCCTCAGAGCT**TAG**

FIGURE 287

MVNVKTNLGRNIYQFQYLSPPQYCMLLEEDEDAYKKQFSQYIKNSVTPDMMEEMYKKAHAAVPENPVYEKKPKKE
VKKKRWNRSKMSLAQKKDWVAQKKASFLRA

FIGURE 288

GCTGACTCCAGTGTCCCGAGAGGCGCCGCTTCTTCCGCTTTCTCGTCAGGCTCCTGCAACCCCAGGCATGAACCA
AGGTTTCTGAACTACTGGGCGGGAGCCAACGTCTCTTCTTTCTCCCGCTCTGGCGGAGGCTTTGTCGCTGCGGGC
TGGGCCCCAGGGTGTCCCC**ATG**GCGGGGCCGCGGGTGGAGGTCGATGGCAGCATCATGGAAGGGGGCGGCCAGA
TCCTGAGAGTCTCTACGGCCTTGAGCTGTCTCCTAGGCCTCCCCTTGCGGGTGCAGAAGATCCGAGCCGGCCGGA
GCACGCCAGGCCTGAGGCCTCAACATTTATCTGGACTGGAAATGATTCGAGATTTGTGTGATGGGCAACTGGAGG
GGGCAGAAATTGGCTCAACAGAAATAACCTTTACACCAGAGAAGATCAAAGGTGGAATCCACACAGCAGATACCA
AGACAGCAGGGAGTGTGTGCCTCTTGATGCAGGTCTCAATGCCGTGTGTTCTCTTTGCTGCTTCTCCATCAGAAC
TTCATTTGAAAGGTGGAACTAATGCTGAAATGGCACCACAGATCGATTATACAGTGATGGTCTTCAAGCCAATTG
TTGAAAAATTTGGTTTCATATTTAATTGTGACATTAAAACAAGGGGATATTACCCAAAAGGGGGTGGTGAAGTGA
TTGTTCGAATGTCACCAGTTAAACAATTGAACCCTATAAATTTAACTGAGCGTGGCTGTGTGACTAAGATATATG
GAAGAGCTTTCGTTGCTGGTGTTTTGCCATTTAAAGTAGCAAAAGATATGGCAGCGGCAGCAGTTAGATGCATCA
GAAAGGAGATCCGGGATTTGTATGTTAACATCCAGCCTGTTCAAGAACCTAAAGACCAAGCATTTGGCAATGGAA
ATGGAATAATAATTATTGCTGAGACCTCCACTGGCTGTTTGTTTGCTGGATCATCGCTTGGTAAACGAGGTGTAA
ATGCAGACAAAGTTGGAATTGAAGCTGCCGAAATGCTATTAGCAAATCTTAGACATGGTGGTACTGTGGATGAGT
ATCTGCAAGACCAGCTGATTGTTTTCATGGCATTAGCCAATGGAGTTTCCAGAATAAAAACAGGACCAGTTACAC
TCCATACGCAAACCGCGATACATTTTGCTGAACAAATAGCAAAGGCTAAATTTATTGTGAAGAAATCAGAAGATG
AAGAAGACGCCGCTAAAGATACTTATATTATTGAATGCCAAGGAATTGGGATGACAAATCCAAATCTA**TAG**AGTA
TTTGCCTCTTAAATGATACCTCATTGATATATTGCACTATTTCATAAATACTATAAAATAATGACTAGGAAGTAA
CTTATTAAAGGCTATGACTTAAATTTGAAGATGAAGTACAGTGTTCTAGGTTTGCTGAGAAGGCTTCATTAAATT
AATCTCACTTTGAATATCTCCTGAGAGATGGACAATGAAATATCAGTTGGTGGATATGTGTGATAGCTGATTTCA
ATATTGAAGTATTGAAATAAAATATTCTTTACACCTGAG

FIGURE 289

MAGPRVEVDGSIMEGGGQILRVSTALSCLLGLPLRVQKIRAGRSTPGLRPQHLSGLEMIRDLCDGQLEGAEIGST
EITFTPEKIKGGIHTADTKTAGSVCLLMQVSMPCVLFAASPSELHLKGGTNAEMAPQIDYTVMVFKPIVEKFGFI
FNCDIKTRGYYPKGGGEVIVRMSPVKQLNPINLTERGCVTKIYGRAFVAGVLPFKVAKDMAAAAVRCIRKEIRDL
YVNIQPVQEPKDQAFGNGNGIIIIAETSTGCLFAGSSLGKRGVNADKVGIEAAEMLLANLRHGGTVDEYLQDQLI
VFMALANGVSRIKTGPVTLHTQTAIHFAEQIAKAKFIVKKSEDEEDAAKDTYIIECQGIGMTNPNL

FIGURE 290

GCTTTTCCTTGCTACCTGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACTTAAAGGGAAACTTT
CACA<u>**ATG**</u>TCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTT
AGGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAA
TCTGAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGGTCGTGCTATTGTTGCCATTGAAAACCCTGCTGATGTCAG
TGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAATTTGCTGCTGCCACTGGAGCCACTCCAATTGC
TGGCCGCTTCACTCCTGGAACCTTCACTAACCGGATCCAGGCAGCCTTCCGGGAGCCACGGCTTGTTGTGGTTAC
TGACCCCAGGGCTGACCACCAGCCTCTCACAGAGGCATCTTATGTTAACCTACCTACCATTGCGCTGTGTAACAC
AGATTCTCCTCTGTGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAACTCACTCAGTGGGTTTGATGTG
GTGGATGCTGGCTCGGGAAGTTCTGCGCATGTGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCTGA
TCTGTACTTCGACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAGAAGGCAGTGACCAAGGA
GGAATTTCAGGGTGAATGGACTGCTCCAGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAGACTGGTCTGA
AGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCCTACTGAAGACTGGAGCGCTCAGCCTGCCACGGAAGA
CTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGACTGGTCT<u>**TAA**</u>GCTGTTCTTGC
ATAGGCTCTTAAGCAGCATGGAAAAATGGTTGATGGAAAATAAACATCAGTTTCT

FIGURE 291

MSGALDVLQMKEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAGRAIVAIENPADVSV
ISSRNTGQRAVLKFAAATGATPIAGRFTPGTFTNRIQAAFREPRLVVVTDPRADHQPLTEASYVNLPTIALCNTD
SPLCYVDIAIPCNNKGTHSVGLMWWMLAREVLRMCGTISREHPWEVMPDLYFDRDPEEIEKEEQAAAEKAVTKEE
FQGEWTAPAPEFTATQPEVADWSEGVQVPSVPIQQFPTEDWSAQPATEDWSAAPTAQATEWVGATTDWS

FIGURE 292

GGCACGAGGAAGAATCAGGAGCTTAGGATGTATTAACACCAACTCATTAATATACTAACCGGACAATGTTCTACA
AACAATTCTACATTGTAAAGGACTGGATTGGCACAAAATAAAATAATTTTATTTTATTCAGCTTATAATATGACT
CGATGGAGGAAAATTTGATAAGCATGAGAGAAGACCATTCTTTTCATGTTCGTTACAGAATGGAAGCTTCTTGCC
TAGAGCTGGCCTTGGAAGGGGAACGTCTATGTAAATCAGGAGACTGCCGCGCTGGCGTGTCATTCTTTGAAGCTG
CAGTTCAAGTTGGAACTGAAGACCTAAAAACACTTAGCGCTATTTACAGCCAGTTGGGCAATGCTTATTTCTATT
TGCATGATTATGCCAAAGCATTAGAATATCACCATCATGATTTAACCCTTGCAAGGACTATTGGAGACCAGCTGG
GGGAAGCGAAAGCTAGTGGTAATCTGGGAAACACCTTAAAAGTTCTTGGGAATTTTGACGAAGCCATAGTTTGTT
GTCAGCGACACCTAGATATTTCCAGAGAGCTTAATGACAAGGTGGGAGAAGCAAGAGCACTTTACAATCTTGGGA
ATGTGTATCATGCCAAAGGGAAAAGTTTTGGTTGCCCTGGTCCCCAGGATGTAGGAGAATTTCCAGAAGAAGTGA
GAGATGCTCTGCAGGCAGCCGTGGATTTTTATGAGGAAAACCTATCATTAGTGACTGCTTTGGGTGACCGAGCGG
CACAAGGACGTGCCTTTGGAAATCTTGGAAACACACATTACCTCCTTGGCAACTTCAGGGATGCAGTTATAGCTC
ATGAGCAGCGTCTCCTTATTGCAAAAGAATTTGGAGATAAAGCAGCTGAAAGAAGAGCATATAGCAACCTTGGAA
ATGCATATATATTTCTTGGTGAATTTGAAACTGCCTCGGAATACTACAAGAAGACACTACTGTTGGCCCGACAGC
TTAAAGACCGAGCTGTAGAAGCACAGTCTTGTTACAGTCTTGGAAATACATATACTTTACTTCAAGACTATGAAA
AGGCCATTGATTATCATCTGAAGCACTTAGCAATTGCTCAAGAGCTGAATGATAGAATTGGTGAAGGAAGAGCAT
GTTGGAGCTTAGGAAATGCATACACAGCACTAGGAAATCATGATCAAGCAATGCATTTTGCTGAAAAGCACTTGG
AAATTTCAAGAGAGGTTGGGGATAAAAGTGGTGAACTAACAGCACGACTTAATCTCTCAGACCTTCAAATGGTTC
TTGGTCTGAGCTACAGCACAAATAACTCCATAATGTCTGAAAATACTGAAATTGATAGCAGTTTGAATGGTGTAC
TCCCCAAGTTGGGACGCCGGCATAGTATGGAAAATATGGAACTTATGAAGTTAACACCAGAAAAGGTACAGAACT
GGAACAGTGAAATTCTTGCTAAGCAAAAACCTCTTATTGCCAAACCTTCTGCAAAGCTACTCTTTGTCAACAGAC
TGAAGGGGAAAAAATACAAAACGAATTCCTCCACTAAAGTTCTCCAAGATGCCAGTAATTCTATTGACCACCGAA
TTCCAAATTCTCAGAGGAAAATCAGTGCAGATACTATTGGAGATGAAGGGTTCTTTGACTTATTAAGCCGATTTC
AAAGCAATAGGATGGATGATCAGAGATGTTGCTTACAAGAAAAGAACTGCCATACAGCTTCAACAACAACTTCTT
CCACTCCCCCTAAAATGATGCTAAAAACATCATCTGTTCCTGTGGTATCCCCCAACACGGATGAGTTTTTAGATC
TTCTTGCCAGCTCACAGAGTCGCCGTCTGGATGACCAGAGGGCTAGTTTCAGTAATTTGCCAGGGCTTCGTCTAA
CACAAAACAGCCAGTCGGTACTTAGCCACCTGATGACTAATGACAACAAAGAGGCTGATGAAGATTTCTTTGACA
TCCTTGTAAAATGTCAAGGATCCAGATTAGATGATCAAAGATGTGCTCCACCACCTGCTACCACAAAGGGTCCGA
CAGTACCAGATGAAGACTTTTTCAGCCTTATTTTACGGTCCCAGGGAAAGAGAATGGATGAACAGAGAGTTCTTT
TACAAAGAGATCAAAACAGAGACACTGACTTTGGGCTAAAGGACTTTTTGCAAAATAATGCTTTGTTGGAGTTTA
AAAATTCAGGGAAAAAATCGGCAGACCATTAGTTACTATGGATTTATTTTTTTCCTTTCAAACACGGTAAGGAA
ACAATCTATTACTTTTTTCCTTAAAAGGAGAATTTATAGCACTGTAATACAGCTTAAAATATTTTTAGAATGATG
TAAATAGTTAA

FIGURE 293

MREDHSFHVRYRMEASCLELALEGERLCKSGDCRAGVSFFEAAVQVGTEDLKTLSAIYSQLGNAYFYLHDYAKAL
EYHHHDLTLARTIGDQLGEAKASGNLGNTLKVLGNFDEAIVCCQRHLDISRELNDKVGEARALYNLGNVYHAKGK
SFGCPGPQDVGEFPEEVRDALQAAVDFYEENLSLVTALGDRAAQGRAFGNLGNTHYLLGNFRDAVIAHEQRLLIA
KEFGDKAAERRAYSNLGNAYIFLGEFETASEYYKKTLLLARQLKDRAVEAQSCYSLGNTYTLLQDYEKAIDYHLK
HLAIAQELNDRIGEGRACWSLGNAYTALGNHDQAMHFAEKHLEISREVGDKSGELTARLNLSDLQMVLGLSYSTN
NSIMSENTEIDSSLNGVLPKLGRRHSMENMELMKLTPEKVQNWNSEILAKQKPLIAKPSAKLLFVNRLKGKKYKT
NSSTKVLQDASNSIDHRIPNSQRKISADTIGDEGFFDLLSRFQSNRMDDQRCCLQEKNCHTASTTTSSTPPKMML
KTSSVPVVSPNTDEFLDLLASSQSRRLDDQRASFSNLPGLRLTQNSQSVLSHLMTNDNKEADEDFFDILVKCQGS
RLDDQRCAPPPATTKGPTVPDEDFFSLILRSQGKRMDEQRVLLQRDQNRDTDFGLKDFLQNNALLEFKNSGKKSA
DH

FIGURE 294

AAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTATTCACTTGACCCGGAGAACCCCACGAAATCATGCAAATC
AAGAGGTTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACG
AAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACCATTCCGACGTTACAATGGTGGAGT
TGGCAGGTGTGCGCAGGCCCTGCACATGCTTAAAAACACAGAGAGTAATGCTGAACTTAAGGGTTTAGATGTAGA
TTCTCTGGTCATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCCGGACCTACAGAGCTCATGGTCG
GATTAACCCATACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAAAGGAACAGATTGTTCCTAAACC
AGAAGAGGAGGTTGCCCAGAAGAAAAGGATATCCCAGAAGAAACTGAAGAAACAAAAACTTATGGCACGGGAGTA
AATTCAGCAT

FIGURE 295

GCAGGCTCTGCCTGTGGCCACTAGCAGAGAAGCTGCTGTCCTTCCACCACCAGCACCGGACCACCTGCTCCAAGA
CCAGCCTCCTGGGGGGACCAGGCACCCGGCCTTCACTGGCACCCAGGGAGCCGTCCTCAGCAGCGTCAACATGTC
AAGGCCCAGCAGCAGAGCCATTTACTTGCACCGGAAGGAGTACTCCCAGAACCTCACCTCAGAGCCCACCCTCCT
GCAGCACAGGGTGGAGCACTTGATGACATGCAAGCAGGGGAGTCAGAGAGTCCAGGGGCCCGAGGATGCCTTGCA
GAAGCTGTTCGAGATGGATGCACAGGGCCGGGTGTGGAGCCAAGACTTGATCCTGCAGGTCAGGGACGGCTGGCT
GCAGCTGCTGGACATTGAGACCAAGGAGGAGCTGGACTCTTACCGCCTAGACAGCATCCAGGCCATGAATGTGGC
GCTCAACACATGTTCCTACAACTCCATCCTGTCCATCACCGTGCAGGAGCCGGGCCTGCCAGGCACTAGCACTCT
GCTCTTCCAGTGCCAGGAAGTGGGGGCAGAGCGACTGAAGACCAGCCTGCAGAAGGCTCTGGAGGAAGAGCTGGA
GCAAAGACCTCGACTTGGAGGCCTTCAGCCAGGCCAGGACAGATGGAGGGGGCCTGCTATGGAAAGGCCGCTCCC
TATGGAGCAGGCACGCTATCTGGAGCCGGGGATCCCTCCAGAACAGCCCCACCAGAGGACCCTAGAGCACAGCCT
CCCACCATCCCCAAGGCCCCTGCCACGCCACACCAGTGCCCGAGAACCAAGTGCCTTTACTCTGCCTCCTCCAAG
GCGGTCCTCTTCCCCCGAGGACCCAGAGAGGGACGAGGAAGTGCTGAACCATGTCCTAAGGGACATTGAGCTGTT
CATGGGAAAGCTGGAGAAGGCCCAGGCAAAGACCAGCAGGAAGAAGAAATTTGGGAAAAAAAACAAGGACCAGGG
AGGTCTCACCCAGGCACAGTACATTGACTGCTTCCAGAAGATCAAGCACAGCTTCAACCTCCTGGGAAGGCTGGC
CACCTGGCTGAAGGAGACAAGTGCCCCTGAGCTCGTACACATCCTCTTCAAGTCCCTGAACTTCATCCTGGCCAG
GTGCCCTGAGGCTGGCCTAGCAGCCCAAGTGATCTCACCCCTCCTCACCCCTAAAGCTATCAACCTGCTACAGTC
CTGTCTAAGCCCACCTGAGAGTAACCTTTGGATGGGGTTGGGCCCAGCCTGGACCACTAGCCGGGCCGACTGGAC
AGGCGATGAGCCCCTGCCCTACCAACCCACATTCTCAGATGACTGGCAACTTCCAGAGCCCTCCAGCCAAGCACC
CTTAGGATACCAGGACCCTGTTTCCCTTCGGCGGGGAAGTCATAGGTTAGGGAGCACCTCACACTTTCCTCAGGA
GAAGACACACAACCATGACCCTCAGCCTGGGGACCCCAACTCCAGGCCCTCCAGCCCCAAACCTGCCCAGCCAGC
CCTGAAAATGCAAGTCTTGTACGAGTTTGAAGCTAGGAACCCACGGGAACTGACTGTGGTCCAGGGAGAGAAGCT
GGAGGTTCTGGACCACAGCAAGCGGTGGTGGCTGGTGAAGAATGAGGCGGGACGGAGCGGCTACATTCCAAGCAA
CATCCTGGAGCCCCTACAGCCGGGGACCCCTGGGACCCAGGGCCAGTCACCCTCTCGGGTTCCAATGCTTCGACT
TAGCTCGAGGCCTGAAGAGGTCACAGACTGGCTGCAGGCAGAGAACTTCTCCACTGCCACGGTGAGGACACTTGG
GTCCCTGACGGGGAGCCAGCTACTTCGCATAAGACCTGGGGAGCTACAGATGCTATGTCCACAGGAGGCCCCACG
AATCCTGTCCCGGCTGGAGGCTGTCAGAAGGATGCTGGGGATAAGCCCTTAGGCACCAGCTTAGACACCTCCAAG
AACCAGGCCCCGCTGATGCAAGATGGCAGATCTGATACCCATTAGAGCCCCGAGAATTCCTCTTCTGGATCCCAG
TTTGCAGCAAACCCCACACCCCAGCTCACACAGCAAAAACAATGGACAGGCCCAGAGGCTGAAGCAAACAGTGTC
CCTTCTGGCTGTGTTGGAGCCTCCCCAGTAACCACCTATTTATTTACCTCTTTCCCAAACCTGGAGCATTTATG
CCTAGGCTTGTCAAGAATCTGTTCAGTCCCTCTCCTTCTCAATAAAAGCATCTTCAAGCTTGT

FIGURE 296

GGGAGAAAGCCTGTTGCGTGGAAGATAAGGCGGCGCGGGAAGTGGACACAGGGTGGGCTGGAGCTCAGATCTAAC
TGGACTCTCGCTCCTGCTGGCTGGAC**ATG**GAGGATTTGGAGGAAGATGTAAGGTTTATTGTGGATGAGACCTTGG
ACTTTGGGGGGCTGTCACCATCTGACAGCCGTGAGGAGGAAGACATAACAGTGTTGGTGACTCCAGAGAAACCAC
TTCGACGGGGCCTCTCCCACCGAAGTGACCCAAATGCAGTGGCACCTGCCCCCCAGGGTGTGAGGCTCAGCCTAG
GCCCCCTCAGTCCAGAGAAGCTGGAGGAGATCCTCGATGAGGCCAACCGGCTGGCCGCTCAGCTGGAGCAGTGTG
CCCTGCAGGATCGGGAGAGCGCAGGCGAGGGCCTGGGGCCTCGCCGAGTGAAGCCCAGTCCTCGGCGGGAGACCT
TTGTGCTGAAGGATAGTCCTGTCCGAGACCTGCTGCCCACTGTGAACTCTTTGACGCGGAGCACCCCCTCCCCAA
GCAGCCTGACGCCTCGACTCCGGAGTAATGATAGGAAGGGGTCAGTCAGGGCTCTCCGGGCTACATCTGGAAAGA
GGCCCTCCAACATGAAGAGGGAGTCACCCACTTGCAATCTGTTCCCTGCATCCAAAAGCCCAGCATCTTCTCCTC
TTACCCGATCGACTCCCCCAGTCCGGGGGAGAGCCGGGCCCAGTGGGAGAGCAGCAGCCAGCCCACCCACCCCCA
TCAGATCCGTCCTGGCCCCACAGCCTTCTACCAGCAACTCTCAACGCCTGCCCCGGCCGCAGGGAGCAGCTGCTA
AATCTTCCAGTCAACTGCCCATTCCCTCGGCCATCCCCAGGCCTGCCAGCCGAATGCCACTCACCAGCCGGAGTG
TGCCACCTGGCAGAGGTGCCCTACCTCCGGATTCTCTGTCAACTCGAAAAGGGCTTCCAAGACCAAGCACTGCAG
GACACAGAGTGCGGGAAAGTGGACACAAGGTTCCTGTTTCCCAGCGACTAAATCTTCCTGTCATGGGTGCCACTC
GCAGCAATCTGCAGCCCCCCAGGAAAGTGGCAGTCCCAGGACCTACCAGG**TAA**AGAGATCAGGACAGCAAGCAAG
ACTTCAGTAGCAAACCACTACAGTCAGTACCTGGACTCGCCTCTACCCAGCAGACCCTGACTCCAGCAGATTCTG
GCCCAGGGACAGGAGGAAGAGATGCCACCAGGGCTGGTCTCCCAGGAGTAGAGACCATGGGAAATGGGGTGGATT
AGGATTGAGCTGGAGAAGACTTAAACTCTCTGGGTTGAAAGAAGATTAGGGGAAAAGAGGTCACCTTCCAGCAGT
GAAATGAACAAATAGAAGATGAGAAGTACAGGCAAGTGGTTTGTCTTTATCCACCCCCACTGTTGTGGTCAGCCC
CAGAGAATTTTATCTTCTTCCTTGGCATTGGTTCACTGGACATTTCCACGTGAGCGGCCTCCGTAGCTAACCTCC
CTGCCCTCTGAGGAGCCATCTTCCTGAATCGCATTCTCTACTGGACTCTGGCCTGCTTGGAGAGGTGGCAGCAGG
CACCTGGTCTTCAGAAATTGTTTCCTGTGAATTCTGTGACTCCTAATAGGCCAGTTTGTGATAAGCTTACTCTAT
GAGTCTTCATTTTTCTAAAATAAAGTGAATGTATTTTTAAAAAAAAAAAAAAAAAAA

FIGURE 297

MEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVLVTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLE
EILDEANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSPVRDLLPTVNSLTRSTPSPSSLTPRLRS
NDRKGSVRALRATSGKRPSNMKRESPTCNLFPASKSPASSPLTRSTPPVRGRAGPSGRAAASPPTPIRSVLAPQP
STSNSQRLPRPQGAAAKSSSQLPIPSAIPRPASRMPLTSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGH
KVPVSQRLNLPVMGATRSNLQPPRKVAVPGPTR

FIGURE 298

GCAGTGCGGCGGTCACAGGCTGAGTGCTGCGGCGCGATCCTTGCTTCCCTGAGCGTTGGCCCGGGAGGAAAGAAG
ATGGTGCTGGATCTGGATTTGTTTCGGGTGGATAAAGGAGGGGACCCAGCCCTCATCCGAGAGACGCAGGAGAAG
CGCTTCAAGGACCCGGGACTAGTGGACCAGCTGGTGAAGGCAGACAGCGAGTGGCGACGATGTAGATTTCGGGCA
GACAACTTGAACAAGCTGAAGAACCTATGCAGCAAGACAATCGGAGAGAAAATGAAGAAAAAAGAGCCAGTGGGA
GATGATGAGTCTGTCCCAGAGAATGTGCTGAGTTTCGATGACCTTACTGCAGACGCTTTAGCTAACCTGAAAGTC
TCACAAATCAAAAAAGTCCGACTCCTCATTGATGAAGCCATCCTGAAGTGTGACGCGGAGCGGATAAAGTTGGAA
GCAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACCCATCAGTAACGATGAGGAT
GTGGACAACAAAGTAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTG
ATGGTAGATGGCTTTGAAGGCGAAAAGGGGGCCGTGGTGGCTGGGAGTCGAGGGTACTTCTTGAAGGGGGTCCTG
GTGTTCCTGGAACAGGCTCTCATCCAGTATGCCCTTCGCACCTTGGGAAGTCGGGGCTACATTCCCATTTATACC
CCCTTTTTCATGAGGAAGGAGGTCATGCAGGAGGTGGCACAGCTCAGCCAGTTTGATGAAGAACTTTATAAGGTG
ATTGGCAAAGGCAGTGAAAAGTCTGATGACAACTCCTATGATGAGAAGTACCTGATTGCCACCTCAGAGCAGCCC
ATTGCTGCCCTGCACCGGGATGAGTGGCTCCGGCCGGAGGACCTGCCCATCAAGTATGCTGGCCTGTCTACCTGC
TTCCGTCAGGAGGTGGGCTCCCATGGCCGTGACACCCGTGGCATCTTCCGAGTCCATCAGTTTGAGAAGATTGAA
CAGTTTGTGTACTCATCACCCCATGACAACAAGTCATGGGAGATGTTTGAAGAGATGATTACCACCGCAGAGGAG
TTCTACCAGTCCCTGGGGATTCCTTACCACATTGTGAATATTGTCTCAGGTTCTTTGAATCATGCTGCCAGTAAG
AAGCTTGACCTGGAGGCCTGGTTTCCGGGCTCAGGAGCCTTCCGTGAGTTGGTCTCCTGTTCTAATTGCACGGAT
TACCAGGCTCGCCGGCTTCGAATCCGATATGGGCAAACCAAGAAGATGATGGACAAGGTGGAGTTTGTCCATATG
CTCAATGCTACCATGTGCGCCACTACCCGTACCATCTGCGCCATCCTGGAGAACTACCAGACAGAGAAGGGCATC
ACTGTGCCTGAGAAATTGAAGGAGTTCATGCCGCCAGGACTGCAAGAACTGATCCCCTTTGTGAAGCCTGCGCCC
ATTGAGCAGGAGCCATCAAAGAAGCAGAAGAAGCAACATGAGGGCAGCAAAAAGAAAGCAGCAGCAAGAGACGTC
ACCCTAGAAAACAGGCTGCAGAACATGGAGGTCACCGATGCT**TGA**ACATTCCTGCCTCCCTATTTGCCAGGCTTT
CATTTCTGTCTGCTGAGATCTCAGAGCCTGCCCAACAGCAGGGAAGCCAAGCACCCATTCATCCCCCTGCCCCCA
TCTGACTGCGTAGCTGAGAGGGGAACAGTGCCATGTACCACACAGATGTTCCTGTCTCCTCGCATGGGCATAGGG
ACCCATCATTGATGACTGATGAAACCATGTAATAAAGCATCTCTGGGGAGGGCTTAGGACTCTTCCTCAGTCTTC
TTCCCCGGGCTTGAACCCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 299

MVLDLDLFRVDKGGDPALIRETQEKRFKDPGLVDQLVKADSEWRRCRFRADNLNKLKNLCSKTIGEKMKKKEPVG
DDESVPENVLSFDDLTADALANLKVSQIKKVRLLIDEAILKCDAERIKLEAERFENLREIGNLLHPSVPISNDED
VDNKVERIWGDCTVRKKYSHVDLVVMVDGFEGEKGAVVAGSRGYFLKGVLVFLEQALIQYALRTLGSRGYIPIYT
PFFMRKEVMQEVAQLSQFDEELYKVIGKGSEKSDDNSYDEKYLIATSEQPIAALHRDEWLRPEDLPIKYAGLSTC
FRQEVGSHGRDTRGIFRVHQFEKIEQFVYSSPHDNKSWEMFEEMITTAEEFYQSLGIPYHIVNIVSGSLNHAASK
KLDLEAWFPGSGAFRELVSCSNCTDYQARRLRIRYGQTKKMMDKVEFVHMLNATMCATTRTICAILENYQTEKGI
TVPEKLKEFMPPGLQELIPFVKPAPIEQEPSKKQKKQHEGSKKKAAARDVTLENRLQNMEVTDA

FIGURE 300

CAGAGTGCCCTTTCTCCCCGCCTCTTCCCCCTCCCGGGAGCTGCCAGTACTTGACGTGGCGTCACCGCCCTCTAC
CCTCGCTTTGCGTGCGTGTTTGCGTACAGCGGAGGTGGCGGCGCGGGCAGGTCGGAGCTCGGAGCTGCTGCTTCT
GGTTCTCTTGTGGCCACCGTCGCTGTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTC
AGAAGCCGACGCAGCTCGACGCAGGGGCCGGCAGGAGGGTGGGCGATCGCGTGTCGGAGGGCGCCGCGCGGGCAG
GCGGGCGGGCGCCAGAGGGGGAAAGAGGCGGGGGCGGCGGGTCAGCCGCTGGCCGGGCCGGCGGGGGA**ATG**TCGA
TGCCTGACGCGATGCCGCTGCCCGGGGTCGGGGAGGAGCTGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGT
ACTCCTTCATGGCCACCGTCACCAAGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCA
AATTCCCCACCAAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACAGTTCAG
CTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGCAAACCAACTCCAAGGGCAGCA
GCAATTTCTGTGTGAAGAACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGT
CTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACAC
ACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTA
ACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCG
AGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGG
ATGATGGGGGAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGG
AAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACG
TCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGA
GGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTG
CTGCTCTCAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGG
ATGGGTTCAGGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGA
ATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACAG
AAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCT
GGCCAGATGGCAAACGAGTTGTCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCT
TTGTTCTGTCCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACA
AGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTTGCATCTGCCATCATTTGATGCCC
ACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGGGACTCAACAAAAATGGGCCATTCAAACCTAATTATT
ACAGATAC**TAA**TGGACCATACTACCAAGGACCAGTCCACCTGAACCACACACTCTAAAGAAATATTTTTTAAGAT
AACTTTTATTTTCTTCTTACTCCTTTCCTCTTGATTTTTTTCCTATAATTTCATTCTTGTTTTTTCATCTCATTA
TCCAAGTTCTGCAGACCACACAGGAACTTGCTTCATGGCTCTTTAGATGAAATAGAAGTTCAGGGTCCCTCACTC
TAGTCACTAAAGAAGGATTTTACTCCCCCAGCCCAGAAAGGTGATTCTTCTCTTTACCATTTCTGGGGACTTTAG
TCTTAATTAGGTACCTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGC
CTTAAAAGAGCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAGAAGCAGGGATGGTACCTAC
CCGGCAGGTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCCTGCGTAAAG
GTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCAGGAGGCCCACTTGGATTTATAGT
ATAGCCCTTCCTCCACTCCCACCAGACTTGCTCATTTTTCGAGTTTTAACTAGACTACACTCTATTTGAGTTTA
ATTTTGTCCTCTAGGATTTATTCTGTTGTCCAAAAAAAAAAAAAAAAAAAA

FIGURE 301

MSMPDAMPLPGVGEELKQAKEIEDAEKYSFMATVTKAPKKQIQFADDMQEFTKFPTKTGRRSLSRSISQSSTDSY
SSAASYTDSSDDEVSPREKQQTNSKGSSNFCVKNIKQAEFGRREIEIAEQDMSALISLRKRAQGEKPLAGAKIVG
CTHITAQTAVLIETLCALGAQCRWSACNIYSTQNEVAAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDGWQANM
ILDDGGDLTHWVYKKYPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKFDNLYCCRESILDG
LKRTTDVMFGGKQVVVCGYGEVGKGCCAALKALGAIVYIITEIDPICALQACMDGFRVVKLNEVIRQVDVVITCTG
NKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQVDHVIWPDGKRVVLLAEGRLLNLSCSTV
PTFVLSITATTQALALIELYNAPEGRYKQDVYLLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKP
NYYRY

FIGURE 302A

GCTTATGGCGGCGCTGGAGAGGGGGCGCTGAGCTGTTGGGTATGAAGTGTAACAGAACAGACTTTACCACCTGAA
ACTGCTGCTTCAAGTTCAGATCAGGCAAGGAACAAACCTCGTAACAACTAACAAGACCAAAGAAGAGTACACTTA
AGTTGAAGACACAACACTTGATCTGAAACAAGAAGTTTGTGCCTACTCAACAGCTTTGAAAGAGCACTTCCCAAC
GCTGCTAGTAGTCTTTGTTTTCTTCAGTGCTGTACTGTGAGATTGCCCGGTACAGCAGCAGTTGTATTCTTTATT
AGCTTGGTAGATCATTTTCTCTCGCTCTTTTTTTAATACTAGCAACTTTCATCCTTTGAAACGTGTGCTGAAAA
AGAAGAATCAGCAAATACTACTGAAAGTGCAATATTTGAGTATCACTGCGAGATGAGCTTTGATCCAAACCTTCT
CCACAACAATGGACATAATGGGTACCCTAATGGTACTTCAGCAGCACTGCGTGAAACTGGGGTTATTGAAAAACT
GTTAACCTCTTACGGATTTATTCAGTGTTCAGAACGTCAAGCTAGACTTTTCTTCCACTGTTCACAGTATAATGG
CAACCTGCAAGACTTAAAAGTAGGAGATGATGTTGAATTTGAAGTATCATCGGACCGACGGACTGGGAAACCCAT
TGCTGTTAAACTGGTGAAGATAAAACAAGAAATCCTCCCTGAAGAACGAATGAATGGACAAGTTGTGTGCGCTGT
TCCTCACAACTTAGAGAGTAAATCTCCAGCTGCCCCGGGTCAGAGTCCAACAGGGAGTGTATGCTACGAACGTAA
TGGGGAAGTGTTTTATCTGACTTACACCCCTGAAGATGTCGAAGGGAACGTTCAGCTGGAAACTGGAGATAAAAT
AAACTTTGTAATTGATAACAATAAACATACTGGTGCTGTAAGTGCTCGCAACATTATGCTGTTGAAAAAGAAACA
AGCCCGCTGTCAGGGAGTAGTTTGTGCCATGAAGGAGGCATTTGGCTTTATTGAAAGAGGTGATGTTGTAAAAGA
GATATTCTTTCACTATAGTGAATTTAAGGGTGACTTAGAAACCTTACAGCCTGGCGATGATGTGGAATTCACAAT
CAAGGACAGAAATGGTAAAGAAGTTGCAACAGATGTCAGACTATTGCCTCAAGGAACAGTCATTTTTGAAGATAT
CAGCATTGAACATTTTGAAGGAACTGTAACCAAAGTTATCCCAAAAGTACCCAGTAAAAACCAGAATGACCCATT
GCCAGGACGCATCAAAGTTGACTTTGTGATCCCTAAAGAACTTCCCTTTGGAGACAAAGATACGAAATCCAAGGT
GACCCTGCTGGAAGGTGACCATGTTAGGTTTAATATTTCAACAGACCGACGTGACAAATTAGAGCGAGCAACCAA
TATAGAAGTTCTGTCAAATACATTTCAGTTCACTAATGAAGCCCGAGAAATGGGTGTGATTGCTGCCATGAGAGA
TGGTTTTGGTTTCATCAAGTGTGTGGATCGTGATGTTCGTATGTTCTTCCACTTCAGTGAAATTCTGGATGGGAA
CCAGCTCCATATTGCAGATGAAGTAGAGTTTACTGTGGTTCCTGATATGCTCTCTGCTCAAAGAAATCATGCTAT
TAGGATTAAAAAACTTCCCAAGGGCACGGTTTCATTTCATTCCCATTCAGATCACCGTTTTCTGGGCACGGTAGA
AAAAGAAGCCACTTTTTCCAATCCTAAAACCACTAGCCCAAATAAAGGCAAAGAGAAGGAGGCTGAGGATGGCAT
TATTGCTTATGATGACTGTGGGGTGAAACTGACTATTGCTTTTCAAGCCAAGGATGTGGAAGGATCTACTTCTCC
TCAAATAGGAGATAAGGTTGAATTTAGTATTAGTGACAAACAGAGGCCTGGACAGCAGGTTGCAACTTGTGTGCG
ACTTTTAGGTCGTAATTCTAACTCCAAGAGGCTCTTGGGTTATGTGGCAACTCTGAAGGATAATTTTGGATTTAT
TGAAACAGCCAATCATGATAAGGAAATCTTTTTCCATTACAGTGAGTTCTCTGGTGATGTTGATAGCCTGGAACT
GGGGGACATGGTCGAGTATAGCTTGTCCAAAGGCAAAGGCAACAAAGTCAGTGCAGAAAAAGTGAACAAAACACA
CTCAGTGAATGGCATTACTGAGGAAGCTGATCCCACCATTTACTCTGGCAAAGTAATTCGCCCCCTGAGGAGTGT
TGATCCAACACAGACTGAGTACCAAGGAATGATTGAGATTGTGGAGGAGGGCGATATGAAAGGTGAGGTCTATCC
ATTTGGCATCGTTGGGATGGCCAACAAAGGGGATTGCCTGCAGAAAGGGGAGAGCGTCAAGTTCCAATTGTGTGT
CCTGGGCCAAAATGCACAAACTATGGCTTACAACATCACACCCCTGCGCAGGGCCACAGTGGAATGTGTGAAAGA
TCAGTTTGGCTTCATTAACTATGAAGTAGGAGATAGCAAGAAGCTCTTTTTCCATGTGAAAGAAGTTCAGGATGG
CATTGAGCTACAGGCAGGAGATGAGGTGGAGTTCTCAGTGATTCTTAATCAGCGCACTGGCAAGTGCAGCGCCTG
TAATGTTTGGCGAGTCTGTGAGGGCCCCAAGGCTGTTGCAGCTCCTCGACCTGATCGGTTGGTCAATCGCTTGAA
GAATATCACTCTGGATGATGCCAGTGCTCCTCGCCTAATGGTTCTTCGTCAGCCAAGGGGACCAGATAACTCAAT
GGGGTTTGGTGCAGAAAGAAAGATCCGTCAAGCTGGTGTCATTGACTAACCACATCCACAAAGCACACCATTAAT
CCACTATGATCAAGTTGGGGGGAATCTGGTGAAGGGTTCTGAATATCTCCCTCTTCATCCCTCCCGAAATCTGGA
ATACTTATTCTATTGAGCTATTACACCAGTTTTAACACCTTCCTCGTGTTATGTTTAAAAAAATAAATAAATTTA
AGAAAACCATTTTAAATAATGCACAGTTGCAGCCTGGAAAAACTTAAGGTGGCGCCTTATAGTATCAATTTTAGG
AGCTTTATTTGGTGCATTTAACGCAACTGGTAATTGCAGAATCCACTTTGCCTGTGTAAGTGAAAAATATAGACT
GTTATCTTGTTGGCCCTATGAAATTCTGCACTTTTCATTATATACTCTACCTTCATTAATTACTTCTGGCAAGAT
GTTCTGCCTTAGCACTCAGTTGCATTCTTTTCCTTTTTCTTCCTGTTCATTATGCTTTAATTCTGAGGACCATAT
GAGGGTAGAATATATTATCTTTTAAAAATTACAAAAATTTGTATAGGCAAACCATTTCTTAAAGTTGATGGCCAA
ATTTTAAAATGTTATTTTTCATATCATTTATAATCTTGTCACAATCCACTTAAAGAAGTTTGGTTATATTTCAGT
GAAAATTTTCTTCCAGAGTAGGTTTTTTTTCGTGGGTTGGGGGGTAACTTTACTACAATTAGTAAGTATGGTGCA
GAATTTCATGCAAATGAGGAGTGCCAGCAGTGTGATAATTTAAACATATTTAAACAAAAACAAAAAAAAATGAATG

FIGURE 302B

CACAAACTTGCTGCTGCTTAGATCACTGCAGCTTCTAGGACCCGGTTTCTTTTACTGATTTAAAAACAAAACAAA
AAAAAATAAAAAAGTTGTGCCTGAAATGAATCTTGTTTTTTTTTATAAGTAGCCGCCTGGTTACTGTGTCCTGTA
AAATACAGACACTTGACCCTTGGTGTAGCTTCTGTTCAACTTTATATCACGGGAATGGATGGGTCTGATTTCTTG
GCCCTCTTCTTGAATTGGCCATATACAGGGTCCCTGGCCAGTGGACTGAAGGCTTTGTCTAAGATGACAAGGGTC
AGCTCAGGGGATGTGGGGGAGGGCGGTTTTATCTTCCCCCTTGTCGTTTGAGGTTTTGATCTCTGGGTAAAGAGG
CCGTTTATCTTTGTAAACACGAAACATTTTTGCTTTCTCCAGTTTTCTGTTAATGGCGAAAGAATGGAAGCGAAT
AAAGTTTTACTGATTTTTGAGACACT

FIGURE 303

MSFDPNLLHNNGHNGYPNGTSAALRETGVIEKLLTSYGFIQCSERQARLFFHCSQYNGNLQDLKVGDDVEFEVSS
DRRTGKPIAVKLVKIKQEILPEERMNGQVVCAVPHNLESKSPAAPGQSPTGSVCYERNGEVFYLTYTPEDVEGNV
QLETGDKINFVIDNNKHTGAVSARNIMLLKKKQARCQGVVCAMKEAFGFIERGDVVKEIFFHYSEFKGDLETLQP
GDDVEFTIKDRNGKEVATDVRLLPQGTVIFEDISIEHFEGTVTKVIPKVPSKNQNDPLPGRIKVDFVIPKELPFG
DKDTKSKVTLLEGDHVRFNISTDRRDKLERATNIEVLSNTFQFTNEAREMGVIAAMRDGFGFIKCVDRDVRMFFH
FSEILDGNQLHIADEVEFTVVPDMLSAQRNHAIRIKKLPKGTVSFHSHSDHRFLGTVEKEATFSNPKTTSPNKGK
EKEAEDGIIAYDDCGVKLTIAFQAKDVEGSTSPQIGDKVEFSISDKQRPGQQVATCVRLLGRNSNSKRLLGYVAT
LKDNFGFIETANHDKEIFFHYSEFSGDVDSLELGDMVEYSLSKGKGNKVSAEKVNKTHSVNGITEEADPTIYSGK
VIRPLRSVDPTQTEYQGMIEIVEEGDMKGEVYPFGIVGMANKGDCLQKGESVKFQLCVLGQNAQTMAYNITPLRR
ATVECVKDQFGFINYEVGDSKKLFFHVKEVQDGIELQAGDEVEFSVILNQRTGKCSACNVWRVCEGPKAVAAPRP
DRLVNRLKNITLDDASAPRLMVLRQPRGPDNSMGFGAERKIRQAGVID

FIGURE 304

GCTGAAG**ATG**GGAGCCACTCTCAAAATCATGCTGGATAACACCTACATGAAAAAGTGTGACGAGAACATCCTGTG
GCTGGACTACAAGAACATCTGCAAGGTGATGGAAGTGGGCAGCAAGATCTACGTGGATGATGGGCTTATTTCTCT
CCAGGTAAAGCAGAAAGGTGCTGACTTCCTGGTGACGGAGGTGGAAACTGGTGGTTCCTCGGGCAGCAAGAAGGG
TGTGAACCTTCCTGGGGCTGCTGTGGACTTGCCTGCTGTGTCAGAGGACATCCAGGACCTGAATTTTGGGGTCGA
GCAGGATGTCGATATGGTGTTTGCGTCGTTCATCCGCAAGGCATCTGATGTCCATGAAGTTAGGGAGGCCCTGGG
AGAGAAGGGAAAGAAAACACTCCACCCTCCACCTTCCATTTTCCCCCACTACTGCAGCACCTCCGGGCCTGTTGC
TATAGAGCCTACCTGTATATCAATAAACAACAGC**TGA**AG

FIGURE 305

MGATLKIMLDNTYMKKCDENILWLDYKNICKVMEVGSKIYVDDGLISLQVKQKGADFLVTEVETGGSSGSKKGVN
LPGAAVDLPAVSEDIQDLNFGVEQDVDMVFASFIRKASDVHEVREALGEKGKKTLHPPPSIFPHYCSTSGPVAIE
PTCISINNS

FIGURE 306

AGAAGAAGCTGGCCAAGGATATGGGAGCAACCACC<u>ATG</u>GACCAGAAGTCTCTCTGGGCAGGTGTAGTGGTCTTGC
TGCTTCTCCAGGGAGGATCTGCCTACAAACTGGTTTGCTACTTTACCAACTGGTCCCAGGACCGGCAGGAACCAG
GAAAATTCACCCCTGAGAATATTGACCCCTTCCTATGCTCTCATCTCATCTATTCATTCGCCAGCATCGAAAACA
ACAAGGTTATCATCAAGGACAAGAGTGAAGTGATGCTCTACCAGACCATCAACAGTCTCAAAACCAAGAATCCCA
AACTGAAAATTCTCTTGTCCATTGGAGGGTACCTGTTTGGTTCCAAAGGGTTCCACCCTATGGTGGATTCTTCTA
CATCACGCTTGGAATTCATTAACTCCATAATCCTGTTTCTGAGGAACCATAACTTTGATGGACTGGATGTAAGCT
GGATCTACCCAGATCAGAAAGAAAACACTCATTTCACTGTGCTGATTCATGAGTTAGCAGAAGCCTTTCAGAAGG
ACTTCACAAAATCCACCAAGGAAAGGCTTCTCTTGACTGCGGGCGTATCTGCAGGGAGGCAAATGATTGATAACA
GCTATCAAGTTGAGAAACTGGCAAAAGATCTGGATTTCATCAACCTCCTGTCCTTTGACTTCCATGGGTCTTGGG
AAAAGCCCCTTATCACTGGCCACAACAGCCCTCTGAGCAAGGGGTGGCAGGACAGAGGGCCAAGCTCCTACTACA
ATGTGGAATATGCTGTGGGGTACTGGATACATAAGGGAATGCCATCAGAGAAGGTGGTCATGGGCATCCCCACAT
ATGGGCACTCCTTCACACTGGCCTCTGCAGAAACCACCGTGGGGGCCCCTGCCTCTGGCCCTGGAGCTGCTGGAC
CCATCACAGAGTCTTCAGGCTTCCTGGCCTATTATGAGATCTGCCAGTTCCTGAAAGGAGCCAAGATCACGCGCC
TCCAGGATCAGCAGGTTCCCTACGCAGTCAAGGGGAACCAGTGGGTGGGCTATGATGATGTGAAGAGTATGGAGA
CCAAGGTTCAGTTCTTAAAGAATTTAAACCTGGGAGGAGCCATGATCTGGTCTATTGACATGGATGACTTCACTG
GCAAATCCTGCAACCAGGGCCCTTACCCTCTTGTCCAAGCAGTCAAGAGAAGCCTTGGCTCCTTG<u>TGA</u>AGGATTA
ACTTACAGAGAAGCAGGCAAGATGACCTTGCTGCCTGGGGCCTGCTCTCTCCCAGGAATTCTCATGTGGGATTCC
CCTTGCCAGGCTGGCCTTTGGATCTCTCTTCCAAGCCTTTCCTGACTTCCTCTTAGATCATAGATTGGACCTGGT
TTTGTTTTCCTGCAGCTGTTGACTTGTTGCCCTGAAGTACAATAAAAAAAATTCATTTTGCTCCAGTA

FIGURE 307

MDQKSLWAGVVVLLLLQGGSAYKLVCYFTNWSQDRQEPGKFTPENIDPFLCSHLIYSFASIENNKVIIKDKSEVM
LYQTINSLKTKNPKLKILLSIGGYLFGSKGFHPMVDSSTSRLEFINSIILFLRNHNFDGLDVSWIYPDQKENTHF
TVLIHELAEAFQKDFTKSTKERLLLTAGVSAGRQMIDNSYQVEKLAKDLDFINLLSFDFHGSWEKPLITGHNSPL
SKGWQDRGPSSYYNVEYAVGYWIHKGMPSEKVVMGIPTYGHSFTLASAETTVGAPASGPGAAGPITESSGFLAYY
EICQFLKGAKITRLQDQQVPYAVKGNQWVGYDDVKSMETKVQFLKNLNLGGAMIWSIDMDDFTGKSCNQGPYPLV
QAVKRSLGSL

FIGURE 308

GGGGAGACTTGTGAGCGGCCATCTTGGTCCTGCCCTGACAGATTCTCCTATCGGGGTCACAGGGACGCTAAGATT
GCTACCTGGACTTTCGTTGACC<u>ATG</u>CTGTCCCGGGTGGTACTTTCCGCCGCCGCCACAGCGGCCCCCTCTCTGAA
GAATGCAGCCTTCCTAGGTCCAGGGGTATTGCAGGCAACAAGGACCTTTCATACAGGGCAGCCACACCTTGTCCC
TGTACCACCTCTTCCTGAATACGGAGGAAAAGTTCGTTATGGACTGATCCCTGAGGAATTCTTCCAGTTTCTTTA
TCCTAAAACTGGTGTAACAGGACCCTATGTACTCGGAACTGGGCTTATCTTGTACGCTTTATCCAAAGAAATATA
TGTGATTAGCGCAGAGACCTTCACTGCCCTATCAGTACTAGGTGTAATGGTCTATGGAATTAAAAAATATGGTCC
CTTTGTTGCAGACTTTGCTGATAAACTCAATGAGCAAAAACTTGCCCAACTAGAAGAGGCGAAGCAGGCTTCCAT
CCAACACATCCAGAATGCAATTGATACGGAGAAGTCACAACAGGCACTGGTTCAGAAGCGCCATTACCTTTTTGA
TGTGCAAAGGAATAACATTGCTATGGCTTTGGAAGTTACTTACCGGGAACGACTGTATAGAGTATATAAGGAAGT
AAAGAATCGCCTGGACTATCATATATCTGTGCAGAACATGATGCGTCGAAAGGAACAAGAACACATGATAAATTG
GGTGGAGAAGCACGTGGTGCAAAGCATCTCCACACAGCAGGAAAAGGAGACAATTGCCAAGTGCATTGCGGACCT
AAAGCTGCTGGCAAAGAAGGCTCAAGCACAGCCAGTTATG<u>TAA</u>ATGTATCTATCCCAATTGAGACAGCTAGAAAC
AGTTGACTGACTAAATGGAAACTAGTCTATTTGACAAAGTCTTTCTGTGTTGGTGTCTACTGAAGTTATAGTTTA
CCCTTCCTAAAAATGAAAAGTTTGTTTCATATAGTGAGAGAACGAAATCTCTATCGGCCAGTCAGATGTTTCTCA
TCCTTCTTGCTCTGCCTTTGAGTTGTTCCGTGATCACTTCTGAATAAGCAGTTTGCCTTTATAAAAACTTGCTGC
CTGACTAAAGATTAACAGGTTATAGTTTAAATTTGTAATTAATTCTACCATCTTGCAATAAAGTGACAATTGAAT
AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 309

MLSRVVLSAAATAAPSLKNAAFLGPGVLQATRTFHTGQPHLVPVPPLPEYGGKVRYGLIPEEFFQFLYPKTGVTG
PYVLGTGLILYALSKEIYVISAETFTALSVLGVMVYGIKKYGPFVADFADKLNEQKLAQLEEAKQASIQHIQNAI
DTEKSQQALVQKRHYLFDVQRNNIAMALEVTYRERLYRVYKEVKNRLDYHISVQNMMRRKEQEHMINWVEKHVVQ
SISTQQEKETIAKCIADLKLLAKKAQAQPVM

FIGURE 310

GCGGGGAGCCGGCCCGGAGCGCAGTTTCCAGTGGGGCCGGGGTTTCACCCGGGCCCTCTCTGTTTGAACCGAACC
CGACAAATGGGCGC<u>ATG</u>ACGATGGAGAGCAGGGAAATGGACTGCTATCTCCGTCGCCTCAAACAGGAGCTGATGT
CCATGAAGGAGGTGGGTGATGGCTTACAGGATCAGATGAACTGCATGATGGGTGCACTGCAAGAACTGAAGCTCC
TCCAGGTGCAGACAGCACTGGAACAGCTGGAGATCTCTGGAGGGGGTCCTGTGCCAGGCAGCCCTGAAGGTCCCA
GGACCCAGTGCGAGCACCCTTGTTGGGAGGGTGGCAGAGGTCCTGCCAGGCCCACAGTCTGTTCCCCCTCCAGTC
AACCTTCTCTTGGCAGCAGCACCAAGTTTCCATCCCATAGGAGTGTCTGTGGAAGGGATTTAGCCCCCTTGCCCA
GGACACAGCCACATCAAAGCTGTGCTCAGCAGGGGCCAGAGCGAGTGGAACCGGATGACTGGACCTCCACGTTGA
TGTCCCGGGGCCGGAATCGACAGCCTCTGGTGTTAGGGGACAACGTTTTTGCAGACCTGGTGGGCAATTGGCTAG
ACTTGCCAGAACTGGAGAAGGGTGGGGAGAAGGGTGAGACTGGGGGGGCACGTGAACCCAAAGGAGAGAAAGGCC
AGCCCCAGGAGCTGGGCCGCAGGTTCGCCCTGACAGCAAACATCTTTAAGAAGTTCTTGCGTAGTGTGCGGCCTG
ACCGTGACCGGCTGCTGAAGGAGAAGCCAGGCTGGGTGACACCCATGGTCCCTGAGTCCCGAACCGGCCGCTCAC
AGAAGGTCAAGAAGCGGAGCCTTTCCAAGGGCTCTGGACATTTCCCCTTCCCAGGCACCGGGGAGCACAGGCGAG
GGGAGAATCCCCCCACAAGCTGCCCCAAGGCCCTGGAGCACTCACCCTCAGGATTTGATATTAACACAGCTGTTT
GGGTC<u>**TGA**</u>ATCCTAGAGACAGAAAGTTGACTGAGCCTGAAAGGGCCAGGTCCCAGTGCTGGGCCCCTGGGGAGGA
GGGAGGGTGGGCGGTATGGCTCTCGAAAGCCCAACTCCAAGTTCCTTTCCCCCAGAAAGCGGGGAGAAGCCAGAG
TTCTTGGCTCAGGACTGAAGGGAAGGTGGTTGGGAGAGGCTGTCTTGGGGGCTAGCTGGTGGAGGAGGTAAGAGT
AGCTGGAGAGTGAGCTGTGCGTGTGTGTGTGTGTGTGTGCATGTGTGTGTCTGTCTGGCATGCATGCACTCACTT
TGGGGCTGGAGGTGACAGTAGGTGAGGGCAGAGGAGGAGATCAGAAAATCCCTCTGACATCTCCACTGCCCCCAA
AGACCTCCGTTGAACATTCTGTATGGAAAAGAGCCCTGGAGCATCAGGTTCCCCAGATAGGCCCCCAAATAAAGA
CCTGTCTATGGCTCTCCCAA

FIGURE 311

MTMESREMDCYLRRLKQELMSMKEVGDGLQDQMNCMMGALQELKLLQVQTALEQLEISGGGPVPGSPEGPRTQCE
HPCWEGGRGPARPTVCSPSSQPSLGSSTKFPSHRSVCGRDLAPLPRTQPHQSCAQQGPERVEPDDWTSTLMSRGR
NRQPLVLGDNVFADLVGNWLDLPELEKGGEKGETGGAREPKGEKGQPQELGRRFALTANIFKKFLRSVRPDRDRL
LKEKPGWVTPMVPESRTGRSQKVKKRSLSKGSGHFPFPGTGEHRRGENPPTSCPKALEHSPSGFDINTAVWV

FIGURE 312A

GGCACGAGGCTGGGGCGCAGAGCAGCGGCGGGAGGAGGCGGACACGTGGCAACAGCGGTAGCAGCCCGGGCGGCG
GCAGCAACAGCGGCGGCGGCATCGGCCCGAGCCGCCGGCCGCCCTCCCACCCTCCCGCCCCGCGGCAGCCCTAGC
TCCCTCCACTTGGCTCCCCTGGTCCCGCTCGCTCGGCCGGGAGCTGCTCTGTGCTTTTCTCTCTGATTCTCCAGC
GACAGGACCCGGCGCCGGGCACTGAGCACCGCCACC**ATG**GGGAAGGGGGTTGGACGTGATAAGTATGAGCCTGCA
GCTGTTTCAGAACAAGGTGATAAAAAGGGCAAAAAGGGCAAAAAAGACAGGGACATGGATGAACTGAAGAAAGAA
GTTTCTATGGATGATCATAAACTTAGCCTTGATGAACTTCATCGTAAATATGGAACAGACTTGAGCCGGGGATTA
ACATCTGCTCGTGCAGCTGAGATCCTGGCGCGAGATGGTCCCAACGCCCTCACTCCCCCTCCCACTACTCCTGAA
TGGATCAAGTTTTGTCGGCAGCTCTTTGGGGGGTTCTCAATGTTACTGTGGATTGGAGCGATTCTTTGTTTCTTG
GCTTATAGCATCCAAGCTGCTACAGAAGAGGAACCTCAAAACGATAATCTGTACCTGGGTGTGGTGCTATCAGCC
GTTGTAATCATAACTGGTTGCTTCTCCTACTATCAAGAAGCTAAAAGTTCAAAGATCATGGAATCCTTCAAAAAC
ATGGTCCCTCAGCAAGCCCTTGTGATTCGAAATGGTGAGAAAATGAGCATAAATGCGGAGGAAGTTGTGGTTGGG
GATCTGGTGGAAGTAAAAGGAGGAGACCGAATTCCTGCTGACCTCAGAATCATATCTGCAAATGGCTGCAAGGTG
GATAACTCCTCGCTCACTGGTGAATCAGAACCCCAGACTAGGTCTCCAGATTTCACAAATGAAAACCCCCTGGAG
ACGAGGAACATTGCCTTCTTTTCAACCAATTGTGTTGAAGGCACCGCACGTGGTATTGTTGTCTACACTGGGGAT
CGCACTGTGATGGGAAGAATTGCCACACTTGCTTCTGGGCTGGAAGGAGGCCAGACCCCCATTGCTGCAGAAATT
GAACATTTTATCCACATCATCACGGGTGTGGCTGTGTTCCTGGGTGTGTCTTTCTTCATCCTTTCTCTCATCCTT
GAGTACACCTGGCTTGAGGCTGTCATCTTCCTCATCGGTATCATCGTAGCCAATGTGCCGGAAGGTTTGCTGGCC
ACTGTCACGGTCTGTCTGACACTTACTGCCAAACGCATGGCAAGGAAAAACTGCTTAGTGAAGAACTTAGAAGCT
GTGGAGACCTTGGGGTCCACATCCACCATCTGCTCTGATAAAACTGGAACTCTGACTCAGAACCGGATGACAGTG
GCCCACATGTGGTTTGACAATCAAATCCATGAAGCTGATACGACAGAGAATCAGAGTGGTGTCTCTTTTGACAAG
ACTTCAGCTACCTGGCTTGCTCTGTCCAGAATTGCAGGTCTTTGTAACAGGGCAGTGTTTCAGGCTAACCAGGAA
AACCTACCTATTCTTAAGCGGGCAGTTGCAGGAGATGCCTCTGAGTCAGCACTCTTAAAGTGCATAGAGCTGTGC
TGTGGTTCCGTGAAGGAGATGAGAGAAAGATACGCCAAAATCGTCGAGATACCCTTCAACTCCACCAACAAGTAC
CAGTTGTCTATTCATAAGAACCCCAACACATCAGAGCCCCAACACCTGTTGGTGATGAAGGGCGCCCCAGAAAGG
ATCCTAGACCGTTGCAGCTCTATCCTCCTCCACGGCAAGGAGCAGCCCCTGGATGAGGAGCTGAAAGACGCCTTT
CAGAACGCCTATTTGGAGCTGGGGGGCCTCGGAGAACGAGTCCTAGGTTTCTGCCACCTCTTTCTGCCAGATGAA
CAGTTTCCTGAAGGGTTCCAGTTTGACACTGACGATGTGAATTTCCCTATCGATAATCTGTGCTTTGTTGGGCTC
ATCTCCATGATTGACCCTCCACGGGCGGCCGTTCCTGATGCCGTGGGCAAATGTCGAAGTGCTGGAATTAAGGTC
ATCATGGTCACAGGAGACCATCCAATCACAGCTAAAGCTATTGCCAAAGGTGTGGGCATCATCTCAGAAGGCAAT
GAGACCGTGGAAGACATTGCTGCCCGCCTCAACATCCCAGTCAGCCAGGTGAACCCCAGGGATGCCAAGGCCTGC
GTAGTACACGGCAGTGATCTAAAGGACATGACCTCCGAGCAGCTGGATGACATTTTGAAGTACCACACTGAGATA
GTGTTTGCCAGGACCTCCCCTCAGCAGAAGCTCATCATTGTGGAAGGCTGCCAAAGACAGGGTGCTATCGTGGCT
GTGACTGGTGACGGTGTGAATGACTCTCCAGCTTTGAAGAAAGCAGACATTGGGGTTGCTATGGGGATTGCTGGC
TCAGATGTGTCCAAGCAAGCTGCTGACATGATTCTTCTGGATGACAACTTTGCCTCAATTGTGACTGGAGTAGAG
GAAGGTCGTCTGATCTTTGATAACTTGAAGAAATCCATTGCTTATACCTTAACCAGTAACATTCCCGAGATCACC
CCGTTCCTGATATTTATTATTGCAAACATTCCACTACCACTGGGGACTGTCACCATCCTCTGCATTGACTTGGGC
ACTGACATGGTTCCTGCCATCTCCCTGGCTTATGAGCAGGCTGAGAGTGACATCATGAAGAGACAGCCCAGAAAT
CCCAAAACAGACAAACTTGTGAATGAGCGGCTGATCAGCATGGCCTATGGGCAGATTGGAATGATCCAGGCCCTG
GGAGGCTTCTTTACTTACTTTGTGATTCTGGCTGAGAACGGCTTCCTCCCAATTCACCTGTTGGGCCTCCGAGTG
GACTGGGATGACCGCTGGATCAACGATGTGGAAGACAGCTACGGGCAGCAGTGGACCTATGAGCAGAGGAAAATC
GTGGAGTTCACCTGCCACACAGCCTTCTTCGTCAGTATCGTGGTGGTGCAGTGGGCCGACTTGGTCATCTGTAAG
ACCAGGAGGAATTCGGTCTTCCAGCAGGGGATGAAGAACAAGATCTTGATATTTGGCCTCTTTGAAGAGACAGCC
CTGGCTGCTTTCCTTTCCTACTGCCCTGGAATGGGTGTTGCTCTTAGGATGTATCCCCTCAAACCTACCTGGTGG
TTCTGTGCCTTCCCCTACTCTCTTCTCATCTTCGTATATGACGAAGTCAGAAAACTCATCATCAGGCGACGCCCT
GGCGGCTGGGTGGAGAAGGAAACCTACTAT**TAG**CCCCCCGTCCTGCACGCCGTGGAGCATCAGGCCACACACTCT
GCATCCGACACCCACCCCCTCTTTGTGTACTTCAGTCTTGGAGTTTGGAACTCTACCCTGGTAGGAAAGCACCGC
AGCATGTGGGGAAGCAAGACGTCCTGGAATGAAGCATGTAGCTCTATGGGGGGAGGGGGGAGGGCTGCCTGAAAA
CCATCCATCTGTGGAAATGACAGCGGGGAAGGTTTTTATGTGCCTTTTTGTTTTTGTAAAAAAGGAACACCCGGA

FIGURE 312B

AAGACTGAAAGAATACATTTTATATCTGGATTTTTACAAATAAAGATGGCTATTATAATGGAAAAAAAAAAAAAA
AAAAA

FIGURE 313

MGKGVGRDKYEPAAVSEQGDKKGKKGKKDRDMDELKKEVSMDDHKLSLDELHRKYGTDLSRGLTSARAAEILARD
GPNALTPPPTTPEWIKFCRQLFGGFSMLLWIGAILCFLAYSIQAATEEEPQNDNLYLGVVLSAVVIITGCFSYYQ
EAKSSKIMESFKNMVPQQALVIRNGEKMSINAEEVVVGDLVEVKGGDRIPADLRIISANGCKVDNSSLTGESEPQ
TRSPDFTNENPLETRNIAFFSTNCVEGTARGIVVYTGDRTVMGRIATLASGLEGGQTPIAAEIEHFIHIITGVAV
FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICS
DKTGTLTQNRMTVAHMWFDNQIHEADTTENQSGVSFDKTSATWLALSRIAGLCNRAVFQANQENLPILKRAVAGD
ASESALLKCIELCCGSVKEMRERYAKIVEIPFNSTNKYQLSIHKNPNTSEPQHLLVMKGAPERILDRCSSILLHG
KEQPLDEELKDAFQNAYLELGGLGERVLGFCHLFLPDEQFPEGFQFDTDDVNFPIDNLCFVGLISMIDPPRAAVP
DAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAARLNIPVSQVNPRDAKACVVHGSDLKDMTS
EQLDDILKYHTEIVFARTSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGIAGSDVSKQAADMIL
LDDNFASIVTGVEEGRLIFDNLKKSIAYTLTSNIPEITPFLIFIIANIPLPLGTVTILCIDLGTDMVPAISLAYE
QAESDIMKRQPRNPKTDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLPIHLLGLRVDWDDRWINDVED
SYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFEETALAAFLSYCPGMG
VALRMYPLKPTWWFCAFPYSLLIFVYDEVRKLIIRRRPGGWVEKETYY

FIGURE 314A

TTCCAAAACTGTTCTCTGGAGCTATAAGTGGATTGCCAGAAATGAGAGATTAGGAGCTGGGAGAAGAGGAAGCGC
CTTGTGTTGTGTCTCCTGGAGGCTGCCGACATGAAGTGCTTTTTCCCGGTGCTGAGCTGTCTGGCTGTGCTGGGT
GTGGTGTCAGCACAGCGGCAGGTCACCGTTCAGGAAGGACCCTTGTACCGCACGGAGGGCTCCCACATCACTATC
TGGTGCAATGTGAGTGGCTACCAGGGACCTTCTGAGCAGAATTTCCAGTGGTCCATTTACCTGCCTTCGTCGCCA
GAGCGAGAGGTGCAGATCGTCAGCACCATGGACTCTTCCTTCCCCTATGCCATCTACACCCAGCGCGTCCGCGGA
GGGAAGATCTTCATAGAAAGAGTCCAGGGGAACTCAACCCTATTGCACATCACAGATCTTCAGGCCCGGGATGCC
GGGGAGTATGAATGCCACACACCCAGCACTGATAAGCAATACTTTGGGAGTTACAGTGCAAAGATGAACCTAGTG
GTGATCCCAGACTCCCTGCAGACCACTGCCATGCCCCAGACTCTGCACAGAGTGGAGCAGGACCCGCTGGAGCTC
ACTTGTGAGGTGGCCTCAGAGACCATTCAGCACAGCCACCTGTCTGTGGCCTGGCTCCGGCAGAAAGTTGGCGAG
AAGCCCGTGGAGGTCATCTCCCTGAGCCGAGATTTCATGCTTCACTCCAGCAGCGAATATGCCCAGAGGCAGAGC
CTGGGGGAGGTGCGGCTGGACAAGCTGGGGAGGACCACCTTCCGCCTCACCATCTTCCACCTGCAGCCTTCTGAC
CAGGGCGAATTCTACTGCGAGGCCGCCGAGTGGATCCAGGATCCGGATGGGTCGTGGTATGCTATGACCCGAAAG
CGTTCCGAGGGAGCCGTGGTCAACGTCCAGCCAACTGACAAAGAATTCACTGTTCGGCTGGAGACAGAGAAGCGG
CTGCACACGGTGGGCGAGCCGGTGGAGTTCAGATGCATCCTGGAGGCTCAGAATGTTCCCGACCGTTACTTTGCT
GTCTCCTGGGCCTTCAACAGCTCGCTCATCGCCACCATGGGTCCTAACGCTGTGCCTGTCCTCAACAGCGAATTT
GCTCACCGGGAAGCCAGGGGACAGCTTAAGGTGGCCAAAGAGAGCGACAGTGTCTTTGTGCTGAAGATCTACCAC
CTCCGCCAGGAAGATAGCGGGAAATACAACTGCCGGGTGACTGAGCGAGAGAAAACCGTGACCGGGGAATTCATT
GATAAGGAGAGCAAGCGTCCCAAGAACATCCCCATCATAGTCCTCCCCCTCAAGAGCAGCATCTCCGTGGAGGTG
GCCAGCAATGCCAGCGTCATCCTTGAGGGCGAGGACCTGCGCTTCTCCTGCAGTGTCCGCACGGCAGGCAGGCCG
CAGGGTCGCTTCTCTGTCATCTGGCAGCTTGTGGACAGGCAGAACCGCCGCAGCAATATCATGTGGCTAGACCGG
GATGGCACCGTGCAGCCAGGCTCGTCCTACTGGGAGCGCAGCAGCTTTGGGGGCGTCCAGATGGAGCAGGTGCAG
CCCAACTCGTTCAGCCTGGGCATCTTCAACAGCAGGAAGGAGGACGAGGGCCAGTATGAATGCCATGTGACTGAA
TGGGTGCGGGCAGTGGATGGCGAGTGGCAGATTGTTGGGGAGCGCCGGGCCAGCACTCCCATCTCCATCACAGCT
CTTGAAATGGGCTTCGCAGTCACAGCCATCTCCCGGACACCGGGGGTGACCTACAGCGACTCCTTTGACTTGCAG
TGTATCATCAAACCCCACTACCCTGCCTGGGTCCCCGTGTCGGTGACATGGCGGTTCCAGCCGGTGGGCACGGTG
GAGTTCCATGACTTGGTGACCTTCACCCGGGACGGAGGGGTCCAGTGGGGGGACAGGTCCTCCAGCTTCCGAACC
CGAACTGCCATCGAGAAGGCTGAGTCCAGCAACAACGTCCGCCTAAGCATCAGCCGAGCCAGTGACACGGAAGCA
GGCAAGTACCAGTGTGTGGCAGAGCTGTGGCGGAAGAACTACAACAACACCTGGACGCGACTGGCGGAGAGGACC
TCCAACCTGCTGGAGATCAGGGTGCTGCAGCCAGTGACAAAGCTGCAGGTGAGCAAATCGAAGAGGACCCTCACC
CTGGTGGAAAACAAGCCCATTCAGTTGAACTGCTCAGTCAAGTCTCAGACTAGCCAGAACTCCCACTTTGCGGTG
CTCTGGTATGTCCACAAGCCCTCGGATGCCGATGGCAAGCTTATCCTGAAGACCACCCACAACTCCGCCTTTGAA
TACGGTACTTACGCCGAGGAGGAGGGCCTGAGAGCCAGGCTCCAGTTTGAGAGGCATGTGTCGGGGGGCCTGTTC
AGCCTCACCGTCCAGAGAGCCGAGGTCAGCGACAGCGGCAGCTACTACTGCCACGTGGAGGAGTGGCTGCTGAGC
CCCAACTACGCCTGGTACAAGCTGGCAGAGGAGGTTTCTGGGCGCACAGAAGTCACTGTGAAACAGCCAGACAGC
CGCCTGAGGCTCAGCCAAGCCCAGGGGAACCTGTCGGTTCTGGAGACCCGGCAGGTACAGCTGGAGTGTGTGGTT
CTCAACCGCACCAGCATAACCTCCCAGCTCATGGTGGAATGGTTTGTATGGAAGCCCAACCACCCTGAGCGGGAG
ACTGTGGCCCGCTTGAGCCGTGACGCCACCTTCCACTATGGAGAGCAGGCAGCCAAGAACAATCTGAAGGGGCGG
CTGCATTTGGAGAGTCCTTCCCCCGGCGTGTACCGTCTCTTCATCCAGAACGTGGCTGTGCAGGACAGCGGGACC
TACAGCTGCCATGTGGAGGAGTGGCTGCCCAGCCCCAGTGGCATGTGGTATAAGCGGGCAGAGGACACCGCTGGG
CAGACAGCTCTGACAGTCATGCGACCAGATGCTTCCCTGCAGGTGGACACAGTGGTCCCCAATGCCACGGTCTCT
GAGAAGGCAGCTTTCCAGCTGGACTGTAGCATCGTGTCCCGCTCCAGCCAGGACTCCCGCTTCGCTGTGGCCTGG
TATTCCCTGAGGACTAAAGCTGGGGGGAAAAGGAGCAGCCCTGGCCTGGAAGAACAGGAAGAGGAAAGGGAGGAG
GAGGAGGAGGAGGACGACGACGACGACGACGACCCAACAGAGCGGACGGCCCTGCTGAGCGTGGGCCCAGATGCT
GTCTTTGGCCCAGAGGGCAGTCCTTGGGAGGGCAGGCTTCGCTTCCAGAGGCTCTCCCCGGTGCTCTACCGGCTC
ACAGTGCTGCAGGCAAGCCCCCAAGATACAGGCAATTACTCCTGCCATGTGGAGGAGTGGCTGCCCAGCCCTCAG
AAGGAATGGTACCGGCTGACGGAGGAGGAGTCAGCCCCCATCGGCATCCGTGTTCTAGATACAAGTCCCACCCTC
CAGTCCATCATCTGCTCCAACGACGCACTCTTCTACTTCGTCTTCTTCTACCCTTTCCCCATCTTTGGCATTCTT
ATCATCACCATCCTTCTGGTGCGTTTCAAGAGCCGGAACTCCAGCAAGAACTCTGATGGGAAGAATGGGGTGCCT

FIGURE 314B

CTGCTGTGGATCAAAGAGCCACACCTCAACTACTCCCCTACTTGCCTGGAGCCCCCTGTTCTCAGTATCCATCCA
GGGGCCATAGACTAAGCGGGTGATGCCCCAGCGGATGTTGGCCACGGAGGAGCTGAGGCTCTCCCTTTCTCTGTG
ATTGGACAGTTGACAGCACCCAAACTCTGGGGTGCATGTGTGTGGAAAGTTGTCAGACTTGAAAAGTGTTCCAAG
TTCCCAGTCAGTCACAGAGACAGACTGCCTCTCGGTGGCAGTCTTGGTTGGTTAGCTATTTGCGCGCAAATGTTG
TGATCCTGCCATTATAGATTTCTTGTTTCTGTTTTTAGTAATGTAGTGAGTAGCTCCAGGTGCCACATCTACTCA
CAGATTTATCTAGTATTCTCAGATAGATGTTACAGGGCTTCTTATTCTTTGTAATGTACTCTTTTTAAATCCCTT
TAGTTTACCCTTTTTGGATTCCTTAATGTGGACGAATTTCTCTTACGTACAACTGACAGCAAAAGGAAGGGCGAA
CTTTCTAGTGACAAGGAATCTCTTCCAAGACTTTGTTTTTGCACATTTGAAAATGCCACCCATGGATCAAAATAT
ACCCAAACGTTTTTTACTTTCTTAACAAGACTTAAGAATTGTGTGTAGTGTGGGCAAAATTTGTATGTTGTCTTT
TCCCTCAGCTGGAGTTATTGGAACCACTTTGTAGTCAAGACGAAAGCACTGAATTTTGCTTCAAAGAACTGTGTA
TGTACAAGAGAAATCCTGCATAACCCCATTAGGAGTAGATGGTGCCCGGCCTATCTGTCAGGGAGGCAAAAAAGG
CTTCATCCCATCCTTGCCAAAAAATAAGAAAACTGTCTTGGAGAATGGGTCAGAAGCCCCAAACGGCACACACTT
TCCAAATTAAAGTGGGCAGGGGCTGCTTTTAGCAGCTGCTGACCTGCAGATTTGTCAAAGCCAGTGACTAGAGAA
GGAAGGGAGAAAGGCTGGCTGTTGGCTTGCTCTGAGCTGCAAGGATGGTCTCTAACTGATTAACTGTGAGCAGGT
GGGCCTGTGTCTTCAGGTGCTTTGCCAAACTCTTAAAAGAAAGTGTCCAGTGAACTTGGAAGTGGGCCCCCTGAGC
TGAGCACAGGGCCAAAGCAGCCATGGCAGACACCTGACGGAGGGCACGGGGCTGGCTGACACTAAGTTTGGTGGG
ACAGTGAGGGGTGGGAGGGGGGTTTCCAGGGCCTGGTGTTGGAGAGTGCAGAGAAATATCTACCTCCCTGGAGGT
GTGAAGACTAGGTTTTTCTTCTTCCTTCCAATTAGATTTTCCTTAATTATAGTGATGTCTTCCTTATTCATTTTT
CTCTCCCTGCCTCTCACTGCCATAAGAATATCAGCCTGGGGGCAGTCCAGACGCAGCCCTTTGTCATCCTTTCTG
TTTGCCTAGTCTCAGCAGACTGTGATCACAAGGCATTGTCTGTGGGATTTTTCCTTTCCCTTTCTTGATCTCTCT
TGTGGTTCTAGGTTGTTTGGTTGTTCATTGTTATGGTGGCTTTTTATTTTAACGCCCCTTGAGCCCCATGATGGC
TGGTGTCACCCTGTTCTTTTACACTGTTGGGCCAGGTGCTGCTTGTCCTTCTTAGGGCATCATCAATTGCAAATA
TTTCCTTTTGCTCCCTTTATGAAGATGTTCTTATACCCTTGCTTTCCCATATTTTTCTGGCCAAGCATGCCATCT
CCTTTACTCTGGGAACTTACATCCTGAATCCCAAGAGGGGGTCACAGTTTGGAAAAAGTCATCAGGGATTCTGGA
ACTAAGTCTGATAAAAGATTCCAGTGAAGCCCTGTTCTGAGAACGAGCAGACTGCAGGGGAGGCCATGGGATTCC
CCAGGCCAGTGTCTGTGCTGATCCTTCAAGGGTCTGCAGGTATGCAGGTGGCCTGGGCTGCTCGGCAGATACTTT
GCTGATTCCCAGCTGAGGGGAGCATGGTGGCGATTGCTCAGCCATTTTCTGACAGACACACAGACCTGCCTTTTC
TCCCCCAAGTATACCGTACCCTCCTGTGAGACAGTGTGTGCAGGCACCACCACCTTAATCCTGCTGTTGCCTGAC
ATGCTGATTCTCATTTATTATGCTGCATCAACACATTAGAGGTACAGGAGCGGCTCAGTCATGAAAAAAGAAGGT
CTTTTGCCCCATTTCTTTATTTCAGAGATGTGGGCTTTCAGTGGGAATTTGCTGACTCCTACTTTATAGGCTGAG
TCAATGAGGGAAGATGACTGGCGTTTCCTCTGTCTAAATGGGAGGTTGCCAGAGCGCTGGCTGGGACTAGGATGT
GTAACTAAGATTTCAGTTTGAAATCTTAGATTTCAGTTCACGGCGATAAAGAAGTAGGTGCTGCACACAAATATG
TAAAGCAATTGTAGGAAATTTGAAAGGAAAAAAAGAAACCGAAGCCAGTATTTTAATAATTGCTTTTTCTGTGTA
TTTTGTATTGGGCTGGGGGATAGCATCAAAGGTTGAACTTTTTGAGCTTTCTATGAAAAACCCCAGGACCTTCTT
TCTTTGGCCATTTCTATGGAAATGCGATGTCAGATGGATGGTAATGGTGCCCTCCAGTGGCTGTGAGACCTCATT
GCGCATTGTCTACTGGAGCTTTAGTCTTCTGAGACGGAGGAAAACTGCTGAATACTCTGGATTCATCTATGTCTA
CAATGTTGCATTTATGAAAAACTACACTGTGCTAGGCGCATTCTAGGACATGAATATGACCACACCCTCTTTCAC
CGGGTGTTTCTGTAGCAAGTTTTCATATTCTTTTCAAACAATGGTTTCTCTGCGTTAATTATTGAGGAAAAAAAA
AGATGGGGTAAGAAAACTACCCATGCATGATGTAGAGAGCTGTTGATTTGTTTCTGTTTTTTTAAAGGAAAACTA
TTTGTAAGATGTTGCACTAAAACATTTTATATACACTTCAGAGACCTGTAGTAAATTATGTTGAAAAT

FIGURE 315A

GCTCTTTGCCGAGGGCGTGTGGTGAGAGTCCCCACAGCGACCCTGGTTCGAGTGGTGGGCACTGAGCTGGTCATC
CCCTGCAACGTCAGTGACTATGATGGCCCCAGCGAGCAAAACTTTGACTGGAGCTTCTCATCTTTGGGGAGCAGC
TTTGTGGAGCTTGCAAGCACCTGGGAGGTGGGGTTCCCAGCCCAGCTGTACCAGGAGCGGCTGCAGAGGGGCGAG
ATCCTGTTAAGGCGGACTGCCAACGACGCCGTGGAGCTCCACATAAAGAACGTCCAGCCTTCAGACCAAGGCCAC
TACAAATGTTCAACCCCCAGCACAGATGCCACTGTCCAGGGAAACTATGAGGACACAGTGCAGGTTAAAGTGCTG
GCCGACTCCCTGCACGTGGGCCCCAGCGCGCGGCCCCCGCCGAGCCTGAGCCTGCGGGAGGGGGAGCCCTTCGAG
CTGCGCTGCACCGCCGCCTCCGCCTCGCCGCTGCACACGCACCTGGCGCTGCTGTGGGAGGTGCACCGCGGCCCG
GCCAGGCGGAGCGTCCTCGCCCTGACCCACGAGGGCAGGTTCCACCCGGGCCTGGGGTACGAGCAGCGCTACCAC
AGTGGGGACGTGCGCCTCGACACCGTGGGCAGCGACGCCTACCGCCTCTCAGTGTCCCGGGCTCTGTCTGCCGAC
CAGGGCTCCTACAGGTGTATCGTCAGCGAGTGGATCGCCGAGCAGGGCAACTGGCAGGAAATCCAAGAAAAGGCC
GTGGAAGTTGCCACCGTGGTGATCCAGCCATCAGTTCTGCGAGCAGCTGTGCCCAAGAATGTGTCTGTGGCTGAA
GGAAAGGAACTGGACCTGACCTGTAACATCACAACAGACCGAGCCGATGACGTCCGGCCCGAGGTGACGTGGTCC
TTCAGCAGG**ATG**CCTGACAGCACCCTACCTGGCTCCCGCGTGTTGGCGCGGCTTGACCGTGATTCCCTGGTGCAC
AGCTCGCCTCATGTTGCTTTGAGTCATGTGGATGCACGCTCCTACCATTTACTGGTTCGGGATGTTAGCAAAGAA
AACTCTGGCTACTATTACTGCCACGTGTCCCTGTGGGCACCCGGACACAACAGGAGCTGGCACAAAGTGGCAGAG
GCCGTGTCTTCCCCAGCTGGTGTGGGTGTGACCTGGCTAGAACCAGACTACCAGGTGTACCTGAATGCTTCCAAG
GTCCCCGGGTTTGCGGATGACCCCACAGAGCTGGCATGCCGGGTGGTGGACACGAAGAGTGGGGAGGCGAATGTC
CGATTCACGGTTTCGTGGTACTACAGGATGAACCGGCGCAGCGACAATGTGGTGACCAGCGAGCTGCTTGCAGTC
ATGGACGGGGACTGGACGCTAAAATATGGAGAGAGGAGCAAGCAGCGGGCCCAGGATGGAGACTTTATTTTTTCT
AAGGAACATACAGACACGTTCAATTTCCGGATCCAAAGGACTACAGAGGAAGACAGAGGCAATTATTACTGTGTT
GTGTCTGCCTGGACCAAACAGCGGAACAACAGCTGGGTGAAAAGCAAGGATGTCTTCTCCAAGCCTGTTAACATA
TTTTGGGCATTAGAAGATTCCGTGCTTGTGGTGAAGGCGAGGCAGCCAAAGCCTTTCTTTGCTGCCGGAAATACA
TTTGAGATGACTTGCAAAGTATCTTCCAAGAATATTAAGTCGCCACGCTACTCTGTTCTCATCATGGCTGAGAAG
CCTGTCGGCGACCTCTCCAGTCCCAATGAAACGAAGTACATCATCTCTCTGGACCAGGATTCTGTGGTGAAGCTG
GAGAATTGGACAGATGCATCACGGGTGGATGGCGTTGTTTTAGAAAAAGTGCAGGAGGATGAGTTCCGCTATCGA
ATGTACCAGACTCAGGTCTCAGACGCAGGGCTGTACCGCTGCATGGTGACAGCCTGGTCTCCTGTCAGGGGCAGC
CTTTGGCGAGAAGCAGCAACCAGTCTCTCCAATCCTATTGAGATAGACTTCCAAACCTCAGGTCCTATATTTAAT
GCTTCTGTGCATTCAGACACACCATCAGTAATTCGGGGAGATCTGATCAAATTGTTCTGTATCATCACTGTCGAG
GGAGCAGCACTGGATCCAGATGACATGGCCTTTGATGTGTCCTGGTTTGCGGTGCACTCTTTTGGCCTGGACAAG
GCTCCTGTGCTCCTGTCTTCCCTGGATCGGAAGGGCATCGTGACCACCTCCCGGAGGGACTGGAAGAGCGACCTC
AGCCTGGAGCGCGTGAGTGTGCTGGAATTCTTGCTGCAAGTGCATGGCTCCGAGGACCAGGACTTTGGCAACTAC
TACTGTTCCGTGACTCCATGGGTGAAGTCACCAACAGGTTCCTGGCAGAAGGAGGCAGAGATCCACTCCAAGCCC
GTTTTTATAACTGTGAAGATGGATGTGCTGAACGCCTTCAAGTATCCCTTGCTGATCGGCGTCGGTCTGTCCACG
GTCATCGGGCTCCTGTCCTGTCTCATCGGGTACTGCAGCTCCCACTGGTGTTGTAAGAAGGAGGTTCAGGAGACA
CGGCGCGAGCGCCGCAGGCTCATGTCGATGGAGATGGAC**TAG**GCTGGCCCGGGAGGGGAGTGACAGAGGGACGTT
CTAGGAGCAATTGGGGCAAGAAGAGGACAGTGATATTTTAAAACAAAGTGTGTTACACTAAAAACCAGTCCTCTC
TAATCTCAGGTGGGACTTGGCGCTCTCTCTTTTCTGCATGTCAAGTTCTGAGCGCGGACATGTTTACCAGCACAC
GGCTCTTCTTCCCACGGCACTTTCTGATGTAACAATCGAGTGTGTGTTTTCCCAACTGCAGCTTTTTAATGGTTA
ACCTTCATCTAATTTTTTTTCTCCCACTGGTTTATAGATCCTCTGACTTGTGTGTGTTTATAGCTTTTGTTTCGC
GGGGTTGTGGTGAGGAAGGGGTGATGGCATGCGGAGTTCTTTATCTTCAGTGAGAATGTGCCTGCCCGCCTGAGA
GCCAGCTTCCGCGTTGGAGGCACGTGTTCAGAGAGCTGCTGAGCGCCACCCTCTACCCGGCTGACAGACAACACA
GACCTGTGCCGAAGGCTAATTTGTGGCTTTTACGACCCTACCCCACCCCCTGTTTTCAGGGGTTTAGACTACATT
TGAAATCCAAACTTGGAGTATATAACTTCTTATTGAGCCCAACTGCTTTTTTTTTTTTTTTTTTGCTTCTCTGC
CCCTTTTCCATTTCTTTTGTATTTGTTTTCTGTGAGAGCACTGAAATGGCAGCCCTGGAATCTACAATTTGGCTC
TCCACTGAGCACCTTATCTTGCCACCTTAGCCTTAAGAATGAATATGAAGAAAAATACACAGCCACCTCTGTCCA
GGGCAGTAAGAAGGGCTGCAAGGAAGGGGAGGATGGGGACAAGGAAAGGATCAGATACCTGCTCCAGTAGTTGTG
AGGCCACTGTGTCTCAGGGGACTCCAGGAGGAGCAGAAGAGGGATCCCACGAAGTTATTCTTACGCAGCTGGGGC
CAGGAGGGTCAGAGTGGTGCCAGGTGCAAGTTAGGCTAAAGAAGCCACCACTATTCCTCTCTCTTGCCCATTGTG

FIGURE 315B

GGGGGCAAAGGCATTGGTCACCAAGAGTCTTGCAGGGGGACCCACAGATATGCCATGTCCTTCACACGTGCTTGG
GCTCCTTAACCTGAAGGCAAATTGCTACTTGCAAGACTGACTGACTTCAAGGAATCAGAAATTACCTAGAAGCAC
CATGTTTTTTCTATGACCTTTTCAGTCCTTCAGGTCATTTTAAGGTCCACTGCAGGGGGTTAGTGAGAAAGGGTA
TACTTTGTGGTATGTTTTGCTTTCCTAATAGGGACATGAAGGAAACCCAGCAATTTGCTGTTATGTGAATGGCCT
GTAGAGCAGAGTCAAGAGCGGTGTGCTTTGCCCGACTGCTCCCATCAGGAATAGGAGAGTAGACAGAGATCTTCC
ACATCCCAGGCTTCTGCTGCTGCTTTAAAAGCTCTGTCCTTGGAGCCTCCCGCTCCCTGAAGTGTCTCGCCCCCT
GCACAGCACTGGCCTTTCGGAAGCATCCCAGTAGGGTTTTCTGAGGCTCGCTGGTGACTCATGCCCTAATTGCAA
TCCTCTGCTTTTATCTTGACTTTGAAGGATCTAACACTGCTCTCTCTTCCAAAGGGGAAAAAAAGATTCATTTGT
TTTGAGCAATAAACTAATACAAAATGATGGCCATTCATGTGCAGCTCTTTGTCACCATGGGCCGGATGAGTTGTG
CTCCTCCTGGCTCACCATTTCCCCCTGCTCCCCCACAGCCGGTTCTGCACTTATCACCGAGTCGCCCCTGGAAGC
AGATTCCCATTGAGTTTTCCCCACCAAGGGGACCATGCACATGGTAGAAACATTAGATTCTGCATTGACAGTAGC
CTTTCCTTGGCCCGGGCCTGTGGTGGGAAGACGGGCAACAAGTATACCCCACCAGGGCCTGAGTGACTAGAGGAA
GAGGACGAGGCCTTGTTGGCACTAGATTTGGGTATTTTCTGCATGTCATAACATATCCTAACTGCTATTTCAGAA
GAGGCAGCTTGTAGGTGATTGTACAAGTGAGAATTAAAGAGAGAACAGATATTTAAACAGGTGCTGTATTAGTAA
CAGCCAGTGCCCTTTCAGCCCTTGCATCTATTAAAAGGAGATTCAGGATTTTATTGGCACAGGCCCTTCTTAGTA
GGAAGAAAGGGTGCTTAGCTTTGGACCTGACCGGGTGTGTGTAAAACCATGGACTGAGTCACAGCAGACACTCGA
TGGTGGTAAATGTGATGGGTGCTTACACACTGTACCTTTTCCTTTCATACTGATGCTGCAGTTCAGGGCTGGAGT
TGTTAAGGCATTGACCTCCACCCACCTGCCCCATGTCCACTGGGCTGCCCAAGCTGCATGTCACCTGAGGGCTGG
CAGGAAGGGGCGAGAAATCCCAGGGCATTGTACCAAGGACCTAGTTCCTTCTAGGGATATAAATTTCCAGGAATG
TGTATTTTTAATGTGGTGAGATGCACTCTTTTGTTGTACCAAATAGGGCTCCCCACCCCACCCCTGCGACAAGTG
CTCTTCTAGAACAGGTTCCTACCAGCAGCACTGGTGTGAATGAAAGAGAGACCCAGCCGCGTCTCACACAGGTGG
AATTGCACTTCTTAACAAAAAGGAACTTTATAAAAGTTTGGGATTTTTTTTCCTAATCATAAAAATAGCCCCAGA
AAGAGCCTAAGCTATGTTCAGATAGAAGCCTCGAAATTCCTGTAAATTGTTTACTTTATGATGTTTACATACACG
TTTCACTTTGAAAAAAAATGCAAATCGACTTTTTAACAACTGTTGAGATGTTTCATGGGACAGTAGAACTCTGAC
TCACCAACTGGGCTAAATTTTAATTTAAAAATGTATTTATTTGAGTGTCTTTCCCCCCCTCACCCTCACCATCTG
AGGGGCTCCCTGAGATCTTGGTAGAGGAGGCCCCTCCTGCCCAGACCTTCGTTTGTTTCCCCGGTGGCCCTTGCT
TCTTGCTTTGCAGACTGCCTGCAGCCATGATTTTGTCACTGACATCTGTGAGCCAAAGACTGAGCCTTTTTGGCA
GGAATAATAAGCAATACTACACAACTTGCTACTTTCAGAAAACTTTTTTTTAGCTTCACCGATGACAACAGAGGA
AGAAGGGAACTGGGATTTGGGTAAGTTCTCCTCCACTGTTTGACCAAATTCTCAGTGATAAATATGTGTGCAGAT
CCCTAGAAGAGAAAACGCTGACTTTCTTTTTAAGTGTGGCACATAAGGATCTGCAGAATTTTCCGTAGACAAAGA
AAGGATCTTGTGTATTTTTGTCCATATCCAATGTTATATGAACTAATTGTATTGTTTTATACTGTGACCACAAAT
ATTATGCAATGCACCATTTGTTTTTTATTTCATTAAAGGAAGTTTAATTT

FIGURE 316

MPDSTLPGSRVLARLDRDSLVHSSPHVALSHVDARSYHLLVRDVSKENSGYYYCHVSLWAPGHNRSWHKVAEAVS
SPAGVGVTWLEPDYQVYLNASKVPGFADDPTELACRVVDTKSGEANVRFTVSWYYRMNRRSDNVVTSELLAVMDG
DWTLKYGERSKQRAQDGDFIFSKEHTDTFNFRIQRTTEEDRGNYYCVVSAWTKQRNNSWVKSKDVFSKPVNIFWA
LEDSVLVVKARQPKPFFAAGNTFEMTCKVSSKNIKSPRYSVLIMAEKPVGDLSSPNETKYIISLDQDSVVKLENW
TDASRVDGVVLEKVQEDEFRYRMYQTQVSDAGLYRCMVTAWSPVRGSLWREAATSLSNPIEIDFQTSGPIFNASV
HSDTPSVIRGDLIKLFCIITVEGAALDPDDMAFDVSWFAVHSFGLDKAPVLLSSLDRKGIVTTSRRDWKSDLSLE
RVSVLEFLLQVHGSEDQDFGNYYCSVTPWVKSPTGSWQKEAEIHSKPVFITVKMDVLNAFKYPLLIGVGLSTVIG
LLSCLIGYCSSHWCCKKEVQETRRERRRLMSMEMD

FIGURE 317

GTCCATTTTGTCGGTAGAGGCAGAAGGAGAAGGTCGGATTGTAGAAGCTGGGGTGGCCGGCAGCTCGCTCATCGG
TGTTCGTGGGCTTTGTCGGTCCGTGCCTCGTCTCTCCCTGGAAAGGGAGGGAGGCTTCAACGTCGAGAGGGAGCC
GCTGCCGCGTTAGTTCCGAGCTTGAAGTCACTAGGACTTCTCTCAAACTTGAGTGCTGAGGAGACTCAGATGTTG
GCCTCAGCTCCTAGGCTGAACTCAGCAGATCGGCCCATGAAAACTTCTGTATTGAGACAAAGGAAGGGATCTGTC
AGAAAGCAACACTTGTTATCTTGGGCTTGGCAGCAAGGAAGAGGACAGGTAGTGGAGATCCTGCAATCTGAAAAG
CAGACTGAAAGGTGACAAAGAAGCTGAAGATGGGTGGTAGAGAGAGGTATAACATTCCAGCCCCTCAATCTAGAA
ATGTTAGTAAGAACCAACAACAGCTTAACAGACAGAAGACCAAGGAACAGAATTCCCAGATGAAGATTGTTCATA
AGAAAAAAGAAAGAGGACATGGTTATAACTCATCAGCAGGTGCCTGGCAGGCCATGAAAAATGGGGGGAAGAACA
AAAATTTTCCAAATAATCAAAGTTGGAATTCTAGCTTATCAGGTCCCAGCTTACTTTTTAAATCTCAAGCTAAAC
AGAACTATGCTGGTGCCAAATTTAGTGAGCCGCCATCACCAAGTGTTCTTCCCAAACCACCAAGCCACTGGGTCC
CTGTTTCCTTTAATCCTTCAGATAAGGAAATAATGACATTTCAACTTAAAACCTTACTTAAAGTACAGGTATAAA
ATAAGACAAATGTTTAAGTTTAGTTATGTTCACAGATAGTTGTCAATTGGTCTGAAACAAATTTGCTAGGGAATC
TATTTGTGTAGAACTAATTAATGTAAAAAAAATAGACTTCATCTCGTGTTGTGTGCACTGTGATATAATGGTAGT
ATCAGTGCAACTTAAACTAATGATTGTAATTGATATTAAGTGTTCTCAACTGAGTAACTTTTAAGTGGAAACCAA
GTTTAGATTTGGGGAGTGGTAAAGGAATCAGCTTTTTCTATTGTTAGGGGAAGATAGTAATTTATCATTCATGGA
CCAGTAGATTGTTGAAAGTTGGTGAATCGGATTATAAGCTTCTGGCTAACACAAGGATTCAGAATTAGGTAAACA
TCTGAAGGTTTAGTATATTAGAAACACCCAAACCAGTAATATGCTAACCTGATGCACTGCTGAAAGAAAATGTGA
ATTTTTCGTAATAATTGCATTTTAGTGAATTGTACAGTGGGTGGAAAGGGCATTTGGAGCTCATTAGAATGAGAC
ATAGTACACCCCAATGGCCCTGTTTATTAAATGTAGTGGATTAAGTGTCTGTCAACAAATACACCAAAACCATTT
TTTATAGAAACAGTATTTAATGGTCACTCAATAGCTTTCAAAATACATTTTTGTATTACAGCACTGCACAAGCTA
TTCTAATAGTGATCTGGCCTCCTCATTCCTGCCAAGCTTGCTTTGGGGAGTTGGATAATGTGAAAATTTTAAGTA
CCTAGGGGAGAAAGAGCCATGTAAATATCTGTAATAAACTTGTAGCATATGTAAAGTTTTCTTGGCCTTTATCTT
ACAAAAATGGAATATTTTAGTATGAATTTGCTGAATGTAAGACCGTGGACTGTTTTTTATAATATGGCCTAATTT
TAAAGGTCCAAAATAACTTGTTTTTAAAGTTTGCCCTTGTGCTAAAGTGCCAGTGTATGTATGTTATACTTGATT
TGGTTGTAAACTATATTTCAAAGTAAACCCTAGTGTAATAAGTTTTATAACTAAAAAGGTTTAAGCTGCTAAAAC
TATTTTTAAGAGATGTGAAATGCAGTATGGGACTATCTTTTTTTCCTCCTCTAAGCCCAAAGATTAACTAGAGTC
CCTCCAACCTTATAGATTTTTGGCTTTCACAATCTTATAACCTAGGATACAGGTAGTTTCGAGTATGGTGCCAGT
GATGTTTTGTTTTTGTTTGGTCAAGGGGTAGGTGCAACCCAATGGACCACTTATGCAAAAGATGTAAACTCTTGC
ATAATACATCGATAACATGTTTTGCCAACTTTAAATGCTTAAACATAAGCGAAACCAGTAGCAAGTATGTGGGTC
AGTTTAAAAATTTTGATTGTTAATGCCCTATTTTCTAATTTGGCACCTCTTTTGATGCCTAAGCAGGTAAGCAGA
TGCCTAAGCTGTATTTCTCCAAATAAATCAAGAGGAAGTACTGCCCAAGTTAAATATTGATAGCCTAAAGACAAA
TTCATGTAGTACTTAATGTACATGATATGAATTTGAAGCATAAAATTAAATTTTTCCCCATTG

FIGURE 318A

TTTCAGCCAAACTTCGGGCGGCGGCTGAGGCGGCGGCCGAGGAGCGGCGGACTCGGGGCGCGGGGAGTCGAGGCA
TTTGCGCCTGGGCTTCGGAGCGTAGCGCCAGGGCCTGAGCCTTTGAAGCAGGAGGAGGGGAGGAGAGAGTGGGGC
TCCTCTATCGGGACCCCCTCCCCATGTGGATCTGCCCAGGCGGCGGCGGCGGCGGCGGAGGAGGAGGCGACCGAG
AAGATGCCCGCCCTGCGCCCCGCTCTGCTGTGGGCGCTGCTGGCGCTCTGGCTGTGCTGCGCGGCCCCCGCGCAT
GCATTGCAGTGTCGAGATGGCTATGAACCCTGTGTAAATGAAGGAATGTGTGTTACCTACCACAATGGCACAGGA
TACTGCAAATGTCCAGAAGGCTTCTTGGGGGAATATTGTCAACATCGAGACCCCTGTGAGAAGAACCGCTGCCAG
AATGGTGGGACTTGTGTGGCCCAGGCCATGCTGGGGAAAGCCACGTGCCGATGTGCCTCAGGGTTTACAGGAGAG
GACTGCCAGTACTCAACATCTCATCCATGCTTTGTGTCTCGACCCTGCCTGAATGGCGGCACATGCCATATGCTC
AGCCGGGATACCTATGAGTGCACCTGTCAAGTCGGGTTTACAGGTAAGGAGTGCCAATGGACGGATGCCTGCCTG
TCTCATCCCTGTGCAAATGGAAGTACCTGTACCACTGTGGCCAACCAGTTCTCCTGCAAATGCCTCACAGGCTTC
ACAGGGCAGAAATGTGAGACTGATGTCAATGAGTGTGACATTCCAGGACACTGCCAGCATGGTGGCACCTGCCTC
AACCTGCCTGGTTCCTACCAGTGCCAGTGCCCTCAGGGCTTCACAGGCCAGTACTGTGACAGCCTGTATGTGCCC
TGTGCACCCTCACCTTGTGTCAATGGAGGCACCTGTCGGCAGACTGGTGACTTCACTTTTGAGTGCAACTGCCTT
CCAGGTTTTGAAGGGAGCACCTGTGAGAGGAATATTGATGACTGCCCTAACCACAGGTGTCAGAATGGAGGGGTT
TGTGTGGATGGGGTCAACACTTACAACTGCCGCTGTCCCCCACAATGGACAGGACAGTTCTGCACAGAGGATGTG
GATGAATGCCTGCTGCAGCCCAATGCCTGTCAAAATGGGGGCACCTGTGCCAACCGCAATGGAGGCTATGGCTGT
GTATGTGTCAACGGCTGGAGTGGAGATGACTGCAGTGAGAACATTGATGATTGTGCCTTCGCCTCCTGTACTCCA
GGCTCCACCTGCATCGACCGTGTGGCCTCCTTCTCTTGCATGTGCCCAGAGGGGAAGGCAGGTCTCCTGTGTCAT
CTGGATGATGCATGCATCAGCAATCCTTGCCACAAGGGGGCACTGTGTGACACCAACCCCCTAAATGGGCAATAT
ATTTGCACCTGCCCACAAGGCTACAAAGGGGCTGACTGCACAGAAGATGTGGATGAATGTGCCATGGCCAATAGC
AATCCTTGTGAGCATGCAGGAAAATGTGTGAACACGGATGGCGCCTTCCACTGTGAGTGTCTGAAGGGTTATGCA
GGACCTCGTTGTGAGATGGACATCAATGAGTGCCATTCAGACCCCTGCCAGAATGATGCTACCTGTCTGGATAAG
ATTGGAGGCTTCACATGTCTGTGCATGCCAGGTTTCAAAGGTGTGCATTGTGAATTAGAAATAAATGAATGTCAG
AGCAACCCTTGTGTGAACAATGGGCAGTGTGTGGATAAAGTCAATCGTTTCCAGTGCCTGTGTCCTCCTGGTTTC
ACTGGGCCAGTTTGCCAGATTGATATTGATGACTGTTCCAGTACTCCGTGTCTGAATGGGGCAAAGTGTATCGAT
CACCCGAATGGCTATGAATGCCAGTGTGCCACAGGTTTCACTGGTGTGTTGTGTGAGGAGAACATTGACAACTGT
GACCCCGATCCTTGCCACCATGGTCAGTGTCAGGATGGTATTGATTCCTACACCTGCATCTGCAATCCCGGGTAC
ATGGGCGCCATCTGCAGTGACCAGATTGATGAATGTTACAGCAGCCCTTGCCTGAACGATGGTCGCTGCATTGAC
CTGGTCAATGGCTACCAGTGCAACTGCCAGCCAGGCACGTCAGGGGTTAATTGTGAAATTAATTTTGATGACTGT
GCAAGTAACCCTTGTATCCATGGAATCTGTATGGATGGCATTAATCGCTACAGTTGTGTCTGCTCACCAGGATTC
ACAGGGCAGAGATGTAACATTGACATTGATGAGTGTGCCTCCAATCCCTGTCGCAAGGGTGCAACATGTATCAAC
GGTGTGAATGGTTTCCGCTGTATATGCCCCGAGGGACCCCATCACCCCAGCTGCTACTCACAGGTGAACGAATGC
CTGAGCAATCCCTGCATCCATGGAAACTGTACTGGAGGTCTCAGTGGATATAAGTGTCTCTGTGATGCAGGCTGG
GTTGGCATCAACTGTGAAGTGGACAAAAATGAATGCCTTTCGAATCCATGCCAGAATGGAGGAACTTGTGACAAT
CTGGTGAATGGATACAGGTGTACTTGCAAGAAGGGCTTTAAAGGCTATAACTGCCAGGTGAATATTGATGAATGT
GCCTCAAATCCATGCCTGAACCAAGGAACCTGCTTTGATGACATAAGTGGCTACACTTGCCACTGTGTGCTGCCA
TACACAGGCAAGAATTGTCAGACAGTATTGGCTCCCTGTTCCCCAAACCCTTGTGAGAATGCTGCTGTTTGCAAA
GAGTCACCAAATTTTGAGAGTTATACTTGCTTGTGTGCTCCTGGCTGGCAAGGTCAGCGGTGTACCATTGACATT
GACGAGTGTATCTCCAAGCCCTGCATGAACCATGGTCTCTGCCATAACACCCAGGGCAGCTACATGTGTGAATGT
CCACCAGGCTTCAGTGGTATGGACTGTGAGGAGGACATTGATGACTGCCTTGCCAATCCTTGCCAGAATGGAGGT
TCCTGTATGGATGGAGTGAATACTTTCTCCTGCCTCTGCCTTCCGGGTTTCACTGGGGATAAGTGCCAGACAGAC
ATGAATGAGTGTCTGAGTGAACCCTGTAAGAATGGAGGGACCTGCTCTGACTACGTCAACAGTTACACTTGCAAG
TGCCAGGCAGGATTTGATGGAGTCCATTGTGAGAACAACATCAATGAGTGCACTGAGAGCTCCTGTTTCAATGGT
GGCACATGTGTTGATGGGATTAACTCCTTCTCTTGCTTGTGCCCTGTGGGTTTCACTGGATCCTTCTGCCTCCAT
GAGATCAATGAATGCAGCTCTCATCCATGCCTGAATGAGGGAACGTGTGTTGATGGCCTGGGTACCTACCGCTGC
AGCTGCCCCCTGGGCTACACTGGGAAAAACTGTCAGACCCTGGTGAATCTCTGCAGTCGGTCTCCATGTAAAAAC
AAAGGTACTTGCGTTCAGAAAAAAGCAGAGTCCCAGTGCCTATGTCCATCTGGATGGGCTGGTGCCTATTGTGAC
GTGCCCAATGTCTCTTGTGACATAGCAGCCTCCAGGAGAGGTGTGCTTGTTGAACACTTGTGCCAGCACTCAGGT

FIGURE 318B

GTCTGCATCAATGCTGGCAACACGCATTACTGTCAGTGCCCCCTGGGCTATACTGGGAGCTACTGTGAGGAGCAA
CTCGATGAGTGTGCGTCCAACCCCTGCCAGCACGGGGCAACATGCAGTGACTTCATTGGTGGATACAGATGCGAG
TGTGTCCCAGGCTATCAGGGTGTCAACTGTGAGTATGAAGTGGATGAGTGCCAGAATCAGCCCTGCCAGAATGGA
GGCACCTGTATTGACCTTGTGAACCATTTCAAGTGCTCTTGCCCACCAGGCACTCGGGGCCTACTCTGTGAAGAG
AACATTGATGACTGTGCCCGGGGTCCCCATTGCCTTAATGGTGGTCAGTGCATGGATAGGATTGGAGGCTACAGT
TGTCGCTGCTTGCCTGGCTTTGCTGGGGAGCGTTGTGAGGGAGACATCAACGAGTGCCTCTCCAACCCCTGCAGC
TCTGAGGGCAGCCTGGACTGTATACAGCTCACCAATGACTACCTGTGTGTTTGCCGTAGTGCCTTTACTGGCCGG
CACTGTGAAACCTTCGTCGATGTGTGTCCCCAGATGCCCTGCCTGAATGGAGGGACTTGTGCTGTGGCCAGTAAC
ATGCCTGATGGTTTCATTTGCCGTTGTCCCCCGGGATTTTCCGGGGCAAGGTGCCAGAGCAGCTGTGGACAAGTG
AAATGTAGGAAGGGGGAGCAGTGTGTGCACACCGCCTCTGGACCCCGCTGCTTCTGCCCCAGTCCCCGGGACTGC
GAGTCAGGCTGTGCCAGTAGCCCCTGCCAGCACGGGGGCAGCTGCCACCCTCAGCGCCAGCCTCCTTATTACTCC
TGCCAGTGTGCCCCACCATTCTCGGGTAGCCGCTGTGAACTCTACACGGCACCCCCCCAGCACCCCTCCTGCCACC
TGTCTGAGCCAGTATTGTGCCGACAAAGCTCGGGATGGCGTCTGTGATGAGGCCTGCAACAGCCATGCCTGCCAG
TGGGATGGGGGTGACTGTTCTCTCACCATGGAGAACCCCTGGGCCAACTGCTCCTCCCCACTTCCCTGCTGGGAT
TATATCAACAACCAGTGTGATGAGCTGTGCAACACGGTCGAGTGCCTGTTTGACAACTTTGAATGCCAGGGGAAC
AGCAAGACATGCAAGTATGACAAATACTGTGCAGACCACTTCAAAGACAACCACTGTGACCAGGGGTGCAACAGT
GAGGAGTGTGGTTGGGATGGGCTGGACTGTGCTGCTGACCAACCTGAGAACCTGGCAGAAGGTACCCTGGTTATT
GTGGTATTGATGCCACCTGAACAACTGCTCCAGGATGCTCGCAGCTTCTTGCGGGCACTGGGTACCCTGCTCCAC
ACCAACCTGCGCATTAAGCGGGACTCCCAGGGGGAACTCATGGTGTACCCCTATTATGGTGAGAAGTCAGCTGCT
ATGAAGAAACAGAGGATGACACGCAGATCCCTTCCTGGTGAACAAGAACAGGAGGTGGCTGGCTCTAAAGTCTTT
CTGGAAATTGACAACCGCCAGTGTGTTCAAGACTCAGACCACTGCTTCAAGAACACGGATGCAGCAGCAGCTCTC
CTGGCCTCTCACGCCATACAGGGGACCCTGTCATACCCTCTTGTGTCTGTCGTCAGTGAATCCCTGACTCCAGAA
CGCACTCAGCTCCTCTATCTCCTTGCTGTTGCTGTTGTCATCATTCTGTTTATTATTCTGCTGGGGGTAATCATG
GCAAAACGAAAGCGTAAGCATGGCTCTCTCTGGCTGCCTGAAGGTTTCACTCTTCGCCGAGATGCAAGCAATCAC
AAGCGTCGTGAGCCAGTGGGACAGGATGCTGTGGGGCTGAAAAATCTCTCAGTGCAAGTCTCAGAAGCTAACCTA
ATTGGTACTGGAACAAGTGAACACTGGGTCGATGATGAAGGGCCCCAGCCAAAGAAAGTAAAGGCTGAAGATGAG
GCCTTACTCTCAGAAGAAGATGACCCCATTGATCGACGGCCATGGACACAGCAGCACCTTGAAGCTGCAGACATC
CGTAGGACACCATCGCTGGCTCTCACCCCTCCTCAGGCAGAGCAGGAGGTGGATGTGTTAGATGTGAATGTCCGT
GGCCCAGATGGCTGCACCCCATTGATGTTGGCTTCTCTCCGAGGAGGCAGCTCAGATTTGAGTGATGAAGATGAA
GATGCAGAGGACTCTTCTGCTAACATCATCACAGACTTGGTCTACCAGGGTGCCAGCCTCCAGGCCCAGACAGAC
CGGACTGGTGAGATGGCCCTGCACCTTGCAGCCCGCTACTCACGGGCTGATGCTGCCAAGCGTCTCCTGGATGCA
GGTGCAGATGCCAATGCCCAGGACAACATGGGCCGCTGTCCACTCCATGCTGCAGTGGCAGCTGATGCCCAAGGT
GTCTTCCAGATTCTGATTCGCAACCGAGTAACTGATCTAGATGCCAGGATGAATGATGGTACTACACCCCTGATC
CTGGCTGCCCGCCTGGCTGTGGAGGGAATGGTGGCAGAACTGATCAACTGCCAAGCGGATGTGAATGCAGTGGAT
GACCATGGAAAATCTGCTCTTCACTGGGCAGCTGCTGTCAATAATGTGGAGGCAACTCTTTTGTTGTTGAAAAAT
GGGGCCAACCGAGACATGCAGGACAACAAGGAAGAGACACCTCTGTTTCTTGCTGCCCGGGAGGGGAGCTATGAA
GCAGCCAAGATCCTGTTAGACCATTTTGCCAATCGAGACATCACAGACCATATGGATCGTCTTCCCCGGGATGTG
GCTCGGGATCGCATGCACCATGACATTGTGCGCCTTCTGGATGAATACAATGTGACCCCAAGCCCTCCAGGCACC
GTGTTGACTTCTGCTCTCTCACCTGTCATCTGTGGGCCCAACAGATCTTTCCTCAGCCTGAAGCACACCCCAATG
GGCAAGAAGTCTAGACGGCCCAGTGCCAAGAGTACCATGCCTACTAGCCTCCCTAACCTTGCCAAGGAGGCAAAG
GATGCCAAGGGTAGTAGGAGGAAGAAGTCTCTGAGTGAGAAGGTCCAACTGTCTGAGAGTTCAGTAACTTTATCC
CCTGTTGATTCCCTAGAATCTCCTCACACGTATGTTTCCGACACCACATCCTCTCCAATGATTACATCCCCTGGG
ATCTTACAGGCCTCACCCAACCCTATGTTGGCCACTGCCGCCCCTCCTGCCCCAGTCCATGCCCAGCATGCACTA
TCTTTTTCTAACCTTCATGAAATGCAGCCTTTGGCACATGGGGCCAGCACTGTGCTTCCCTCAGTGAGCCAGTTG
CTATCCCACCACCACATTGTGTCTCCAGGCAGTGGCAGTGCTGGAAGCTTGAGTAGGCTCCATCCAGTCCCAGTC
CCAGCAGATTGGATGAACCGCATGGAGGTGAATGAGACCCAGTACAATGAGATGTTTGGTATGGTCCTGGCTCCA
GCTGAGGGCACCCATCCTGGCATAGCTCCCCAGAGCAGGCCACCTGAAGGGAAGCACATAACCACCCCTCGGGAG
CCCTTGCCCCCCATTGTGACTTTCCAGCTCATCCCTAAAGGCAGTATTGCCCAACCAGCGGGGGCTCCCCAGCCT

FIGURE 318C

CAGTCCACCTGCCCTCCAGCTGTTGCGGGCCCCCTGCCCACCATGTACCAGATTCCAGAAATGGCCCGTTTGCCC
AGTGTGGCTTTCCCCACTGCCATGATGCCCCAGCAGGACGGGCAGGTAGCTCAGACCATTCTCCCAGCCTATCAT
CCTTTCCCAGCCTCTGTGGGCAAGTACCCCACACCCCCTTCACAGCACAGTTATGCTTCCTCAAATGCTGCTGAG
CGAACACCCAGTCACAGTGGTCACCTCCAGGGTGAGCATCCCTACCTGACACCATCCCCAGAGTCTCCTGACCAG
TGGTCAAGTTCATCACCCCACTCTGCTTCTGACTGGTCAGATGTGACCACCAGCCCTACCCCTGGGGGTGCTGGA
GGAGGTCAGCGGGGACCTGGGACACACATGTCTGAGCCACCACACAACAACATGCAGGTTTATGCGTGAGAGAGT
CCACCTCCAGTGTAGAGACATAACTGACTTTTGTAAATGCTGCTGAGGAACAAATGAAGGTCATCCGGGAGAGAA
ATGAAGAAATCTCTGGAGCCAGCTTCTAGAGGTAGGAAAGAGAAGATGTTCTTATTCAGATAATGCAAGAGAAGC
AATTCGTCAGTTTCACTGGGTATCTGCAAGGCTTATTGATTATTCTAATCTAATAAGACAAGTTTGTGGAAATGC
AAGATGAATACAAGCCTTGGGTCCATGTTTACTCTCTTCTATTTGGAGAATAAGATGGATGCTTATTGAAGCCCA
GACATTCTTGCAGCTTGGACTGCATTTTAAGCCCTGCAGGCTTCTGCCATATCCATGAGAAGATTCTACACTAGC
GTCCTGTTGGGAATTATGCCCTGGAATTCTGCCTGAATTGACCTACGCATCTCCTCCTCCTTGGACATTCTTTTG
TCTTCATTTGGTGCTTTTGGTTTTGCACCTCTCCGTGATTGTAGCCCTACCAGCATGTTATAGGGCAAGACCTTT
GTGCTTTTGATCATTCTGGCCCATGAAAGCAACTTTGGTCTCCTTTCCCCTCCTGTCTTCCCGGTATCCCTTGGA
GTCTCACAAGGTTTACTTTGGTATGGTTCTCAGCACAAACCTTTCAAGTATGTTGTTTCTTTGGAAAATGGACAT
ACTGTATTGTGTTCTCCTGCATATATCATTCCTGGAGAGAGAAGGGGAGAAGAATACTTTTCTTCAACAAATTTT
GGGGGCAGGAGATCCCTTCAAGAGGCTGCACCTTAATTTTTCTTGTCTGTGTGCAGGTCTTCATATAAACTTTAC
CAGGAAGAAGGGTGTGAGTTTGTTGTTTTTCTGTGTATGGGCCTGGTCAGTGTAAAGTTTTATCCTTGATAGTCT
AGTTACTATGACCCTCCCCACTTTTTTAAAACCAGAAAAAGGTTTGGAATGTTGGAATGACCAAGAGACAAGTTA
ACTCGTGCAAGAGCCAGTTACCCACCCACAGGTCCCCCTACTTCCTGCCAAGCATTCCATTGACTGCCTGTATGG
AACACATTTGTCCCAGATCTGAGCATTCTAGGCCTGTTTCACTCACTCACCCAGCATATGAAACTAGTCTTAACT
GTTGAGCCTTTCCTTTCATATCCACAGAAGACACTGTCTCAAATGTTGTACCCTTGCCATTTAGGACTGAACTTT
CCTTAGCCCAAGGGACCCAGTGACAGTTGTCTTCCGTTTGTCAGATGATCAGTCTCTACTGATTATCTTGCTGCT
TAAAGGCCTGCTCACCAATCTTTCTTTCACACCGTGTGGTCCGTGTTACTGGTATACCCAGTATGTTCTCACTGA
AGACATGGACTTTATATGTTCAAGTGCAGGAATTGGAAAGTTGGACTTGTTTTCTATGATCCAAAACAGCCCTAT
AAGAAGGTTGGAAAAGGAGGAACTATATAGCAGCCTTTGCTATTTTCTGCTACCATTTCTTTTCCTCTGAAGCGG
CCATGACATTCCCTTTGGCAACTAACGTAGAAACTCAACAGAACATTTTCCTTTCCTAGAGTCACCTTTTAGATG
ATAATGGACAACTATAGACTTGCTCATTGTTCAGACTGATTGCCCCTCACCTGAATCCACTCTCTGTATTCATGC
TCTTGGCAATTTCTTTGACTTTCTTTTAAGGGCAGAAGCATTTTAGTTAATTGTAGATAAAGAATAGTTTTCTTC
CTCTTCTCCTTGGGCCAGTTAATAATTGGTCCATGGCTACACTGCAACTTCCGTCCAGTGCTGTGATGCCCATGA
CACCTGCAAAATAAGTTCTGCCTGGGCATTTTGTAGATATTAACAGGTGAATTCCCGACTCTTTTGGTTTGAATG
ACAGTTCTCATTCCTTCTATGGCTGCAAGTATGCATCAGTGCTTCCCACTTACCTGATTTGTCTGTCGGTGGCCC
CATATGGAAACCCTGCGTGTCTGTTGGCATAATAGTTTACAAATGGTTTTTTCAGTCCTATCCAAATTTATTGAA
CCAACAAAAATAATTACTTCTGCCCTGAGATAAGCAGATTAAGTTTGTTCATTCTCTGCTTTATTCTCTCCATGT
GGCAACATTCTGTCAGCCTCTTTCATAGTGTGCAAACATTTTATCATTCTAAATGGTGACTCTCTGCCCTTGGAC
CCATTTATTATTCACAGATGGGGAGAACCTATCTGCATGGACCTCTGTGGACCACAGCGTACCTGCCCCTTTCTG
CCCTCCTGCTCCAGCCCCACTTCTGAAAGTATCAGCTACTGATCCAGCCACTGGATATTTTATATCCTCCCTTTT
CCTTAAGCACAATGTCAGACCAAATTGCTTGTTTCTTTTTCTTGGACTACTTTAATTTGGATCCTTTGGGTTTGG
AGAAAGGGAATGTGAAAGCTGTCATTACAGACAACAGGTTTCAGTGATGAGGAGGACAACACTGCCTTTCAAACT
TTTTACTGATCTCTTAGATTTTAAGAACTCTTGAATTGTGTGGTATCTAATAAAAGGGAAGGTAAGATGGATAAT
CACTTTCTCATTTGGGTTCTGAATTGGAGACTCAGTTTTTATGAGACACATCTTTTATGCCATGTATAGATCCTC
CCCTGCTATTTTTGGTTTATTTTTATTGTTATAAATGCTTTCTTTCTTTGACTCCTCTTCTGCCTGCCTTTGGGG
ATAGGTTTTTTTGTTTGTTTATTTGCTTCCTCTGTTTTGTTTTAAGCATCATTTTCTTATGTGAGGTGGGGAAGG
GAAAGGTATGAGGGAAAGAGAGTCTGAGAATTAAAATATTTTAGTATAAGCAATTGGCTGTGATGCTCAAATCCA
TTGCATCCTCTTATTGAATTTGCCAATTTGTAATTTTTGCATAATAAAGAACCAAAGGTGTAATGTTTTGTTGAG
AGGTGGTTTAGGGATTTTGGCCCTAACCAATACATTGAATGTATGATGACTATTTGGGAGGACACATTTATGTAC
CCAGAGGCCCCCACTAATAAGTGGTACTATGGTTACTTCCTTGTGTACATTTCTCTTAAAAGTGATATTATATCT
GTTTGTATGAGAAACCCAGTAACCAATAAAATGACCGCATATTCCTGACTAAACGTAGTAAGGAAAATGCACACT

FIGURE 318D

TTGTTTTTACTTTTCCGTTTCATTCTAAAGGTAGTTAAGATGAAATTTATATGAAAGCATTTTTATCACAAAATA
AAAAAGGTTTGCCAAGCTCAGTGGTGTTGTATTTTTTATTTTCCAATACTGCATCCATGGCCTGGCAGTGTTACC
TCATGATGTCATAATTTGCTGAGAGAGCAAATTTTCTTTTCTTTCTGAATCCCACAAAGCCTAGCACCAAACTTC
TTTTTTTCTTCCTTTAATTAGATCATAAATAAATGATCCTGGGGAAAAAGCATCTGTCAAATAGGAAACATCACA
AAACTGAGCACTCTTCTGTGCACTAGCCATAGCTGGTGACAAACAGATGGTTGCTCAGGGACAAGGTGCCTTCCA
ATGGAAATGCGAAGTAGTTGCTATAGCAAGAATTGGGAACTGGGATATAAGTCATAATATTAATTATGCTGTTAT
GTAAATGATTGGTTTGTAACATTCCTTAAGTGAAATTTGTGTAGAACTTAATATACAGGATTATAAAATAATATT
TTGTGTATAAATTTGTTATAAGTTCACATTCATACATTTATTTATAAAGTCAGTGAGATATTTGAACATG

FIGURE 319

GAGGAGGAGGAGGAGATGACTGGGGAGCGGGAGCTGGAGAATACTGCCCAGTTACTCTAGCGCGCCAGGCCGAAC
CGCAGCTTCTTGGCTTAGGTACTTCTACTCACAGCGGCCGATTCCGAGGCCAACTCCAGCAATGGCTTTTGCAAA
TCTGCGGAAAGTGCTCATCAGTGACAGCCTGGACCCTTGCTGCCGGAAGATCTTGCAAGATGGAGGGCTGCAGGT
GGTGGAAAAGCAGAACCTTAGCAAAGAGGAGCTGATAGCGGAGCTGCAGGACTGTGAAGGCCTTATTGTTCGCTC
TGCCACCAAGGTGACCGCTGATGTCATCAACGCAGCTGAGAAACTCCAGGTGGTGGGCAGGGCTGGCACAGGTGT
GGACAATGTGGATCTGGAGGCCGCAACAAGGAAGGGCATCTTGGTTATGAACACCCCCAATGGGAACAGCCTCAG
TGCCGCAGAACTCACTTGTGGAATGATCATGTGCCTGGCCAGGCAGATTCCCCAGGCGACGGCTTCGATGAAGGA
CGGCAAATGGGAGCGGAAGAAGTTCATGGGAACAGAGCTGAATGGAAAGACCCTGGGAATTCTTGGCCTGGGCAG
GATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCTTTGGGATGAAGACTATAGGGTATGACCCCATCATTTCCCC
AGAGGTCTCGGCCTCCTTTGGTGTTCAGCAGCTGCCCCTGGAGGAGATCTGGCCTCTCTGTGATTTCATCACTGT
GCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCTTTGCCCAGTGCAAGAAGGGGGTGCG
TGTGGTGAACTGTGCCCGTGGAGGGATCGTGGACGAAGGCGCCCTGCTCCGGGCCCTGCAGTCTGGCCAGTGTGC
CGGGGCTGCACTGGACGTGTTTACGGAAGAGCCGCCACGGGACCGGGCCTTGGTGGACCATGAGAATGTCATCAG
CTGTCCCCACCTGGGTGCCAGCACCAAGGAGGCTCAGAGCCGCTGTGGGGAGGAAATTGCTGTTCAGTTCGTGGA
CATGGTGAAGGGGAAATCTCTCACGGGGGTTGTGAATGCCCAGGCCCTTACCAGTGCCTTCTCTCCACACACCAA
GCCTTGGATTGGTCTGGCAGAAGCTCTGGGGACACTGATGCGAGCCTGGGCTGGGTCCCCCAAAGGGACCATCCA
GGTGATAACACAGGGAACATCCCTGAAGAATGCTGGGAACTGCCTAAGCCCCGCAGTCATTGTCGGCCTCCTGAA
AGAGGCTTCCAAGCAGGCGGATGTGAACTTGGTGAACGCTAAGCTGCTGGTGAAAGAGGCTGGCCTCAATGTCAC
CACCTCCCACAGCCCTGCTGCACCAGGGGAGCAAGGCTTCGGGGAATGCCTCCTGGCCGTGGCCCTGGCAGGCGC
CCCTTACCAGGCTGTGGGCTTGGTCCAAGGCACTACGCCTGTACTGCAGGGGCTCAATGGAGCTGTCTTCAGGCC
AGAAGTGCCTCTCCGCAGGGACCTGCCCCTGCTCCTATTCCGGACTCAGACCTCTGACCCTGCAATGCTGCCTAC
CATGATTGGCCTCCTGGCAGAGGCAGGCGTGCGGCTGCTGTCCTACCAGACTTCACTGGTGTCAGATGGGGAGAC
CTGGCACGTCATGGGCATCTCCTCCTTGCTGCCCAGCCTGGAAGCGTGGAAGCAGCATGTGACTGAAGCCTTCCA
GTTCCACTTCTAACCTTGGAGCTCACTGGTCCCTGCCTCTGGGGCTTTTCTGAAGAAACCCACCCACTGTGATCA
ATAGGGAGAGAAAATCCACATTCTTGGGCTGAACGCGGGCCTCTGACACTGCTTACACTGCACTCTGACCCTGTA
GTACAGCAATAACCGTCTAATAAAGAGCCTACCCCC

FIGURE 320

MAFANLRKVLISDSLDPCCRKILQDGGLQVVEKQNLSKEELIAELQDCEGLIVRSATKVTADVINAAEKLQVVGR
AGTGVDNVDLEAATRKGILVMNTPNGNSLSAAELTCGMIMCLARQIPQATASMKDGKWERKKFMGTELNGKTLGI
LGLGRIGREVATRMQSFGMKTIGYDPIISPEVSASFGVQQLPLEEIWPLCDFITVHTPLLPSTTGLLNDNTFAQC
KKGVRVVNCARGGIVDEGALLRALQSGQCAGAALDVFTEEPPRDRALVDHENVISCPHLGASTKEAQSRCGEEIA
VQFVDMVKGKSLTGVVNAQALTSAFSPHTKPWIGLAEALGTLMRAWAGSPKGTIQVITQGTSLKNAGNCLSPAVI
VGLLKEASKQADVNLVNAKLLVKEAGLNVTTSHSPAAPGEQGFGECLLAVALAGAPYQAVGLVQGTTPVLQGLNG
AVFRPEVPLRRDLPLLLFRTQTSDPAMLPTMIGLLAEAGVRLLSYQTSLVSDGETWHVMGISSLLPSLEAWKQHV
TEAFQFHF

FIGURE 321

GGGCAGGGGTGCGGAGGGACCGACGGACGCACGGGCGGGCGGCCGGGAGCCATGGAGCGCGGCCCTGGGGCCCGG
GGGCGCGGGCCGGGGTGGGCTTCCCACGGCACGACATGGAGACCTGTGGTTGCGAGGCTCCCTGGGGCTCGGCTT
GGACCGCGATGGGGCTGGGCCCTGGCCTCCTAACGGGGCTGCTGTCTGGGGCGGTAGCTGGGGGGGCGCTCTCCC
CCCTGCCCGCGACTCGGAGCACCCCACCCCTCCCCTGCCGGGCCAGGCCGGGCGGCGTTGTTGGCGGGGGCCCCG
GTGGAGGCCCGGCCCGGGCGGCGCCCGCC**ATG**AACGGGCTGTCGCTGAGTGAGCTCTGCTGCCTCTTCTGCTGCC
CTCCCTGCCCCGGCCGCATCGCTGCCAAGCTCGCCTTCCTGCCGCCGGAGGCCACCTACTCCCTGGTGCCTGAGC
CCGAGCTGGGGCCTGGTGGGGCCGGGGCCGCCCCCTTGGGGACCCTGAGAGCCTCCTCGGGCGCACCCGGGCGCT
GGAAGCTGCACCTGACGGAGCGTGCCGACTTCCAGTACAGCCAGCGCGAGCTGGACACCATCGAGGTCTTCCCCA
CCAAGAGCGCCCGCGGCAACCGTGTCTCCTGCATGTATGTTCGCTGCGTGCCTGGTGCCAGGTACACGGTCCTCT
TCTCGCACGGCAATGCCGTGGACCTGGGCCAGATGAGCAGCTTCTACATTGGCCTGGGCTCCCGCCTCCACTGCA
ACATCTTCACCTACGACTCCTCCGGCTACGGTGCCAGCTCGGGCAGGCCTTCCGAGAGGAACCTCTATGCCGACA
TCGACGCCACCTGGCAGGCCCTGCGCACCAGGTACGGCATCAGCCCGGACAGCATCATCCTGTACGGGCAGAGCA
TCGGCACGGTGCCCACCATGGACCTGGCCTCGCGCTACGAGTGTGCCGCGGTGGTGCTGCACTCGCCGCTCACCT
CGGGCATGCGCGTCGCCTTCCGCGACACCAAGAAGACCTACTGCTTCGACGCCTTCCCTAACATCGAGAAGGTGT
CCAAGATCACGTCTCCCGTGCTCATCATCCACGGCAGGGAGGACGAGGTGATCGACTTCTCGCACGGGCTGGCGC
TCTACGAGCGCTGCCCCAAGGCGGTGGAGCCGCTGTGGGTGGAGGGCGCCGGGCACAACGACATCGAGCTCTACA
GCCAGTACCTGGAGCGCCTGCGTCGCTTCATCTCCCAGGAGCTGCCCAGCCAGCGCGCC**TAG**CGGCGGCCCCAAC
CAGCCGGACCTCAGCAATAAGGCGGCCCCCGGACCTCACCCCGCGCCGGCCCCCACCCAGGGGCTGCATGTGGAC
CCCCCCGGGCGGCCCAGGGGACCCCGCCCCGACCCAGGGGCTGTGGACGATGTACAGGCAACAGAGCTACGCACT
CCTTTCCTTTTGGAAGCAAGAAGAAAATACGTGAAAACGGAAATTAAAGATTTAAAATT

FIGURE 322

MNGLSLSELCCLFCCPPCPGRIAAKLAFLPPEATYSLVPEPELGPGGAGAAPLGTLRASSGAPGRWKLHLTERAD
FQYSQRELDTIEVFPTKSARGNRVSCMYVRCVPGARYTVLFSHGNAVDLGQMSSFYIGLGSRLHCNIFTYDSSGY
GASSGRPSERNLYADIDATWQALRTRYGISPDSIILYGQSIGTVPTMDLASRYECAAVVLHSPLTSGMRVAFRDT
KKTYCFDAFPNIEKVSKITSPVLIIHGREDEVIDFSHGLALYERCPKAVEPLWVEGAGHNDIELYSQYLERLRRF
ISQELPSQRA

FIGURE 323A

AGCGTGAACCTGGGAGGCAGAGCTTGCAGTGAGCCTAGATCGCGTCACTGCACTCCAGCCTGGGAGACAGAGTGA
GACTCTGTCTCAAAAAAAAAAAAAAAGTCAAAACAAGAGAACATACTAAATGATTCCATTTTTTTATTTATGACTT
CATGACTACCATTAAGAAAATATAACCTGTTGGGAAACTGTTTCTGCCTTGATGATGTTGTACAGACAAGAGATA
AACAGTGAGGAATGTGCTTAGATGTATTGGGAAAGACACGGGTCTGTGGCATTGTCACAAGGGTACACGAATACT
GAGAGTGAATGCTGAAGGAATGATCCCCATTGGTGGTGACCCTCAGGTGAGACTAGGGTGCCTGTGTTTCAGCAA
AGCCTGGGCAATTGGAATGCAGGGCTCCTAAGATTCCATGACACCCCCACCTTCTAATTCTGTTATTGCAACTGC
AGACCGTTACCTGGCACGCTGGCCACAATCTACCTCACTCTTATCAGAGTCTGAGCTACTGGCAGTGCTTTCAGC
TCTGAGTTGAGGCACCTCGAACCTTGTTTTTGTGGTGAAGGATCCTAAAGTGCTGTGGGAGTGATCACATTTTTC
ACAACAGTAAGTCCCTGACTCCACCTCTTCTGCCACAAACGTCAGCATGGTGGTATCAGCCGGCCCTTGGTCCAG
CGAGAAGGCAGAGATGAACATTCTAGAAATCAACGAGAAATTGCGCCCCCAGTTGGCAGAGAACAAACAGCAGTT
CGTAAACCTCAAAGAGATGTTTTCTAACTCAACTGGCCGGCTTCCTGGCCAACCGACAGAAGAAATACAGCAATA
TAAAGTCCTGGTTCACTCTCAGGAACGAGAGCTGACGCAGTTAAAGGAGAAGTTACAGGAAGGGAGAGATGCCTC
CCGCTCATTGAATGAGCATCTCCAGGCCCTCCTCACTCTGGATGAGCCGGACAAGTCCCAGGGGCAGGACCTCCA
AGAACAGCTGGCTGAGGGGTGTAGACTGGCACAGCACCTTGTCCAAAAGCTCAGCCCAGAAAATGACGAAGATGA
GGATGAAGATGTTCAAGTTGAGGAGGATGAGAAAGTGCAGAAATCATCTGCCCCCAGGGAGGTGCAGAAGGCTGA
AGTGAGCAAAGTCCCTGAGGACTCACTGGAGGAATGTGCCATCACTTGTTCAAATAGCCACGGCCCTTGTGACTC
CAACCAGCCTCACAAGAACATCAAAATCACATTTGAGGAAGACGAAGTCAACTCAACTCTGGTTGTAGACAGAGA
ATCCTCTCATGATGAATGTCAGGATGCTCTAAACATTCTCCCAGTCCCTGGCCCCACCTCTTCTGCCACAAACGT
CAGCATGGTGGTATCAGCCGGCCCTTTGTCCAGCGAGAAGGCAGAGATGAACATTCTAGAAATCAATGAGAAATT
GCACCCCCAGCTGGCAGAGAAGAAACAGCAGTTCAGAAACCTCAAAGAGAAATGTTTTCTAACTCAACTGGCCGG
CTTCCTGGCCAACCAGCAGAACAAATACAAGTATGAAGAGTGTAAAGACCTCATAAAATTTATGCTGAGGAATGA
GCGACAGTTCAAGGAGGAGAAGCTTGCAGAGCAGCTGAAGCAAGCTGAGGAGCTCAGGCAATATAAAGTCCTGGT
TCACGCTCAGGAACGAGAGCTGACCCAGTTAAGGGAGAAGTTGCGGGAAGGGAGAGATGCCTCCCGCTCATTGAA
TGAGCATCTCCAGGCCCTCCTCACTCCGGATGAGCCGGACAAGTCCCAGGGGCAGGACCTCCAAGAACAGCTGGC
TGAGGGGTGTAGACTGGCACAGCACCTTGTCCAAAAGCTCAGCCCAGAAAATGACAACGATGACAATGAAGATGT
TCAAGTTGAGGTGGCTGAGAAAGTGCAGAAATCGTCTGCCCCCAGGGAGATGCAGAAGGCTGAAGAAAAGGAAGT
CCCTGAGGACTCACTGGAGGAATGTGCCATCACTTATTCAAATAGCCATGGCCCTTATGACTCCAACCAGCCACA
TAGGAAAACCAAAATCACATTTGAGGAAGACAAAGTCGACTCAACTCTCATTGGCTCATCCTCTCATGTTGAACG
GGAAGATGCTGTACACATTATTCCAGAAAATGAAAGTGATGATGAGGAAGAGGAAGAAAAAGGGCCAGTGTCTCC
CAGGAATCTGCAGGAGTCTGAAGAGGAGGAAGTCCCCCAGGAGTCCTGGGATGAAGGTTATTCGACTCCCTCAAT
TCCTCCTGAAATGTTGGCCTCGTACAAGTCTTACAGCAGCACATTTCACTCATTAGAGGAACAGCAAGTCTGCAT
GGCTGTTGACATAGGCAGACATCGGTGGGATCAAGTGAAAAAGGAGGACCAAGAGGCAACAGGTCCCAGGCTCAG
CAGGGAGCTGCTGGATGAGAAAGGGCCTGAAGTCTTGCAGGACTCACTGTATAGATGTTATTCAACTCCTTCAGG
TTGTCTTGAACTGACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTACGTATTGGAGCAACAGCGTGTTGGCTT
GGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGACCAAGACCCATCATGCCCCAGGCTCAG
CAGGGAGCTGCTGGATGAGAAAGAGCCTGAAGTCTTGCAGGACTCACTGGGTAGATGGTATTCGACTCCTTCAGG
TTATCTTGAACTGCCTGACTTAGGCCAGCCCTACAGCAGTGCTGTTTACTCATTGGAGGAACAGTACCTTGGCTT
GGCTCTTGACTTGGACAGAATTAAAAAGGACCAAGAAGAGGAAGAAGACCAAGGCCCACCATGCCCCAGGCTCAG
CAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGTCTTGCAGGACTCACTGGATAGATGTTATTCAACTCCTTCCAG
TTGTCTTGAACAGCCTGACTCCTGCCAGCCCTATGGAAGTTCCTTTTATGCATTGGAGGAAAAACATGTTGGCTT
TTCTCTTGACGTGGGAGAAATTGAAAAGAAGGGGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAGAAGGAAAG
AAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAACCCACCATGCCCCAGGCTCAACGGCGTGCTGATGGAAGT
GGAAGAGCCTGAAGTCTTGCAGGACTCACTGGATGGATGTTATTCTACTCCGTCAATGTACTTTGAACTACCTGA
CTCATTCCAGCACTACAGAAGTGTGTTTTACTCATTTGAGGAACAGCACATCAGCTTCGCCCTTTACGTGGACAA
TAGGTTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTGTTCCAGATGGAAGTCATATTCCCACAATAAGCAGC
CCTTACTAAGCCGAGAGATGTCATTCCTGCAGGCAGGACCTATAGGCACGTGAAGATTTGAATGAAACTACAGTT
CCATTTGGAAGCCCAGACATAGGATGGGTCAGTGGGCATGGCTCTATTCCTATTCTCAAACCATGCCAGTGGCAA
CCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACACGTTCACATAACTGTGCAGCACATGCCGGGA

FIGURE 323B

GTGATCAGTCAGACATTTTAATTTGAACCACGTATCTCTGGGTAGCTACAAAATTCCTCAGGGATTTCATTTTGC
AGACATGTCTCTGAGCTTCTATACCTGCTCAAGGTCATTGTCATCTTTGTGTTTAGCTCATCCAAAGGTGTTACC
CTGGTTTCAATGAACCTAACCTCATTCTTCGTGTCTTCAGTGTTGGCTTGTTTTAGCTGATCCATCTGTAACACA
GGAGGGATCCTTGGCTGAGGATTGTATTTCAGAACCACCAACTGCTCTTGACAATTGTTAACCCGCTAGGCTCCT
TTGGTTAGAGAAGCCACAGTCCTTCAGCCTCCAATTGGTGTCAGTACTTAGGAAGACCACAGCTAGATGGACAAA
CAGCATTGGGAGGCCTTAGCCCTGCTCCTCTCAATTCCATCCTGTAGAGAACAGGAGTCAGGAGCCGCTGGCAGG
AGACAGCATGTCACCCAGGACTCTGCCGGTGCAGAATATGAACAATGCCATGTTCTTGCAGAAAACGCTTAGCCT
GAGTTTCATAGGAGGTAATCACCAGACAACTGCAGAATGTAGAACACTGAGCAGGACAACTGACCTGTCTCCTTC
ACATAGTCCTTATCACCACAAATCACACAACAAAAAGGAGAAGAGATATTTGGGTTCAAAAAAAGTAAAAAGAT
AATGTAGCTGCATTTCTTTAGTTATTTTGAACCCCAAATATTTCCTCATCTTTTTGTTGTTGTCATGGATGGTGG
TGACATGGACTTGTTTATAGAGGACAGGTCAGCTGTCTGGCTCAATGATCTACATTCTGAAGTTGTCTGAAAATG
TCTTCATGATTAAATTCAGCCTAAACGTTTTGCCGGGAACACTGCAGAGACAATGCTGTGAGTTTCCAACCTCAG
CCCATCTGCGGGCAGAGAAGGTCTAGTTTGTCCATCACCATTATGATATCAGGACTGGTTACTTGGTTAAGGAGG
GGTCTAGGAGATCTGTCCCTTTTAGAGACACCTTACTTATAATGAAGTACTTGGGAAAGCGGTTTTCAAGAGTAT
AAATATCCTGTATTCTAATGATCATCCTCTAAACATTTTATCATTTATTAATCCTCCCTGCCTGTGTCTATTATT
ATATTCATATCTCTACGCTGCAAATTTTGGGTCTCAATTTTTACTGTGCCTTTGTTTTTACTAGTGTCTGCTGTT
GCAAAAAGAAGAAAACATTCTCTGCCTGAGTTTTAATTTTTGTCCAAAGTTAATTTTAATCTATACAATTAAAAC
CTTTTGCCTATCACTCTGGACTTTTGGATTGTTTTTACATTCAGTGTTATAATATTTGATTATGCTGATTGGTT
TTGGTGGGTACTGATGCGAATTAATAAAAACATTTCATTTCC

FIGURE 324A

GTTTTGTAACTCAACTGGCCGGCTTCCTGGCCAAGCAGCAGAACAAATACAAATATGAAGAGTGCAAAGACCTCA
TAAAATCTATGCTGAGGAATGAGCTACAGTTCAAGGAGGAGAAGCTTGCAGAGCAGCTGAAGCAAGCTGAGGAGC
TCAGGTGAGGGGACCCCATGGGGGCAGGCAGGGGGGCAGGTGTGTAAATCTCTGAAGTACAACAGCTCGGTGGGG
AGACTTAAGAGCTAAGCTGGGCCAGGGGAAGGGCAGGAATTGCCATGGCAGGCTCGCTACACACAAATATTTATC
AAACAGAGAAGAAGGATAATAAAAATTTATGGGTTGCAGTGTTTCTCAGAGCCTGTTTTCTTTTTTCAAACAAGT
AATGTTGATGTGAAATTTACATAACACAAAATTAACCAAAGGAGTGTGAACCACACAGCAGCATTCAGTATACTC
AAAATGGTGTGCCATCACCACCCCACTTACCCTAGTGAGAATCACCTCCTGACTGACTGCGGCTTCTCATTCTTT
CACTCAATCAATGTTGCCTTCTCGACCCTGTCATTCTTTTCTTCTTTCGTCTTTTCAATTCGCCCTATCTGCATC
TGGCCTCATTTCTGTACATGGCTTTGTATCTAATGGCCGCAAGATGCACTATGTGTATTTTCACATGGAAATGTC
CATGGCCAGAGTGAGGAACTGAAAGGATGTCTTTTTGAAACGGAATTAGGAAGACACCTACTTTTGTTTACAGAG
GGGAAAGATGAATGGAACATCATCGAGGATCTTGCAGGAGCCCTCTCTGATACAGAGGAAGCCTGTAAACCATTT
TCTATTCTTTCTCTTGGCCACAGACATTCCTTTCAACATGTGCTGACCTTCTGCTTGGAGGTCTCCTTGAGGACA
TTGTCTCAGAAATCTCTGTTGCAATATTTGAACGGATCACTCAACCCTTTCCACTCTTAAATTTTCTCTACCGTC
TCACCTTAGGCAATATAAAGTCCTGGTTCACTCTCAGGAACGAGAGCTGACCCAGTTAAGGGAGAAGTTACGGGA
AGGGAGAGATGCCTCCCGCTCATTGAATGAGCATCTCCAGGCCCTCCTCACTCCGGATGAGCCGGACAAGTCCCA
GGGGCAGGACCTCCAAGAACAGCTGGCTGAGGGGTGTAGACTGGCACAACACCTTGTCCAAAAGCTCAGCCCAGA
AAATGATAACGATGACGATGAAGATGTTCAAGTTGAGGTGGCTGAGAAAGTGCAGAAATCGTCTTCCCCCAGGGA
GATGCAGAAGGCTGAAGAAAAGGAAGTCCCTGAGGACTCACTGGAGGAGTGTGCCATCACTTGTTCAAATAGCCA
TGGCCCTTATGACTCCAACCAGCCACATAGGAAAACCAAAATCACATTTGAGGAAGACAAAGTCGACTCAACTCT
CATTGGCTCATCCTCTCATGTTGAATGGGAGGATGCTGTACACATTATCCCAGAAAATGAAAGTGATGATGAGGA
AGAGGAAGAAAAAGGGCCAGTGTCTCCCAGGAATCTGCAGGAGTCTGAAGAGGAGGAAGTCCCCCAGGAGTCCTG
GGATGAAGGTTATTCGACTCTCTCAATTCCTCCTGAAAGGTTGGCCTCATACCAGTCTTACAGCAGCACATTTCA
CTCATTAGAGGAACAGCAAGTCTGCATGGCTGTTGACATAGGCAGACATCGGTGGGATCAAGTGAAAAAGGAGGA
CCAAGAGGCAACAGGTCCCAGGCTCAGCAGGGAGCTGCTGGCTGAGAAAGAGCCTGAAGTCTTGCAGGACTCACT
GGATAGATGTTATTCAACTCCTTCAGTTTATCTTGGACTGACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTA
CGTATTGGAGCAACAGCGTGTTGGCTTGGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGA
CCAAGACCCATCATGCCCCAGGCTCAGCAGGGAGCTGCTGGCTGAGAAAGAGCCTGAAGTCTTGCAGGACTCACT
GGATAGATGTTATTCGACTCCTTCAGGTTATCTTGAACTGCCTGACTTAGGCCAGCCCTACAGAAGTGCTGTTTA
CTCATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAAAAGGACCAAGAAGAGGAAGAAGA
CCAAGGCCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGTCTTGCAGGACTCACT
GGATAGATGTTATTCAACTCCTTCCAGTTGTCTTGAACAGCCTGACTCCTGCCAGCCCTACAGAAGTTCCTTTTA
TGCATTGGAGGAAAAACATGTTGGCTTTTCTCTTGACGTGGGAGAAATTGAAAAGAAGGGGAAGGGGAAGAAAAG
AAGGGGAAGAAGATCAAAGAAGAAAAGAAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAACCCACCATGCCC
CAGGCTCAACAGCGTGCTGATGGAAGTGGAAGAGCCTGAAGTCTTGCAGGACTCACTGGATAGATGTTATTCGAC
TCCATCAATGTACTTTGAACTACCTGACTCATTCCAGCACTACAGAAGTGTGTTTTACTCATTTGAGGAACAGCA
CATCACCTTTGCCCTTGACATGGACAATAGCTTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTCTTCCAGAT
GGGAGTCATATTCCCACAATAAGCAGCCCTTACTAAGCCGAGAGGTGTCATTCCTGCAGGCAGGACCTATAGGCA
CCTGAAGATTTGAATGAAACTATAGTTCCATTTGGAAGCCCAGACATAGGATGGGTCAGTGGGCATGGCTCTATT
CCTATTCTCAGAGCATGCCAGTGGCAACCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACACGTT
CACATAACTGTGCAGCACATGCCGGGAGTGATCAGCCGGACATTTTAATTTGAACCATGTATCTCTGGGTAGCTA
CAAAATTCCTCAGGGATTTCATTTTGCAGGCATGTCTCTGAGCTTCTATACCTACTCAAGGTCAGTGTCATCTTT
GTGTTTAGTTCATCCAAAGGTGTTACCCTGGTTTCAATGAACCTAACCTCATTATTTGTGTCTTCAGTGTTGGCT
TGTTTTAGCTGATCCATCTGTAACACAGGAGGGATCCTTGGCTGAGGATTGTATTTCAGAACCACCAACTGCTCT
TGACAATTGTTAACCCGCTAGGCTCCTTTGGTTAGAGAAGCCACAGTCCTTCAGCCTCCAATTGGTGTCAGTACT
TAGGAAGACCACAGCTAGATGGACAAACAGCATTGGGAGGCCTTAGCCCTGCTCCTCTCAATTCCATCCTGTAGA
GAACAGGAGTCAGGAGCCGCTGGCAGGAGACAGCATGTCACCCAGGACTCTGCCGGTGCAGAATATGAGCAATGC
CATGTTCTTGCAGAAAACGCTTAGCCTGAGTTTCATAGGAGGTAATCACCAGACAACTGCAGAATGTAGAACACT
GAGCAGGACAACTGACCTGTCTCCTTCACATAGTCCATATCACCACAAATCACACAACAAAAAGGAGAAGAGATA

FIGURE 324B

TTTTGGGTTGAAAAAAAGTAAAAAGATAATTAGCTGCATTTCTTTAGTTATTTTGAACCCCAAATATTTCCTCAT
CTTTTTGTTGTTGTCATTGATGGTGGTGACATGGACTTGTTTATAGAGGACAGGTCAGCTCTCTGGCTCAATGAT
CTACATTCTGAAGTTGTCTGAAAATGTCTTCATGATTAAATTCAGCCTAAACTTTTTGCTGGGAACACTGCAGAG
ACAATGCTGTGAGTTTCCAACCTCAGCCCATCTGCGGGCAGAGAAGGTCTAGTTTGTCCATCACCATTATGATAT
CAGGACTGGTTACTTGGTTAAGGAGGGGTCTAGGAGATCTGTCCCTTTTAGAGACACCTTACTTATAATGAAGTA
CTTGGGAAAGCGGTTTTCAAGAGTATAAATATCCTGTATTCTAATGATCATCCTCTAAACATTTTATCATTTATT
AATCCTCCCTGCCTGTGTCTATTATTATATACATATCTCTACGCTGCAAATTTTGGGTCTCAATTTTTACTGTGC
CTTTGTTTTTACTAGTGTCTGCTGTTGCAAAAAGAAGAAAACATTCTCTGCCTGAGTTTTAATTTTTGTCCAAAG
TTAATTTTAATCTATACAATTAAAACCTTTTGCCTATC

FIGURE 325

MLRNELQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLNEHLQALLTPDEPDKSQGQDL
QEQLAEGCRLAQHLVQKLSPENDNDDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCSNSHGPYD
SNQPHRKTKITFEEDKVDSTLIGSSSHVEWEDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEGY
STLSIPPERTSVGSSEKGGPRGNRSQAQQGAAG

FIGURE 326

CTCCGCGGTCTTCTGAGCGGTCACGTGAACGGCTTCCTGCAGGCTGGCCATGGCGCTTCAAGTTCCCAAGGCTCC
GGGCTTCGCCCAGATGCTCAAGGAGGGAGCGAAACACTTTTCAGAATTAGAAGAGGCTGTGTATAGAAACATACA
AGCTTGCAAGGAGCTTGCCCAAACCACTCGTACAGCATATGGACGAAATGGAATGAAAAAAATGGTTATCAACTA
CTTGGAGAAGTTGTTTGTGACAAATGATGCAGCGACTATTTTAAGAGAACTAGAAGTACAGCATCCTGCTGCAAA
AATGACTGTAATGGCTTCTCATATGCAAGAGCAAGAAGTTGGAGATGGCACAAACATTGTTCTGGTATTTGCTGG
AGCTCTCCTGGAATTAGCTGAAGAACTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAAT
AGCTTGCAGAAAAGCTCATGAGATTCTTCCTAATTTGGTACGTTGTTCTGCAAAAAACCTTCGAGATGTTGATGA
AGTCTCATCTCTACTTCGTACCTCTGTAATGTGTAAACAATATGGTAATGAAGTATTTCTGGCCAAGCTTATTGT
TCAGGCATGCGTATCTATTTTTCCTGATTCTGGCCATTTCAAAGTTGATAACATCAGAGTTTGTAAAATTCTGGG
CTGTGGTATCACTTCCTCTTCAGTATTGCATGGCATGGTTTTTAAGAAGGAAACAGAAGGTGATGTACATCTGTC
AAAGATGCAAAAATAGCAGTGTACTCTTGTCCTTTTGATGGCATGATAACAGAAACTAAGGGAACAGTGTTGATA
AAGACTGATGAAGAATTGATGAATTTAAGTAAGGGAGAAGAAAATCTCATGGATGCATAAGTCAAAGCTATTGCT
GATACTGGTGCAAATGTTGTAGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGCAAACAAATATAAT
ATGATGTTAGTGAAGCTAAACTCAAAATGGGATGTCTGAAGACTCTGTAAAACAGTTGGTGCTACAGCTCTTCCT
AGATTGACACCTCCTGTCCTTGAAGAAATGGGACACTGAGACAGTGTTTACCTCTCAGAAGTTGGAGATACTCAG
GTGGTGGTTTTTAAGCATGAAAAGGAAGATGGCATCATTTCTACCATAGTACTTCAGGGCTCTACAGACAATCTG
ATGGATGACATAGAAAGGGCAGTAGATGATGGTGTTAATACTTTCAAAGTTCTTACAAGGGATAAACGTCTTGTA
CCCGGAGGTGGAGCAACAGAAATTGAATTAGCCAAACAGATCACATCATATGGAGAGACATGTCCTGGACTTGAA
CAGTACGCTATTAAGAAGTTTGCTGAGGCGTTTGAAGCTATTCCCCGTGCACTGGCAGAAATACTCTGGAGAAAA
CTCTGGAGTTAAGGCCAATGAAGTAATCTCTAAACTTTATGCAGTACCTCAAGAAGGAAATAAAAATGTTGGATT
AGATACTGAGGCTGTAGTCCCTGCTGTAACGGACATGTTGGAAGCTGGTGTTCTAGATACTTACCTGGGAAAACA
CTGGTCTATCAAACTCGCTGCTAATGCTGCAGTCACTGTACTTAGAGTGGGTCAGGTAATCATGGCAAAACCAGA
TGGTGGGCCCAAGCCTCCAAGTGGGAAGAAAGACTGGGATGATGACCAAAATGATTGAAATTGGCTTAATTTTTA
CTGTAGGTGAAGGCTGTATTTGTAGTAGTATTCTAAGAATCGCGTGATGTTTTCTTATTCTCCTTACATTAAGAG
GTATTTTGTGTTTGTATTCTTGGCTGGATGTTATAATAAACATATTGTTACTGTC

FIGURE 327

GGGCTTCGCCCAGATGCTCAAGGAGGGAGCGAAACACTTTTCAGAATTAGAAGAGGCTGTGTATAGAAACATACA
AGCTTGCAAGGAGCTTGCCCAAACCACTCGTACAGCATATGGACGAAATGGAATGAAAAAAATGGTTATCAACTA
CTTGGAGAAGTTGTTTGTGACAAATGATGCAGCGACTATTTTAAGAGAACTAGAAGTACAGCATCCTGCTGCAAA
AATGACTGTAATGGCTTCTCATATGCAAGAGCAAGAAGTTGGAGATGGCACAAACATTGTTCTGGTATTTGCTGG
AGCTCTCCTGGAATTAGCTGAAGAACTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAAT
AGCTTGCAGAAAAGCTCATGAGATTCTTCCTAATTTGGTACGTTGTTCTGCAAAAAACCTTCGAGATGTTGATGA
AGTCTCATCTCTACTTCGTACCTCTGTAATGTGTAAACAATATGGTAATGAAGTATTTCTGGCCAAGCTTATTGT
TCAGGCATGCGTATCTATTTTTCCTGATTCTGGCCATTTCAAAGTTGATAACATCAGAGTTTGTAAAATTCTGGG
AACAGTGTTGATAAAGACTGATGAAGAATTGATGAATTTAAGTAAGGGAGAAGAAAATCTCATGGATGCATAAGT
CAAAGCTATTGCTGATACTGGTGCAAATGTTGTAGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGC
AAACAAATATAATATGATGTTAGTGAAGCTAAACTCAAAATGGGATGTCTGAAGACTCTGTAAAACAGTTGGTGC
TACAGCTCTTCCTAGATTGACACCTCCTGTCCTTG

FIGURE 328

GTGGGTAGGAGCTTGCTTATAGAAAAGTGGAATCGAGTAGTCCTTGCTGGTGGAGCCGCTGCCGCCAGGGAACTC
AGGGCCGGCTCCTGTTCCTTCAAGAGTGCTGGAGGCCAAACTTGAAATACAAGTTTAATGTTCCTCGTCGGGCAA
AAGATAAGGATCCGATCTCCCCCGGCCCGGTGTGCAGCAGGAGCGACCAACCCCGACCCGGGTTAAAACTCCCAG
GGACTCTTCGCTGCTGCCACCTCTTGTTCTCTCCCCCGTTCCCACTCGGGGTCTCCCTCAGGGCCGGGAGGCACA
GCGGTCCCTGCTTGCTGAGGGGCTGGATGTACGCATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCC
CGGCGCCCGCAGAAGACTTGTGTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACC**ATG**ATC
ACTGGTGTGTTCAGCATGCGCTTGTGGACCCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACCAGCGG
CGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCTGAAGTTGAAAATG
GTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCCGCTGGAGGAGCAGGTAGAGTGGAAC
CCCCAGCTATTAGAGGTCCCACCCCAAACTCAGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCA
TATTCTCCTTACGACTCTCAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTG
GGCATGCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCTTTCACCA
ACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTGGAGTCCACCCGTTGTTTGCTG
GCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCCATCATCATCCACACTGATGAAGCAGATTCAGAAGTCTTGTAT
CCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGA
ATCTCAGAGGATTTGAAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTC
CTGGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATC
GAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGGGAAAGTCTTCAGATGGCAGTAGGC
CCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAG
CTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGG
CCACCGTTTGCTGTTGACCTGACCATGGAACTTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTAT
TACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGTTCTTGAATGCCATG
TCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACTCAGGTGATGGAAGTTGGAAATGAA
GAG**TAA**CTGATTTATAAAAGCAGGATGTGTTGATTTTAAAATAAAGTGCCTTTATACAATGCCAAAAAAAAAAAA
AAAAAAAAAAAA

FIGURE 329

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGARSPLKPLPLEEQVE
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQ
PGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLHILESNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ
LYYHGKEQVPRGCPDGLCPLDMFLNAMSVYTLSPEKYHALCSQTQVMEVGNEE

FIGURE 330

CTTAAAGTGAAATAATTTTTTGCAAAGGGGTTTCCTCGATTTGGAGCTTTTTTTTTCTTCCACCGTCATTTCTAA
CTCTTAAAACCAACTCAGTTCCATCATGGTGATGTTCAAGAAGATCAAGTCTTTTGAGGTGGTCTTTAACGACCC
TGAAAAGGTGTACGGCAGTGGCGAGAAGGTGGCTGGCCGGGTGATAGTGGAGGTGTGTGAAGTTACTCGTGTCAA
AGCCGTTAGGATCCTGGCTTGCGGAGTGGCTAAAGTGCATCCTCAACAACAATGTGCAGTGAGCATGTGGAAGAA
AAGAAGCAGCTTTACCTACTTGTTTCTTTTTGTCTCTCTTCCTGGACACTCACTTTTTCAGAGACTCAACAGTCT
CTGCAATGGAGTGTGGGTCCACCTTAGCCTCTGACTTCCTAATGTAGGAGGTGGTCAGCAGGCAATCTCCTGGGC
CTTAAAGGATGCGGACTCATCCTCAGCCAGCGCCCATGTTGTGATACAGGGGTGTTTGTTGGATGGTTTAAAAA
TAACTAGAAAAACTCAGGCCCATCCATTTTCTCAGATCTCCTTGAAAATTGAGGCCTTTTCGATAGTTTCGGGTC
AGGTAAAAATGGCCTCCTGGCGTAAGCTTTTCAAGGTTTTTTGGAGGCTTTTTGTAAATTGTGATAGGAACTTTG
GACCTTGAACTTATGTATCATGTGGAGAAGAGCCAATTTAACAAACTAGGAAGATGAAAAGGGAAATTGTGGCCA
AAACTTTGGGAAAA

FIGURE 331

TGACTTGCTCACTATCATGAACTCAAAAGAAACTAGCAATTTTTTAGACTTCTTTTGGGATCCTTGTACCGCATC
CTATACTGCTTTTATGTTCATGTGTGCATTTGTGTACATGTATACACATATTACTCCATAACGAAGCACAGTCTT
CTTTTATACCTTTCCTGGTTGGGGTAGTAGAGGAATTTTACAGCCTACAATCAGACACATCCAGAAGAAGAGTGG
AATATGTATGATACCTTAAAAATCAGCACATTTAACAAAGTATAACTTACTCATGGTTACAACTAAGTTAATGTT
TTTTCCCTTTATTTTTCAAAAGGCTCATTTTTCTCCATTTCTCTACTATCAAAGTCAAGAACTGCCCAATGGCTC
TGTCAAGGAGGCTCCAGCTCCTACTCCCACTTCTCTGGAAGTCTCAAGTCCACCAGATACTACAGAGGAAGAAGA
TCATAAGCCTAAACTCTGCAGGCTGGCTAAAGGTGAAAATGGCTATGGCTTTCACTTAAATGCGATTCGGGGTCT
GCCAGGCTCATTCATCAAAGAGGTACAGAAGGGCGGTCCTGCTGACTTGGCTGGGCTAGAGGATGAGGATGTCAT
CATTGAAGTGAATGGGGTGAATGTGCTAGATGAACCCTATGAGAAGGTGGTGGATAGAATCCAGAGCAGTGGGAA
GAATGTCACACTTCTAGTCTGTGGAAAGAAGGCCTATGATTATTTCCAAGCTAAGAAAATCCCTATTGTTTCCTC
CCTGGCTGATCCACTTGACACCCCTCCAGATTCTAAAGAAGGAATAGTGGTGGAGTCAAAGCATGACTCGCACAT
GGCAAAAGAACGGGCCCACAGTACAGCCTCACATTCTTCTTCCAATTCTGAAGATACAGAGATGTGATGAAAACA
AGCGGCTATTGCAGACGGCTAATTTATGCTTAACTTAGGAAGAGATAAGGTTCCTTGAGCACCAAAGATGATTCA
TAACTCTGTATAGGTGACAGCTGCTTATAAAAGCATCTTAGCAGATAAGCCTATTAAAATTGTGCTTTTGTAACA
ATGTTGTGGTTGCTAGAATAAATACCATTAACAAA

FIGURE 332

GTCCCAACTCTTGGACTCCATTTGCTATTCTCTTCTTTCTCCCCCACACCTATCTGGTGGTGGTAGTGGGCGTTT
ATATTTGCGTTCCTTTTCATTCATTTCTAAATCTCTTAAAAATTTTGGGTTGGGGGTATTGGGGAAGGCAGGAAA
GGGAAAAGGAGAGTAGTAGCTGAAGAGCAAGAGGAGGAC**ATG**GAGATGAAGAAGAAGATTAACCTGGAGTTAAGG
AACAGATCCCCGGAGGAGGTGACAGAGTTAGTCCTTGATAATTGCCTGTGTGTCAATGGGGAAATTGAAGGCCTG
AATGATACTTTCAAAGAACTAGAATTTCTGAGTATGGCTAATGTGGAACTAAGTTCGCTGGCCCGGCTTCCCAGC
TTAAATAAACTTCGAAAATTGGAGCTTAGTGATAATATAATTTCTGGAGGCTTGGAAGTCCTGGCAGAGAAATGT
CCAAATCTTACCTACCTCAATCTGAGTGGAAACAAAATAAAAGATCTCAGTACAGTAGAAGCTCTGCAAAATCTT
AAAAATTTGAAAAGTCTTGACCTGTTTAACTGTGAGATCACAAACCTGGAAGATTATAGAGAAAGTATTTTTGAA
CTACTGCAGCAAATCACATACTTAGATGGATTTGATCAGGAGGATAATGAAGCGCCGGACTCTGAAGAGGAGGAT
GATGAGGATGGAGATGAAGATGATGAAGAGGAAGAGGAAAATGAAGCTGGTCCACCGGAAGGATATGAGGAAGAG
GAGGAGGAAGAGGAAGAGGAGGATGAGGATGAGGATGAAGATGAAGATGAAGCAGGTTCAGAGTTGGGAGAGGGA
GAAGAGGAAGTGGGCCTCTCATACTTAATGAAAGAAGAAATTCAGGATGAAGAAGATGATGATGACTATGTTGAA
GAAGGGGAAGAAGAGGAAGAAGAGGAAGAAGGAGGTCTTCGAGGGGAGAAGAGGAAACGAGATGCTGAAGACGAT
GGAGAGGAAGAAGATGAC**TAG**ATCATTCTAAGACCAGATTCTCTAATGTTTCTGGGTGTGCAATAGAGTGATCAC
ATCTTTGTTTCTTCATGTACGATAGCTATCCCTACAGAAGATAATGTGTAACTTTTTATAGGAAAAGTGTGGTTT
TACTATTTTTGCCTTATCATTCCAAATAAGAACTAGTCTGTTAATGATCATATTGTATGTAGAGAAAAATTTTCA
TTGACTCCCATTGTGGAATTCCCTAGCAATTTATTTAGACTTAATTTTTTAAATTCAAGCTTACTGTATTAGTCA
TTTTTAGCCCATAATTAAAACATGATCACTTTTAAAAAAAAAAAAAAAAAAA

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FIGURE 333

MEMKKKINLELRNRSPEEVTELVLDNCLCVNGEIEGLNDTFKELEFLSMANVELSSLARLPSLNKLRKLELSDNI
ISGGLEVLAEKCPNLTYLNLSGNKIKDLSTVEALQNLKNLKSLDLFNCEITNLEDYRESIFELLQQITYLDGFDQ
EDNEAPDSEEEDDEDGDEDDEEEEENEAGPPEGYEEEEEEEEEEDEDEDEDEDEAGSELGEGEEEVGLSYLMKEE
IQDEEDDDDYVEEGEEEEEEEEGGLRGEKRKRDAEDDGEEEDD

FIGURE 334

GTGGGGTCGCGTTGCCACCCCACGCGGACTCCCCAGCTGGCGCGCCCCTCCCATTTGCCTGTCCTGGTCAGGCCC
CCACCCCCCTTCCCACCTGACCAGCC**ATG**GGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTCGGCCCGG
CCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCATTTTTCT
GGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGACCGACCGGTCAGATGCCCGGC
TCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACA
AGCTGCTTAAGAAGGCAGATGAGGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGA
TGGCCTATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCAC
TTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCCTATTACTTCCTGACTTCAGCCTTTCTGACAGCAGCCA
TTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATGCCTGTGAGAGGAGACGGTACTGGGCTTTGGGCC
TGGTGGTTGGGAGTCACCTACTGACATCGGGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCA
TCTATGCAGTCACTGTTTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCA
GCTCTTGTGTAAGGACTGACTACCTGGAC**TGA**TCGCCTGACAGATCCCACCTGCCTGTCCACTGCCCATGACTGA
GCCCAGCCCCAGCCCGGGGTCCATTGCCCACATTCTCTGTCTCCTTCTCGTCGGTCTACCCCACTACCTCCAGGG
TTTTGCTTTGTCCTTTTGTGACCGTTAGTCTCTAAGCTTTACCAGGAGCAGCCTGGGTTCAGCCAGTCAGTGACT
GGTGGGTTTGAATCTGCACTTATCCCCACCACCTGGGGACCCCCTTGTTGTGTCCAGGACTCCCCCTGTGTCAGT
GCTCTGCTCTCACCCTGCCCAAGACTCACCTCCCTTCCCCTCTGCAGGCCGACGGCAGGAGGACAGTCGGGTGAT
GGTGTATTCTGCCCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGCCTGGGGTGCCCTC
CTGATGTCCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAGGTTGCCAAGAAAAGGGACCTAGTTTA
GCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAAGGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGA
CTGGACATCTTGGTCTTTTTCTCAGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCCTAAACTGCCTTTT
TTTCTTTTTTGAGGTGGGGGGAGGGAGGAGGTATATTGGAACTCTTCTAACCTCCTTGGGCTATATTTTCTCTCC
TCGAGTTGCTCCTCATGGCTGGGCTCATTTCGGTCCCTTTCTCCTTGGTCCCAGACCTTGGGGGAAAGGAAGGAA
GTGCATGTTTGGGAACTGGCATTACTGGAACTAATGGTTTTAACCTCCTTAACCACCAGCATCCCTCCTCTCCCC
AAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGCCACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCAT
GACATCGTAGGGAAGGAGGGGAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTAT
AAACTGTATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATCAAGGTGATTGTGATTTTGACTAATAAA
AAAGAATTTGTAAAAAA

FIGURE 335

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYGLLIFG
AAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIH
GDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG
LWAFITAGGSLRSIQRSSCVRTDYLD

FIGURE 336

TTCCGGTGGGCTAGGTACTGAGCGCGCGAGGCTCTACAGAGTGAAGGTTTAAATCCAAGGTC**ATG**GCAAAACATC
TGAAGTTCATCGCCAGGACTGTGATGGTACAGGAAGGGAACGTGGAAAGCGCATACAGGACCCTAAACAGAATCC
TCACTATGGATGGGCTCATTGAGGACATTAAGCATCGGCGGTATTATGAGAAGCCATGCCGCCGGCGACAGAGGG
AAAGCTATGAAAGGTGCCGGCGGATCTACAACATGGAAATGGCTCGCAAGATCAACTTCTTGATGCGAAAGAATC
GGGCAGATCCGTGGCAGGGCTGC**TGA**GGCCTGTGGGTGGACACCCAGTGCGAAACCCTCATCCAGTTTTCTCTC
CATCTCTTTTCTTTGTACAATCCCATTTCCTATTACCATTCTCTGCAATAAACTCAAATCACATGTCTGCAAAAA

FIGURE 337

MAKHLKFIARTVMVQEGNVESAYRTLNRILTMDGLIEDIKHRRYYEKPCRRRQRESYERCRRIYNMEMARKINFL
MRKNRADPWQGC

FIGURE 338A

ATGTCTCCACTTCTGAGAAGCATCTGTGACATCACTGAAATTTTCAATCAGTATGTCTCTCATGATTGTGATGGA
GCAGCATTAACTAAGAAAGACCTGAAGAACCTCCTTGAAAGGGAATTTGGAGCTGTGCTTCGGAGACCACATGAC
CCTAAGACGGTAGATCTGATCCTGGAACTTCTGGATCTTGACAGTAATGGGCGTGTCGATTTCAACGAATTCCTC
CTATTTATTTTCAAAGTGGCTCAAGCTTGTTACTATGCTCTCGGCCAGGCCACGGGACTGGATGAGGAGAAGCGA
GCCCGGTGTGACGGAAAGGAGAGCCTGTTACAAGATCGCAGGCAAGAAGAAGACCAAAGGAGATTCGAGCCCCGG
GACAGACAACTGGAAGAAGAACCTGGGCAACGACGCAGGCAGAAGAGGCAGGAACAGGAGAGGGAGCTAGCTGAG
GGAGAGGAGCAAAGTGAGAAACAAGAGCGACTTGAACAGCGCGACAGGCAGCGCCGCGACGAGGAGCTGTGGCGG
CAAAGGCAAGAATGGCAAGAACGGGAAGAGCGCCGTGCAGAGGAAGAGCAGCTGCAGAGTTGCAAAGGTCACGAA
ACTGAGGAGTTTCCAGACGAAGAGCAACTGCGAAGGCGGGAGCTGCTGGAGCTGAGGAGGAAGGGCCGCGAGGAG
AAACAGCAGCAAAGGCGAGAGCGGCAAGACAGAGTGTTCCAGGAGGAAGAAGAGAAAGAGTGGAGGAAGCGCGAG
ACAGTGCTCCGGAAGGAAGAAGAGAAGCGCGAACGTTGGCTGAAGCTCGAGGAGGAGGAGAGGCGCGAGCAGCAG
GAGAGGCGCGAGCAGCAACTAAGGCGGGAGCAAGAGGAGAGGCGCGAGCAGCGGCTGAAGCGCCAGGAGGAGGAA
GAGAGGCTCCAGCAGCGGTTGAGGAGCGAGCAACAACTAAGACGCGAGCAGGAGGAGAGGCGCGAGCAGCTGCTG
AAGCGCGAGGAGGAGAAGAGGCTCGAGCAGGAGAGGCGAGAGCAGCGGCTGAAGCGCGAGCAGGAGGAGAGGCGC
GATCAGCTGCTGAAGCGCGAGGAGGAGAGGCGCCAGCAGCGGCTGAAGCGCGAGCAGGAAGAGAGGCTCGAGCAG
CGACTGAAGCGCGAGGAGGTGGAGAGACTCGAGCAGGAGGAGAGGCGCGAGCAGCGGCTGAAGCGCGAGGAGCCG
GAGGAAGAGAGGCGCCAGCAGCTGCTGAAGAGCGAGGAGCAGGAGGAGAGGCGCCAGCAGCAACTAAGGCGCGAG
CAGCAGGAAAGGCGCGAGCAGCGGCTGAAGCGCGAGGAGGAGGAAGAGAGGCTCGAGCAGCGGCTGAAGCGCGAG
CATGAGGAAGAGAGGCGCGAGCAGGAGCTAGCTGAGGAGGAGCAGGAACAGGCCCGGGAGCGGATTAAGAGCCGC
ATCCCGAAGTGGCAGTGGCAGCTAGAAAGCGAGGCCGACGCACGGCAAAGCAAAGTCTACTCGAGGCCCCGCAAG
CAGGAAGGGCAGAGGCGCCGCCAAGAGCAGGAGGAAAAGAGGCGGCGCCGGGAGAGTGAGCTGCAATGGCAGGAG
GAGGAACGGGCTCACCGGCAGCAGCAGGAAGAGGAGCAGCGCCGGGACTTCACATGGCAGTGGCAGGCGGAGGAA
AAGAGCGAGAGGGGGCCGTCAGAGGCTGTCGGCCAGGCCCCCATTGCGGGAGCAGCGGGAGAGGCAGCTGAGGGCC
GAGGAGCGCCAGCAGCGGGAACAACGGTTTCTCCCGGAGGAGGAGGAGAAGGAGCAGCGGCGCCGCCAGCGACGC
GAGAGGGAGAAAGAGCTGCAGTTCCTGGAGGAAGAGGAGCAGCTCCAGCGGCGGGAGCGTGCCCAACAGCTCCAG
GAGGAGGAGGACGGCCTCCAGGAGGATCAGGAGAGGAGGCGAAGCCAGGAGCAGCGCCGCGACCAAAAATGGAGG
TGGCAACTAGAAGAAGAAAGGAAGAGACGCCGCCACACGCTGTACGCCAAGCCAGCCCTACAAGAGCAGCTGAGG
AAGGAACAGCAGCTGCTGCAGGAGGAGGAGGAGGAGCTACAGAGAGAGGAGCGCGAGAAGAGAAGGCGCCAAGAA
CAGGAGAGACAATACCGCGAGGAAGAGCAGCTGCAGCAGGAGGAAGAGCAGCTGCTGAGAGAGGAACGGGAGAAA
AGAAGACGCCAGGAGCGGGAAAGGCAATATCGGAAGGATAAGAAGCTGCAGCAGAAGGAAGAGCAGCTGCTGGGA
GAGGAACCGGAGAAGAGAAGGCGCCAGGAGCGGGAGAAAAAATACCGCGAGGAAGAGGAGTTGCAGCAGGAGGAA
GAGCAGCTGCTGAGAGAGGAACGGGAGAAGAGAAGGCGCCAGGAGTGGGAGAGGCAGTACCGCAAAAAAGACGAG
CTGCAGCAGGAAGAAGAGCAGCTGCTGAGAGAGGAACGGGAGAAAAGAAGACTCCAGGAGCGGGAGAGGCAATAT
CGGGAGGAAGAGGAGCTGCAGCAGGAGGAAGAGCAGCTGCTGGGAGAGGAACGGGAGACGAGAAGGCGCCAGGAG
CTGGAGAGGCAATATCGGAAGGAAGAGGAGCTGCAGCAGGAGGAAGAGCAGCTGCTGAGAGAGGAACCGGAGAAG
AGAAGGCGCCAGGAGCGGGAGAGGCAATGCAGAGAGAATGAACAGTTCCGGCAGTTGGAAGATTCCCAGCTGCGC
GACAGACAATCCCAGCAAGATCTGCAGCACCTGCTGGGTGAACAGCAAGAGCGAGATCGTGAGCAAGAGAGGAGG
CGCTGGCAGCAGCGCGACAGGCATTTCCCAGAGGAAGAACAGCTGGAGCGAGAAGAGCAAAAGGAAGCCAAAAGG
CGCGACAGGAAGTCCCAAGAGGAAAAGCAGTTGCTGAGAGAGGAAAGAGAAGAGAAGAGACGCCGTCAAGAGACA
GACAGAAAATTCCGCGAGGAGGAACAGCTGCTCCAGGAAAGGGAGGAACAGCCGCTGCGCCGCCAAGAGCGTGAC
AGAAAATTCCGCGAAGAGGAACTGCGCCATCAGGAACAAGGGAGAAAATTCCTCGAGGAGGAACAGCGGCTGCGC
CGCCAGGAACGGGAGAGAAAATTCCTTAAGGAGGAACAGCAGCTGCGCTGCCAGGAGCGCGAGCAACAGCTGCGT
CAGGACCGCGACAGAAAATTCCGCGAGGAGGAACAGCAGCTGAGCCGCCAAGAGCGTGACAGAAAATTCCGTGAA
GAGGAACAGCAGGTGCGCCGCCAGGAACGAGAGAGAAAATTCCTGGAGGAGGAACAGCAGCTGCGCCAGGAGCGT
CACAGAAAATTCCGCGAAGAGGAACAGCTGCTCCAGGAAAGGGAAGAACAGCAGCTGCACCGCCAAGAGCGTGAC
AGAAAATTCCTGGAGGAGGAACAACAGCTGCGCCGCCAAGAGCGTGACAGAAAATTCCGCGAACAGGAACTGCGC
AGTCAGGAACCAGAGAGAAAATTCCTCGAGGAGGAACAGCAGCTGCACCGCCAGCAACGGCAGAGAAAATTCCTC
CAGGAGGAACAGCAGCTGCGCCGCCAGGAGCGCGGGCAACAGCGGCGTCAGGACCGTGACAGAAAATTCCGCGAG

FIGURE 338B

GAGGAACAGCTGCGCCAGGAGAGGGAGGAACAGCAGCTGAGCCGCCAAGAGCGTGACAGAAAATTCCGTTTAGAG
GAACAGAAAGTGCGCCGCCAGGAACAAGAGAGAAAATTCATGGAGGACGAACAGCAGCTGCGCCGCCAGGAGGGC
CAACAACAGCTGCGCCAGGAGCGCGACAGAAAATTCCGCGAAGACGAACAGCTGCTCCAGGAAAGGGAAGAACAG
CAGCTGCACCGCCAAGAGCGTGACAGAAAATTCCTCGAGGAGGAACCGCAGCTGCGCCGCCAGGAGCGCGAACAA
CAGCTGCGTCACGACCGCGACAGAAAATTCCGTGAAGAGGAACAGCTGCTCCAGGAAGGGGAGGAACAGCAGCTG
CGCCGCCAAGAGCGTGACAGAAAATTCCGCGAAGAGGAACAGCAGCTCCGCCGTCAGGAACGAGAGAGAAAATTC
CTCCAGGAGGAACAGCAGCTGCGCCGCCAGGAACTGGAGAGAAAATTCCGTGAGGAGGAACAGCTGCGCCAAGAA
ACGGAGCAAGAGCAGCTGCGCCGCCAAGAACGCTACAGAAAAATCCTAGAGGAAGAGCAGCTCCGTCCGGAAAGG
GAAGAACAGCAGCTGCGCCGCCAGGAGCGCGACAGAAAATTCCGCGAGGAGGAACAGCTCCGCCAGGAGAGGGAG
GAACAGCAGCTGCGCAGCCAAGAGTCTGACAGAAAATTCCGCGAGGAGGAACAGCTACGCCAGGAGAGGGAAGAA
CAGCAGCTGCGCCCCCAACAGCGTGACGGAAAGTATCGCTGGGAAGAAGAGCAGCTCCAACTTGAGGAACAAGAG
CAGAGGCTGCGGCAGGAGCGAGACCGGCAGTACCGGGCGGAGGAGCAGTTTGCCACGCAGGAGAAGAGTCGTCGT
GAGGAACAAGAACTATGGCAAGAAGAGGAGCAGAAACGTCGCCAGGAACGGGAAAGGAAATTACGGGAAGAACAC
ATCCGCCGCCAGCAGAAGGAGGAACAGAGGCACCGCCAAGTCGGGGAGATAAAATCCCAAGAAGGGAAGGGCCAT
GGGCGGCTTCTGGAGCCCGGCACTCATCAGTTTGCCAGTGTCCCAGTGCGCTCCAGCCCTCTCTATGAGTACATC
CAAGAGCAGAGATCTCAATACCGCCCT<u>TAA</u>

FIGURE 339

MSPLLRSICDITEIFNQYVSHDCDGAALTKKDLKNLLEREFGAVLRRPHDPKTVDLILELLDLDSNGRVDFNEFL
LFIFKVAQACYYALGQATGLDEEKRARCDGKESLLQDRRQEEDQRRFEPRDRQLEEEPGQRRRQKRQEQERELAE
GEEQSEKQERLEQRDRQRRDEELWRQRQEWQEREERRAEEEQLQSCKGHETEEFPDEEQLRRRELLELRRKGREE
KQQQRRERQDRVFQEEEEKEWRKRETVLRKEEEKRERWLKLEEEERREQQERREQQLRREQEERREQRLKRQEEE
ERLQQRLRSEQQLRREQEERREQLLKREEEKRLEQERREQRLKREQEERRDQLLKREEERRQQRLKREQEERLEQ
RLKREEVERLEQEERREQRLKREEPEEERRQQLLKSEEQEERRQQQLRREQQERREQRLKREEEEEERLEQRLKRE
HEEERREQELAEEEQEQARERIKSRIPKWQWQLESEADARQSKVYSRPRKQEGQRRRQEQEEKRRRRESELQWQE
EERAHRQQQEEEQRRDFTWQWQAEEKSERGRQRLSARPPLREQRERQLRAEERQQREQRFLPEEEEKEQRRRQRR
EREKELQFLEEEEQLQRRERAQQLQEEEDGLQEDQERRRSQEQRRDQKWRWQLEEERKRRRHTLYAKPALQEQLR
KEQQLLQEEEEELQREEREKRRRQEQERQYREEEQLQQEEEQLLREEREKRRRQERERQYRKDKKLQQKEEQLLG
EEPEKRRRQEREKKYREEEELQQEEEQLLREEREKRRRQEWERQYRKKDELQQEEEQLLREEREKRRLQERERQY
REEEELQQEEEQLLGEERETRRRQELERQYRKEEELQQEEEQLLREEPEKRRRQERERQCRENEQFRQLEDSQLR
DRQSQQDLQHLLGEQQERDREQERRRWQQRDRHFPEEEQLEREEQKEAKRRDRKSQEEKQLLREEREEKRRRQET
DRKFREEEQLLQEREEQPLRRQERDRKFREEELRHQEQGRKFLEEEQRLRRQERERKFLKEEQQLRCQEREQQLR
QDRDRKFREEEQQLSRQERDRKFREEEQQVRRQERERKFLEEEQQLRQERHRKFREEEQLLQEREEQQLHRQERD
RKFLEEEQQLRRQERDRKFREQELRSQEPERKFLEEEQQLHRQQRQRKFLQEEQQLRRQERGQQRRQDRDRKFRE
EEQLRQEREEQQLSRQERDRKFRLEEQKVRRQEQERKFMEDEQQLRRQEGQQQLRQERDRKFREDEQLLQEREEQ
QLHRQERDRKFLEEEPQLRRQEREQQLRHDRDRKFREEEQLLQEGEEQQLRRQERDRKFREEEQQLRRQERERKF
LQEEQQLRRQELERKFREEEQLRQETEQEQLRRQERYRKILEEEQLRPEREEQQLRRQERDRKFREEEQLRQERE
EQQLRSQESDRKFREEEQLRQEREEQQLRPQQRDGKYRWEEEQLQLEEQEQRLRQERDRQYRAEEQFATQEKSRR
EEQELWQEEEQKRRQERERKLREEHIRRQQKEEQRHRQVGEIKSQEGKGHGRLLEPGTHQFASVPVRSSPLYEYI
QEQRSQYRP

FIGURE 340

GGGCAAGGCTGGGCCGGGAAGGGCGTGGGTTGAGGAGAGGCTCCAGACCCGCACGCCGCGCGCACAGAGCTCTCA
GCGCCGCTCCCAGCCACAGCCTCCCGCGCCTCGCTCAGCTCCAAC**ATG**GCAAAAATCTCCAGCCCTACAGAGACT
GAGCGGTGCATCGAGTCCCTGATTGCTGTCTTCCAGAAGTATGCTGGAAAGGATGGTTATAACTACACTCTCTCC
AAGACAGAGTTCCTAAGCTTCATGAATACAGAACTAGCTGCCTTCACAAAGAACCAGAAGGACCCTGGTGTCCTT
GACCGCATGATGAAGAAACTGGACACCAACAGTGATGGTCAGCTAGATTTCTCAGAATTTCTTAATCTGATTGGT
GGCCTAGCTATGGCTTGCCATGACTCCTTCCTCAAGGCTGTCCCTTCCCAGAAGCGGACC**TGA**GGACCCCTTGGC
CCTGGCCTTCAAACCCACCCCCTTTCCTTCCAGCCTTTCTGTCATCATCTCCACAGCCCACCCATCCCCTGAGCA
CACTAACCACCTCATGCAGGCCCCACCTGCCAATAGTAATAAAGCAATGTCACTTTTTTAAAACATGAAA

FIGURE 341

MAKISSPTETERCIESLIAVFQKYAGKDGYNYTLSKTEFLSFMNTELAAFTKNQKDPGVLDRMMKKLDTNSDGQL
DFSEFLNLIGGLAMACHDSFLKAVPSQKRT

FIGURE 342

CCGGTGGGGCGGGAAGCCCGGCTTCTGGGGAGGTGCCGCCCCTCCACTGGCGCAGGCCGCCGAGACCCCCAGACG
GACCTCCTAGGGCTAATCTGATAGTGCCTCTGAGGTCGATAGGACTCCACGTGCCACTCCCTGCAGGGTCATCCA
GCAAGTAATTCCTAGACCCGTAGGTGGCCGCAGAGCCGGTTACCTCTGGTTCTGCGCCAGCGTGCCCCACCCGCA
GGACGGCCGGGTTCTTTGATTTGTACACTTTCTAAAACCAAACCCGAGAGGAAGGGCAGGCTCAGGGTGGGGATG
CCCTGAAATATTCGAGAGCAGGACCGTTTCTACTGAAGAGAAGTTTACAAGAACGCTCTGTCTGGGGCGGGCGAG
GCCTCTGCGAGGCGGGTCCGGGAGCGAGGGCAGGGCGTGGCCGCGCGCCCGGGGTCGGGGGAGTCGGGGGCAGG
AAGAGGGGGAGGAGACAGGGCTGGGGGAGCGCCCTGCCGAGCGCCCGCCAGGCTCCTCCCGCTCCCGCGCCGCCT
CCCTCTACCCACCCGCCGCACGTACTAAGGAAGGCGCACAGCCCGCCGCGCTCGCCTCTCCGCCCCGCGTCCAGC
TCGCCCAGCTCGCCCAGCGTCCGCCGCGCCTCGGCCAAGGCTTCAACGGACCACACCAAA**ATG**CCATCTCAAATG
GAACACGCCATGGAAACCATGATGTTTACATTTCACAAATTCGCTGGGGATAAAGGCTACTTAACAAAGGAGGAC
CTGAGAGTACTCATGGAAAAGGAGTTCCCTGGATTTTTGGAAAATCAAAAAGACCCTCTGGCTGTGGACAAAATA
ATGAAGGACCTGGACCAGTGTAGAGATGGCAAAGTGGGCTTCCAGAGCTTCTTTTCCCTAATTGCGGGCCTCACC
ATTGCATGCAATGACTATTTTGTAGTACACATGAAGCAGAAGGGAAAGAAG**TAG**GCAGAAATGAGCAGTTCGCTC
CTCCCTGATAAGAGTTGTCCCAAAGGGTCGCTTAAGGAATCTGCCCCACAGCTTCCCCCATAGAAGGATTTCATG
AGCAGATCAGGACACTTAGCAAATGTAAAAATAAAATCTAACTCTCATTTGACAAGCAGAGAAAGAAAAGTTAAA
TACCAGATAAGCTTTTGATTTTTGTATTGTTTGCATCCCCTTGCCCTCAATAAATAAAGTTCTTTTTTAGTTCC

FIGURE 343

MPSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDLDQCRDGKVGFQSFFSL
IAGLTIACNDYFVVHMKQKGKK

FIGURE 344

CGGCTGAAGCGCCGCCGGCGGGGCTCACTGTGGTGGTGTGAGTGGGAGGCGGCGGCGCTGGTGGCTGCAGCTGGG
GTGAGGCGCGAGGCGGCGCACTCGACGGCTGACTGGAGCAGCGGTAAAGGCGAGGATGGAGACCGAAGGATATAA
GTCAAAGAGTACAGCAGAAA**ATG**TCTACTGAACGGACTTCTTGGACAAGCCTGTCCACCATTCAGAAAATAGCCC
TGGGCCTTGGGATCCCAGCCAGTGCAACAGTTGCCTATATCCTATACCGCAGGTATAGGGAAAGCAGAGAAGAGC
GGCTGACATTTGTTGGGGAAGATGACATTGAGATAGAGATGCGGGTTCCCCAGGAGGCTGTGAAACTCATCATTG
GCCGGCAAGGAGCCAATATTAAACAGCTGCGGAAACAGACAGGTGCTCGGATTGATGTGGACACAGAGGATGTAG
GCGATGAGCGAGTGCTGCTTATCAGTGGTTTTCCTGTTCAGGTGTGCAAGGCCAAAGCAGCAATCCATCAGATCC
TGACAGAGAATACCCCAGTGTCTGAGCAGCTTTCAGTTCCCCAGAGATCTGTGGGCAGAATCATAGGGAGAGGCG
GCGAGACAATTCGTTCTATCTGTAAGGCATCTGGAGCCAAAATTACCTGTGACAAAGAATCAGAAGGGACATTAC
TACTATCAAGACTTATAAAAATCTCAGGAACACAGAAGGAAGTGGCAGCAGCCAAGCATTTGATACTGGAGAAAG
TTTCAGAAGATGAAGAACTTCGGAAGAGAATTGCTCATTCTGCAGAAACCAGGGTCCCACGCAAACAGCCAATCA
GTGTGAGAAGAGAAGACATGACAGAGCCAGGTGGAGCTGGAGAGCCAGCATTATGGAAAAACACCAGTTCTAGCA
TGGAGCCGACTGCACCCCTGGTGACTCCTCCACCCAAAGGAGGAGGCGACATGGCTGTGGTAGTGTCAAAGGAAG
GTTCCTGGGAGAAACCTAGTGATGACAGCTTTCAGAAGTCTGAAGCCCAGGCCATCCCAGAGATGCCCATGTTTG
AAATCCCCAGTCCTGACTTCAGTTTTCATGCTGATGAGTACCTAGAAGTCTACGTTTCTGCTTCTGAGCACCCTA
ACCACTTCTGGATCCAGATCGTTGGCTCCCGCAGCCTGCAATTGGATAAGCTTGTCAATGAGATGACCCAGCACT
ATGAGAATAGTGTGCCTGAAGACTTGACTGTGCATGTAGGAGACATTGTAGCAGCACCTTTACCTACAAATGGTT
CCTGGTATCGAGCCCGGGTCCTCGGCACCTTGGAGAATGGGAACTTGGACCTCTATTTTGTTGACTTTGGAGATA
ATGGAGATTGCCCACTGAAGGACCTCAGGGCTCTCAGGAGTGACTTCCTAAGCCTTCCATTTCAAGCAATAGAAT
GTAGTCTGGCACGGATTGCTCCCTCAGGTGACCAGTGGGAAGAGGAAGCTTTGGATGAGTTTGATAGACTCACTC
ATTGTGCTGACTGGAAGCCTCTGGTAGCCAAGATCTCTAGCTATGTCCAGACTGGGATCTCAACTTGGCCAAAGA
TCTACTTATATGATACTAGCAATGGGAAGAAACTTGATATTGGGCTAGAATTAGTACACAAAGGATACGCAATTG
AGCTTCCTGAAGACATAGAAGAAAACAGAGCTGTCCCAGACATGTTGAAGGACATGGCCACAGAAACAGATGCCT
CTCTCAGCACGTTGCTCACTGAGACCAAAAAGAGCTCTGGAGAGATAACACATACCCTGTCCTGCCTCAGCTTAT
CAGAAGCTGCTTCCATGTCTGGTGATGATAACCTTGAAGATGACTACTTACTCGGAAGTCTGGGCTTCAGTTTGC
TCAGCCATCTGCTTTGCTGTATGTTGCCTGCAATGAACTCGCTGAAGCATGCTCAGCCCTGGAACTGGTGCTACC
AGAGTTCCGTAGGGAACCTTTACTCTTTAGAGGTTCCC**TGA**TATAAATCATTCATAAGACTTCCTACCCTGGAAA
ATGAGTAATGTCTCATTCTTACCTGCAGTTTGTTACTATGTATAAAAGTCTTTTTCTTTAATATGCCTTTAAGTC
TTACCTGTTTACAGCCCATTCTGATGGGTTCTTTGTCATTCTGTTAGTATAACCCAGTACTTTTCCTGCTGCCTG
GAATGCCCTCTTCTATGTTACCTATTCTGTCCGTTGAGATGCCCCAACTTGGGCCAAAGCCAAGAGATCTATGTG
CCTTCTCTGGTTTTCTCCACATCTATAGCACCTCAACTGAAATATATGGATAAAAACAGCCTAACAAAAAAAAAA
AAAAAA

FIGURE 345

MSTERTSWTSLSTIQKIALGLGIPASATVAYILYRRYRESREERLTFVGEDDIEIEMRVPQEAVKLIIGRQGANI
KQLRKQTGARIDVDTEDVGDERVLLISGFPVQVCKAKAAIHQILTENTPVSEQLSVPQRSVGRIIGRGGETIRSI
CKASGAKITCDKESEGTLLLSRLIKISGTQKEVAAAKHLILEKVSEDEELRKRIAHSAETRVPRKQPISVRREDM
TEPGGAGEPALWKNTSSSMEPTAPLVTPPPKGGGDMAVVVSKEGSWEKPSDDSFQKSEAQAIPEMPMFEIPSPDF
SFHADEYLEVYVSASEHPNHFWIQIVGSRSLQLDKLVNEMTQHYENSVPEDLTVHVGDIVAAPLPTNGSWYRARV
LGTLENGNLDLYFVDFGDNGDCPLKDLRALRSDFLSLPFQAIECSLARIAPSGDQWEEEALDEFDRLTHCADWKP
LVAKISSYVQTGISTWPKIYLYDTSNGKKLDIGLELVHKGYAIELPEDIEENRAVPDMLKDMATETDASLSTLLT
ETKKSSGEITHTLSCLSLSEAASMSGDDNLEDDYLLGSLGFSLLSHLLCCMLPAMNSLKHAQPWNWCYQSSVGNL
YSLEVP

FIGURE 346

TTTTTTCTGCTACCGTGACTAAG**ATG**GAAGCGTTTTTGGGGTCGCGGTCCGGACTTTGGGCGGGGGGTCCGGCCC
CAGGACAGTTTTACCGCATTCCGTCCACTCCCGATTCCTTCATGGATCCGGCGTCTGCACTTTACAGAGGTCCAA
TCACGCGGACCCAGAACCCCATGGTGACCGGGACCTCAGTCCTCGGCGTTAAGTTCGAGGGCGGAGTGGTGATTG
CCGCAGACATGCTGGGATCCTACGGCTCCTTGGCTCGTTTCCGCAACATCTCTCGCATTATGCGAGTCAACAACA
GTACCATGCTGGGTGCCTCTGGCGACTACGCTGATTTCCAGTATTTGAAGCAAGTTCTCGGCCAGATGGTGATTG
ATGAGGAGCTTCTGGGAGATGGACACAGCTATAGTCCTAGAGCTATTCATTCATGGCTGACCAGGGCCATGTACA
GCCGGCGCTCGAAGATGAACCCTTTGTGGAACACCATGGTCATCGGAGGCTATGCTGATGGAGAGAGCTTCCTCG
GTTATGTGGACATGCTTGGTGTAGCCTATGAAGCCCCTTCGCTGGCCACTGGTTATGGTGCATACTTGGCTCAGC
CTCTGCTGCGAGAAGTTCTGGAGAAGCAGCCAGTGCTAAGCCAGACCGAGGCCCGCGACTTAGTAGAACGCTGCA
TGCGAGTGCTGTACTACCGAGATGCCCGTTCTTACAACCGGTTTCAAACCGCCACTGTCACCGAAAAAGGTGTTG
AAATAGAGGGACCATTGTCTACAGAGACCAACTGGGATATTGCCCACATGATCAGTGGCTTTGAA**TGA**AATACAG
ATGCATTATCCAGAACTGAAGTTGCCCTACTTTTAACTTTGAACTTGGCTAGTTCAAAGATAGACTCTTCTTTTG
TAAAGTAAATAAATTCTTCAAAATG

FIGURE 347

MEAFLGSRSGLWAGGPAPGQFYRIPSTPDSFMDPASALYRGPITRTQNPMVTGTSVLGVKFEGGVVIAADMLGSY
GSLARFRNISRIMRVNNSTMLGASGDYADFQYLKQVLGQMVIDEELLGDGHSYSPRAIHSWLTRAMYSRRSKMNP
LWNTMVIGGYADGESFLGYVDMLGVAYEAPSLATGYGAYLAQPLLREVLEKQPVLSQTEARDLVERCMRVLYYRD
ARSYNRFQTATVTEKGVEIEGPLSTETNWDIAHMISGFE

FIGURE 348

AATTGGAGGAGTTGTTGTTAGGCCGTCCCGGAGACCCGGTCGGGAGGGAGGAAGGTGGCAAG**ATG**GTGTTGGAAA
GCACTATGGTGTGTGTGGACAACAGTGAGTATATGCGGAATGGAGACTTCTTACCCACCAGGCTGCAGGCCCAGC
AGGATGCTGTCAACATAGTTTGTCATTCAAAGACCCGCAGCAACCCTGAGAACAACGTGGGCCTTATCACACTGG
CTAATGACTGTGAAGTGCTGACCACACTCACCCCAGACACTGGCCGTATCCTGTCCAAGCTACATACTGTCCAAC
CCAAGGGCAAGATCACCTTCTGCACGGGCATCCGCGTGGCCCATCTGGCTCTGAAGCACCGACAAGGCAAGAATC
ACAAGATGCGCATCATTGCCTTTGTGGGAAGCCCAGTGGAGGACAATGAGAAGGATCTGGTGAAACTGGCTAAAC
GCCTCAAGAAGGAGAAAGTAAATGTTGACATTATCAATTTTGGGGAAGAGGAGGTGAACACAGAAAAGCTGACAG
CCTTTGTAAACACGTTGAATGGCAAAGATGGAACCGGTTCTCATCTGGTGACAGTGCCTCCTGGGCCCAGTTTGG
CTGATGCTCTCATCAGTTCTCCGATTTTGGCTGGTGAAGGTGGTGCCATGCTGGGTCTTGGTGCCAGTGACTTTG
AATTTGGAGTAGATCCCAGTGCTGATCCTGAGCTGGCCTTGGCCCTTCGTGTATCTATGGAAGAGCAGCGGCAGC
GGCAGGAGGAGGAGGCCCGGCGGGCAGCTGCAGCTTCTGCTGCTGAGGCCGGGATTGCTACGACTGGGACTGAAG
ACTCAGACGATGCCCTGCTGAAGATGACCATCAGCCAGCAAGAGTTTGGCCGCACTGGGCTTCCTGACCTAAGCA
GTATGACTGAGGAAGAGCAGATTGCTTATGCCATGCAGATGTCCCTGCAGGGAGCAGAGTTTGGCCAGGCGGAAT
CAGCAGACATTGATGCCAGCTCAGCTATGGACACATCTGAGCCAGCCAAGGAGGAGGATGATTACGACGTGATGC
AGGACCCCGAGTTCCTTCAGAGTGTCCTAGAGAACCTCCCAGGTGTGGATCCCAACAATGAAGCCATTCGAAATG
CTATGGGCTCCCTGGCCTCCCAGGCCACCAAGGACGGCAAGAAGGACAAGAAGGAGGAAGACAAGAAG**TGA**GACT
GGAGGGAAAGGGTAGCTGAGTCTGCTTAGGGGACTGCATGGGAAGCACGGAATATAGGGTTAGATGTGTGTTATC
TGTAACCATTACAGCCTAAATAAAGCTTGGCAACTTTT

FIGURE 349

MVLESTMVCVDNSEYMRNGDFLPTRLQAQQDAVNIVCHSKTRSNPENNVGLITLANDCEVLTTLTPDTGRILSKL
HTVQPKGKITFCTGIRVAHLALKHRQGKNHKMRIIAFVGSPVEDNEKDLVKLAKRLKKEKVNVDIINFGEEEVNT
EKLTAFVNTLNGKDGTGSHLVTVPPGPSLADALISSPILAGEGGAMLGLGASDFEFGVDPSADPELALALRVSME
EQRQRQEEEARRAAAASAAEAGIATTGTEDSDDALLKMTISQQEFGRTGLPDLSSMTEEEQIAYAMQMSLQGAEF
GQAESADIDASSAMDTSEPAKEEDDYDVMQDPEFLQSVLENLPGVDPNNEAIRNAMGSLASQATKDGKKDKKEED
KK

FIGURE 350

CTGGTGAGGGGCTGCAGGTGGCGGCGCAGTCTCGGTAGGCGGT**ATG**AGTTTGGCTGGGGGCCGGGCACCCCGGAA
GACCGCTGGGAACCGGCTTTCTGGGCTTTGGAGGCAGAGGAGGAAGATGAGTTCTACCAGACGACTTATGGGGG
TTTCACAGAGGAATCCGGAGATGATGAGTATCAAGGGGACCAGTCAGACACAGAGGACGAAGTGGACTCTGACTT
TGACATTGATGAAGGGGATGAACCATCCAGTGATGGAGAAGCAGAAGAGCCAAGAAGGAAGCGCCGAGTAGTCAC
CAAGGCCTATAAGGAACCTCTCAAGAGCTTAAGGCCTCGAAAGGTCAACACCCCGGCTGGTAGCTCTCAGAAGGC
GCGAGAAGAGAAGGCACTACTGCCATTAGAACTACAAGATGACGGCTCTGACAGTCGGAAGTCTATGCGTCAGTC
TACAGCTGAGCATACACGACAAACGTTCCTTCGGGTACAGGAGAGGCAGGGCCAGTCAAGACGGCGAAAGGGGCC
CCACTGTGAGCGGCCACTAACCCAGGAGGAACTGCTCCGGGAGGCCAAGATCACAGAAGAGCTTAATTTACGGTC
ACTGGAGACATATGAGCGGCTCGAGGCTGATAAAAAGAAGCAGGTTCATAAGAAGCGGAAGTGCCCCGGGCCCAT
AATCACCTATCATTCAGTGACAGTGCCACTTGTTGGGGAGCCAGGCCCCAAGGAAGAGAACGTTGACATAGAAGG
ACTTGATCCTGCTCCCTCGGTGTCTGCATTGACTCCTCATGCTGGGACTGGACCCGTCAACCCCCCTGCTCGCTG
CTCACGTACCTTCATCACTTTTAGTGATGATGCAACTTTCGAGGAATGGTTCCCCCAAGGGCGGCCCCCAAAAGT
CCCTGTTCGTGAGGTCTGTCCAGTGACCCATCGTCCAGCCCTATACCGGGACCCTGTTACAGACATACCCTATGC
CACTGCTCGAGCCTTCAAGATCATTCGTGAGGCTTACAAGAAGTACATTACTGCCCATGGACTGCCGCCCACTGC
CTCAGCCCTGGGCCCCGGCCCGCCACCTCCTGAGCCCCTCCCTGGCTCTGGGCCCCGAGCCTTGCGCCAGAAAAT
TGTCATTAAA**TGA**AGAGATGTCTAGTCCTCAGAAACTTCTTTCCTGCCCTGATTGGGGCTCTTGCTGTTCCGTTT
CTTCTCCCTGCTTCTCCCCTTTGTCATCTCTGATCTTTGCCTAATCTGTTTCTTTTTCCTTTTCCCCTAGTTCTT
ACAGGTTTCGTTGTGTTTTTTAATCTAATAAAATAGAAAGATCCCTTTT

FIGURE 351

MSLAGGRAPRKTAGNRLSGLLEAEEEDEFYQTTYGGFTEESGDDEYQGDQSDTEDEVDSDFDIDEGDEPSSDGEA
EEPRRKRRVVTKAYKEPLKSLRPRKVNTPAGSSQKAREEKALLPLELQDDGSDSRKSMRQSTAEHTRQTFLRVQE
RQGQSRRRKGPHCERPLTQEELLREAKITEELNLRSLETYERLEADKKKQVHKKRKCPGPIITYHSVTVPLVGEP
GPKEENVDIEGLDPAPSVSALTPHAGTGPVNPPARCSRTFITFSDDATFEEWFPQGRPPKVPVREVCPVTHRPAL
YRDPVTDIPYATARAFKIIREAYKKYITAHGLPPTASALGPGPPPPEPLPGSGPRALRQKIVIK

FIGURE 352

CCTGGCTTTGTGCATTGGGTTCTGGTGCCTGATGGACACATTTTTCCAGTTACAGGCCGAATGGTCTCAATGTAG
CTGAAGAACTGTGCCCACTGATCAGTATTACGTATTGCAAATGCAGGAGGTGGCTGTATCTGACAGACCCAGGCC
TTCCAGCTCCGACAGATCCAGTTCTGGGATGGGCATCCTCCAGAAAAGAAAGGAACTGTACTGGCTACTCACAGG
GTCCCTCATAGCTTCCTAGAAAGAAACCACTTGTCAGTCTTCATGCTACAGCAACTTCTTTGTGGCCCATGGCCT
TTCCTTGCTTAGATACTCCACATACTGTTCTCCCCGCAGGGGCGGCGGCCTTGAGGGGCTGCAGAGGCACCCTCC
CACGTCCCGCGCAGTGCAGTGCCTCCGCAGTCCAGAGGGGAGCAGTGCGCCGGGCTCCGAGCCGGACGGGTTTCG
TAATCGCGTCGCCGCCGCTTCCGCCCTCAGCCGGCCCCACCTCTGCCGGCTCGTACTCGGCTCCCCCACCTCGCC
GCAGAGCTAGCCCGGGAAGCCCACACTGGCGGCCACGGAGCAGAGTCCCTCACCCCCACCAGCTGTAGCTGAACG
TCTGGATGGTGGAGAAGAGCAGGTGAGGCCGTGCAGTTGGTCCCCTGGCCCGCCTGCCGCGCCGGCCGGGCCAGG
CGGAGACACACCGGATGCGGGGTGTGGGGGAGGCGGGTGTCCTGGGCTGCAGAGATGCTGGGGTGGTGGGAAAGG
GGTGCGCGCCCGGGGTGGCCGTAGTCATCCACGCTCCTGGGGTGCGCAGGCTGAGGCCGCTGAAGAGTAGAAGGA
AAAGAAGGAACTGGAATGTTGGGGGAGGTGGGAGGGAGAGGGTCCGAAAGATTCCCAGAGAGGTCCCAGTCCGGT
TAAGGGTTGAGAACAGCAGAGAACTTCTAGGTAGAGTTGTGTAGTGGGGGGAGACAGATACGGAATCTGTGTGAT
TGAATATATTTGGGGAGGGGAGGCTTAGGGCCTAGCCCTCTTTCCTCTTAAGCCCCCAGAAGACCTTTCCTGGGG
AAGGGAAGGTTGGTGTTGGGCCTGTCACTTGGCTGAAATATGGAGTCCACACCGCTTCTCCAGAGTCCCTCAGCA
GCCCTCCATGTCTCGGGGTCTCCACACAGGGACCAGCTGCTGCCCCGGGCTTCTAGCCAGAATTGCCCATGCCAT
TCTCTCGATTCTTTCTTTCTCTCCAGCTGCTTCATGTGAGGGCTTGTCAGGCCGCGGGTTGGAGGCCTTAGGGCC
AGAGGCGGTGGGACCGGGAGAACCGGTTTGGGGCCCGAACAGGACCAGAGAACTAGCCTGTACATCCTTCCTCCC
TGGCACCTCTTTCCCATCCCTTCTGCTCACCTCCCAACAGCTCTGAGACCCTCAAGTCCTAGTATGATCTTGGTG
GGGGCGGGGGGTGGCTTTCCCGGTTCCATATTTCACTCTTGCCATTTGGAACTCAGAGAGGTCGAGTTCTGAGCA
CCACTTGGCTCTCAGGACGTGGCCTTATGAGGTCTAATCCTCATCCCTCCTGTTGTTTTCTCAGCCCCTTCCCTA
TTCACTGTGGGGTTGGATTCGGGTGGCTCTTCCGCCTGGGCTGACCAGCTCAGGACTTCATTTTTCCTCAACCCA
CTCTCTTCTGGCTGCTTTAAAGAAGAGTGGCCGCCAGTGGCTCTTACTTCCTTTTCTGGCTTTGTTCCCATCCCC
CACTGCCCTGCGCTACCATCACATTCACCCTGACCTGTCTTCTTCACACTCTGACCCCACCCTCAAGTTTCAGAG
ACCCTAATGTCCTAGGGAATGGAATTTCCTGGTCACTTCTCGTCATCATTGGTCATTTCATGCCAAGTCCCACAC
ACACGCTTTCCCTCCACCCAGCTCTGGTCAGGTCCCTGGAAAAGAAACAGAAATGGCCTTGTTCTCTCCACTGCC
CCTTTCCCTCTCTCCTTCTCCTCCCCCTCTCTTCTCTTCCCTCCCAGCACTATCCACCTCTGTCCCTCAGCTTTG
AGCAGAGTGGGGGATGTTGAGGGAGAGTCCAGTCACAGTACAGCCTGCCTGCTGGTGTTGGGGGTTTCCTCTAAT
TCTTCATTTTTCCCCAACCCTTACCACCTGCCACCACCACCATCAGGACAAACCCTATGACTGACTCACTGACGT
CCCACTGACCACAGCTCCCCTCTCTGGACAGCGTGTTTTAGCTTCCGCTCCTTCTGGTTACTCCTCCCTTCCAGT
GGTGAGAAGAGAAGAGAAAGCCCAGCCTCCTGGGTTCTCCCCTCCCCTAGAAGCTACATTTGAGTGTTTGTGTGA
TCTCATCTCAAGGCTGTT

FIGURE 353

AGTCAGCACGGGGGTGCTGGAAGAGATCGGGAATAATAGCGCAGACCAATGAGCCTAGGGAGATGCTTTCATCGT
CTCTCCTTCCCTCAAGTGTTCTGGAACCTATCATTTGAATTAGCCGAGTCAGGCAGGAGGGGGCGGGGAATCCTT
CCGCCCTTCTTAGGAGGGGCTGCATTGCAGGGGGAGAGTGAACTGACAGACTCAGTCACTGAAGAGGGAAAAGGA
GTGAGAAGACAAAGCCGTCAAAGCCCCAACAGCTTTGTATTTCTCCAGCCCGGCGCAGACCCCGGAGCTCCCGAG
GCACTCCCTCCATCTTTGGAACACGCCAGTAATTGATTGATAACAGGAAGCTATGAGGGACCCTGTGAGTAGCCA
GTACAGTTCCTTTCTTTTCTGGAGGATGCCCATCCCAGAACTGGATCTGTCGGAGCTGGAAGGCCTGGGTCTGTC
AGATACAGCCACCTACAAGGTCAAAGACAGCAGCGTTGGCAAAATGATCGGGCAAGCAACTGCAGCAGACCAGGA
GAAAAACCCTGAAGGTGATGGCCTCCTTGAGTACAGCACCTTCAACTTCTGGAGAGCTCCCATTGCCAGCATCCA
CTCCTTCGAACTGGACTTGCTCTAAGGCCAAGACTTCTCTCTCCCATCACCTTGCCCTCATTGTCTTCCCTCTCA
AGCCCCTTCCTTTCCACTCCTTTCCCATTTTAATCTTGTTCTCTCCCTACTGTGTTGGTGGTGCTGATGAATCTG
CCAGAGTTGAGTTCTATGTATTTATTTATCTATCTGTCTACTCCATTTCTCTCAAAAGCCCTCAAGTCACAAAGT
AAATGGTTCAAGCAATGGAGTACTGGGTCACAGGGATTCCTCCTTTCCCCCCCAAATATTAACTCCAGAAACTAG
GCCTGACTGGGGACACCTGAGAGTAGTATAGTAGTGCAAAATGGAAGACTGATTTTTGACTCTATTATAATCAGC
TTCAGAGATTCCTTAAACCTTCCTAATTTCCTGCTCCAGGGCAGTAAACACAAATATTTCTTCAAGGGGTGATGA
AAACCTCGGAAGTTTTAATTTGAGGTTATCTGCTACGAAACAGTATTTCTAAAAGGCTAAAGTGATAAGTCTCTT
GCTTTTTTTTGATCCTGCTCTTATATTCTTTTTTTTCCTCAGAGAAATCAGGAGGGTAGTTAGAGGTATAAAACA
GGAGGAAATATTATGGAAAATGAAAATAGGGAAAATAATTGAATCATTTTAGAAGTAGCTAATTTCTTTTCTCAA
AAGAGTGTCCCTTCTTCACACCTACTCACTTTACAACTTTGCTCCTAACTGTGGGTTGAAAACTCTAGCTAAAGA
AAGTTATCAAATCTTAACATGCATTCCTACTATTATGATAGTTTTTAAGGTTTCAATTCAATCTTCTGAACGGCA
TAAGTCCTATTTTAGCCTTACCTCCTGCATTTGCAATACGTAATACTGATCAGTGGGCACAGTTCTTCAGCTACA
TTGAGACCCTGAAATGAACAATTATATTCTGACTCGACATCTTGTCCCCAATCCTTCCAAAAATATTGATGGTGA
TTTGTGCTACCATTTACTCGTTTATTTAATAAAGACATTCAATCCC

FIGURE 354

GGGGGCGGGGCGACGCCGGACTCCGGAGCGCCCGCTTACGCAGTTCCTCCCGGGGTCGGAGGCCGATTCGCCGTG
TGGCGGGTTCGAGTCCCGCCTCCTGACTCTGGCCTCTAGTCCCTGAGTCCCGGGCGGGCTGCATTCGTCGGGGAA
ACCTCTCCTCGACCAGGGGCACCTCTACTCGACCAGGGGCGACGGCGTACTTTGGGCTTCATC**ATG**GAGGACTAC
CTGCAGGGTTGTCGAGCTGCTCTGCAGGAGTCCCGACCTCTACATGTTGTGCTGGGAAATGAAGCCTGTGATTTG
GACTCCACAGTGTCTGCTCTTGCCCTGGCTTTTTACCTAGCAAAGACAACTGAGGCTGAGGAAGTCTTTGTGCCA
GTTTTAAATATAAAACGTTCTGAACTACCTCTGCGAGGTGACATTGTCTTCTTTCTTCAGAAGGTTCATATTCCA
GAGAGTATCTTGATTTTTCGGGATGAGATTGACCTCCATGCATTATACCAGGCTGGCCAACTCACCCTCATCCTT
GTCGACCATCATATCTTATCCAAAAGTGACACAGCCCTAGAGGAGGCAGTAGCAGAGGTGCTAGACCATCGACCC
ATCGAGCCGAAACACTGCCCTCCCTGCCATGTTTCAGTTGAGCTGGTGGGGTCCTGTGCTACCCTGGTGACCGAG
AGAATCCTGCAGGGGGCACCAGAGATCTTGGACAGGCAAACTGCAGCCCTTCTGCATGGAACCATCATCCTGGAC
TGTGTCAACATGGACCTTAAAATTGGAAAGGCAACCCCAAAGGACAGCAAATATGTGGAGAAACTAGAGGCCCTT
TTCCCAGACCTACCCAAGAGAAATGATATATTTGATTCCCTACAAAAGGCAAAGTTTGATGTATCAGGACTGACC
ACTGAGCAGATGCTGAGAAAAGACCAGAAGACTATCTATAGACAAGGCGTCAAGGTGGCCATTAGTGCAATATAT
ATGGATTTGGAGGCCTTTCTGCAGAGGTCTAACCTCCTTGCAGATCTCCATGCTTTCTGCCAGGCTCACAGCTAT
GATGTCCTGGTTGCCATGACTATCTTTTTCAACACTCACAATGAGCCAGTGCGGCAGTTGGCTATTTTCTGTCCC
CATGTGGCACTCCAAACAACGATCTGTGAAGTCCTGGAACGCTCCCACTCTCCACCCCTGAAGCTGACCCCTGCC
TCAAGTACCCACCCTAACCTCCATGCCTATCTTCAAGGCAACACCCAGGTCTCTCGAAAGAAACTTCTGCCCCTG
CTCCAGGAAGCCCTGTCAGCATATTTTGACTCCATGAAGATCCCTTCAGGACAGCCTGAGACAGCAGATGTGTCC
AGGGAGCAAGTGGACAAGGAATTGGACAGGGCAAGTAACTCCCTGATTTCTGGCCTGAGTCAAGATGAGGAGGAC
CCTCCGCTGCCCCCGACGCCCATGAACAGCTTGGTGGATGAGTGCCCTCTAGATCAGGGGCTGCCTAAACTCTCT
GCTGAGGCCGTCTTCGAGAAGTGCAGTCAGATCTCACTGTCACAGTCTACCACAGCCTCCCTGTCCAAGAAG**TGA**

CTGTTGAGAGGCGAGGAGGTAGTGGGTGAGGCTACCTGACTCACTTCAAATGCATGTTTTGAGATGTTTGGAGAT
TCAGCAATTCTGTCTTCATTGCTCCAGGATCTGGTATACTGTTCTCATAAAACTGAGAGGAGAAAAAAAGTGAAA
GAAAGCAGCTGCTTTAAGAATGGTTTTCCACCTTTTCCCCCTAATCTCTACCAATCAGACACATTTTATTATTTA
AATCTGCACCTCTCTCTATTTTATTTGCCAGGGGCACGATGTGACATATCTGCAGTCCCAGCACAGTGGGACAAA
AAGAATTTAGACCCCAAAAGTGTCCTCGGCATGGATCTTGAACAGAACCAGTATCTGTCATGGAACTGAACATTC
ATCGATGGTCTCCATGTATTCATTTATTCACTTGTTCATTCAAGTATTTATTGAATACCTGCCTCAAGCTAGAGA
GAAAAGAGAGTGCGCTTTGGAAATTTATTCCAGTTTTCAGCCTACAGCAGATTATCAGCTCGGTGACTTTTCTTT
CTGCCACCATTTAGGTGATGGTGTTTGATTCAGAGATGGCTGAATTTCTATTCTTAGCTTATTGTGACTGTTTCA
GATCTAGTTTGGGAACAGATTAGAGGCCATTGTCTTCTGTCCTGATCAGGTGGCCTGGCTGTTTCTTTGGATCCC
TCTGTCCCAGAGCCACCCAGAACCCTGACTCTTGAGAATCAAGAAAACACCCAGAAAGGCCTTAATGACCTCATA
GGCACTCTTCCAAAAAGACAACAGAACTGGAATGAGAGGCCTGGGTCTGTCTCCTGCCTTAGCAGGCCTATCAAT
TTCTTGTCAATCTCTTTTTTTCCTTGCTCACATTAAAAGGAAGCATGGAGTTCTAATGCTCCCATAAACTATGTA
TTTTGGCAAGACACTTCACTACTCCAGGTCTCACTTTCCCCATCTGTAAAACAGGGTTTGGACTAGGTGTTCCCT
GGTATTCTGTGATCTGCCTCTTGCTGCCATTCTTTCTCTCCTCTGCTTCTCTGTATTTTTCTTCTGTTATCCCTG
GGGGTGCTCAGGTTCACTTGATTGTCTGTATTTCTGTGTGGTTGTAGCAAGGACTCAGCCTCATGTAGCACGAAT
AGGGGTGTGGTTCATGGCGTGTTGACCCAGCAGAGCACTCCCTCCCACTAACTTGTTCTGCATGTGTAGAGTCTC
CCCATTTTTTTTAACGCAACCCTTTCCCCTTTTTCCTACCCCACAGCTCTGTTCCATGTAAGTTGCCAACAGTTT
CACTGAACAGTGGGGTATGTGATGGTTTTGGCATGACATCTTCAGTATGAGGGGGACAGTTTGACTTCACTTTGA
GGGTGTGATGTCTGTAGCTATGTGGAAGGTAAAAATAGTGGTGTGATCATGAACCAAAGGAATTTATGTTTTGTA
ACTTGGGTACTTTATTTTGCATTTTGTTATACTATTAAATAATTTTTTCCTGTT

FIGURE 355

MEDYLQGCRAALQESRPLHVVLGNEACDLDSTVSALALAFYLAKTTEAEEVFVPVLNIKRSELPLRGDIVFFLQK
VHIPESILIFRDEIDLHALYQAGQLTLILVDHHILSKSDTALEEAVAEVLDHRPIEPKHCPPCHVSVELVGSCAT
LVTERILQGAPEILDRQTAALLHGTIILDCVNMDLKIGKATPKDSKYVEKLEALFPDLPKRNDIFDSLQKAKFDV
SGLTTEQMLRKDQKTIYRQGVKVAISAIYMDLEAFLQRSNLLADLHAFCQAHSYDVLVAMTIFFNTHNEPVRQLA
IFCPHVALQTTICEVLERSHSPPLKLTPASSTHPNLHAYLQGNTQVSRKKLLPLLQEALSAYFDSMKIPSGQPET
ADVSREQVDKELDRASNSLISGLSQDEEDPPLPPTPMNSLVDECPLDQGLPKLSAEAVFEKCSQISLSQSTTASL
SKK

FIGURE 356

GAAACAAGCACTGGATTCCATATCCCACTGCCAAAACCGCATGGTTCAGATTATCGCTATTGCAGCTTTCATCAT
AATACACACCTTTGCTGCCGAAACGAAGCCAGACAACAGATTTCCATCAGCAGGATGTGGGGGCTCAAGGTTCTG
CTGCTACCTGTGGTGAGCTTTGCTCTGTACCCTGAGGAGATACTGGACACCCACTGGGAGCTATGGAAGAAGACC
CACAGGAAGCAATATAACAACAAGGTGGATGAAATCTCTCGGCGTTTAATTTGGGAAAAAAACCTGAAGTATATT
TCCATCCATAACCTTGAGGCTTCTCTTGGTGTCCATACATATGAACTGGCTATGAACCACCTGGGGGACATGACC
AGTGAAGAGGTGGTTCAGAAGATGACTGGACTCAAAGTACCCCTGTCTCATTCCCGCAGTAATGACACCCTTTAT
ATCCCAGAATGGGAAGGTAGAGCCCCAGACTCTGTCGACTATCGAAAGAAAGGATATGTTACTCCTGTCAAAAAT
CAGGGTCAGTGTGGTTCCTGTTGGGCTTTTAGCTCTGTGGGTGCCCTGGAGGGCCAACTCAAGAAGAAAACTGGC
AAACTCTTAAATCTGAGTCCCCAGAACCTAGTGGATTGTGTGTCTGAGAATGATGGCTGTGGAGGGGGCTACATG
ACCAATGCCTTCCAATATGTGCAGAAGAACCGGGGTATTGACTCTGAAGATGCCTACCCATATGTGGGACAGGAA
GAGAGTTGTATGTACAACCCAACAGGCAAGGCAGCTAAATGCAGAGGGTACAGAGAGATCCCCGAGGGGAATGAG
AAAGCCCTGAAGAGGGCAGTGGCCCGAGTGGGACCTGTCTCTGTGGCCATTGATGCAAGCCTGACCTCCTTCCAG
TTTTACAGCAAAGGTGTGTATTATGATGAAAGCTGCAATAGCGATAATCTGAACCATGCGGTTTTGGCAGTGGGA
TATGGAATCCAGAAGGGAAACAAGCACTGGATAATTAAAAACAGCTGGGGAGAAAACTGGGGAAACAAAGGATAT
ATCCTCATGGCTCGAAATAAGAACAACGCCTGTGGCATTGCCAACCTGGCCAGCTTCCCCAAGATGTGACTCCAG
CCAGCCAAATCCATCCTGCTCTTCCATTTCTTCCACGATGGTGCAGTGTAACGATGCACTTTGGAAGGGAGTTGG
TGTGCTATTTTTGAAGCAGATGTGGTGATACTGAGATTGTCTGTTCAGTTTCCCCATTTGTTTGTGCTTCAAATG
ATCCTTCCTACTTTGCTTCTCTCCACCCATGACCTTTTTCACTGTGGCCATCAGGACTTTCCCTGACAGCTGTGT
ACTCTTAGGCTAAGAGATGTGACTACAGCCTGCCCCTGACTGTGTTGTCCCAGGGCTGATGCTGTACAGGTACAG
GCTGGAGATTTTCACATAGGTTAGATTCTCATTCACGGGACTAGTTAGCTTTAAGCACCCTAGAGGACTAGGGTA
ATCTGACTTCTCACTTCCTAAGTTCCCTTCTATATCCTCAAGGTAGAAATGTCTATGTTTTCTACTCCAATTCAT
AAATCTATTCATAAGTCTTTGGTACAAGTTTACATGATAAAAAGAAATGTGATTTGTCTTCCCTTCTTTGCACTT
TTGAAATAAAGTATTTATC

FIGURE 357

MWGLKVLLLPVVSFALYPEEILDTHWELWKKTHRKQYNNKVDEISRRLIWEKNLKYISIHNLEASLGVHTYELAM
NHLGDMTSEEVVQKMTGLKVPLSHSRSNDTLYIPEWEGRAPDSVDYRKKGYVTPVKNQGQCGSCWAFSSVGALEG
QLKKKTGKLLNLSPQNLVDCVSENDGCGGGYMTNAFQYVQKNRGIDSEDAYPYVGQEESCMYNPTGKAAKCRGYR
EIPEGNEKALKRAVARVGPVSVAIDASLTSFQFYSKGVYYDESCNSDNLNHAVLAVGYGIQKGNKHWIIKNSWGE
NWGNKGYILMARNKNNACGIANLASFPKM

FIGURE 358

GGCACGAGGAAGGAAC**ATG**GCCCTGTATCAGAGGTGGCGGTGTCTCCGGCTCCAAGGTTTACAGGCTTGCAGGCT
ACACACGGCAGTTGTGTCGACCCCTCCACGCTGGTTGGCAGAGCGGCTTGGCCTTTTTGAGGAGCTGTGGGCTGC
TCAGGTAAAGAGATTAGCAAGCATGGCACAGAAGGAACCCCGGACTATTAAGATATCACTTCCTGGAGGCCAGAA
AATTGATGCTGTGGCATGGAACACAACCCCCTACCAACTAGCCCGGCAGATCAGTTCAACACTGGCAGATACTGC
AGTGGCTGCTCAAGTGAATGGAGAACCTTATGATCTGGAGCGGCCCTTGGAGACAGATTCTGACCTCAGATTTCT
GACATTCGATTCCCCAGAGGGGAAAGCAGTGTTCTGGCACTCCAGCACCCATGTCCTGGGGGCAGCAGCTGAACA
ATTCCTAGGTGCTGTTCTCTGCAGAGGTCCAAGTACAGAATATGGCTTTTACCATGATTTCTTCCTGGGAAAGGA
GAGGACAATCCGGGGCTCAGAGCTGCCTGTTTTGGAGCGGATTTGCCAGGAACTTACAGCTGCTGCTCGACCCTT
CCGGAGGCTAGAGGCTTCACGGGATCAGCTTCGCCAGTTGTTCAAGGATAACCCCTTTAAGCTTCACTTGATTGA
GGAGAAAGTGACAGGTCCAACAGCAACAGTATATGGGTGTGGCACATTGGTTGACCTTTGCCAGGGCCCCCACCT
TCGGCATACTGGACAGATTGGAGGACTGAAGCTGCTATCGAACTCATCATCCTTATGGAGGTCTTCAGGGGCCCC
AGAGACACTGCAGAGAGTGTCAGGGATTTCCTTCCCCACAACAGAATTGCTGAGGGTCTGGGAAGCATGGAGGGA
GGAAGCAGAATTGCGGGACCACCGGCGCATTGGGAAGGAACAGGAGCTCTTCTTCTTCCATGAACTGAGCCCTGG
GAGCTGCTTCTTCCTGCCACGAGGGACAAGGGTGTATAATGCACTAGTGGCGTTTATCAGGGCTGAGTATGCCCA
TCGTGGTTTCTCCGAGGTGAAAACTCCCACACTGTTTTCTACGAAGCTCTGGGAACAGTCAGGGCACTGGGAGCA
TTATCAGGAAGACATGTTTGCCGTGCAGCCCCCAGGCTCTGACAGGCCTCCCAGCTCCCAGAGTGACGATTCTAC
CAGGCATATCACAGATACACTCGCCCTCAAGCCTATGAACTGCCCTGCACACTGCCTGATGTTCGCCCACCGGCC
CAGATCCTGGCGGGAACTGCCCCTGCGACTAGCTGACTTTGGGGCTCTACACCGGGCCGAAGCCTCTGGTGGTCT
GGGGGGACTGACCCGACTGCGGTGCTTCCAGCAGGATGACGCTCACATCTTCTGTACAACAGATCAGCTGGAAGC
AGAGATCCAAAGCTGTCTTGATTTCCTCCGTTCCGTCTATGCCGTTCTTGGCTTCTCCTTCCGCCTGGCACTGTC
CACCCGGCCATCTGGCTTCCTGGGGGACCCTTGCCTTTGGGACCAGGCCGAACAGGTCCTTAAACAGGCCCTGAA
GGAATTTGGAGAACCCTGGGACCTCAACTCTGGAGATGGTGCCTTCTATGGACCTAAGATTGACGTGCACCTCCA
CGATGCCCTGGGCCGGCCACATCAGTGTGGGACAATTCAGCTTGACTTCCAACTGCCCCTGAGATTTGACCTCCA
GTATAAGGGGCAGGCGGGTGCCCTGGAGCGTCCAGTCCTCATTCACCGAGCAGTGCTCGGTTCTGTGGAAAGACT
GTTGGGAGTGCTGGCAGAAAGCTGCGGGGGGAAATGGCCACTGTGGCTGTCCCCGTTCCAGGTGGTGGTCATCCC
TGTGGGGAGTGAGCAAGAGGAATACGCCAAAGAGGCACAGCAGAGCCTGCGGGCTGCAGGACTGGTCAGTGACCT
GGATGCAGACTCTGGACTGACCCTCAGCCGGAGAATCCGCCGGGCCCAGCTTGCCCACTACAATTTTCAGTTTGT
GGTTGGCCAGAAAGAGCAAAGTAAGAGAACAGTGAACATTCGGACTCGAGATAATCGTCGCCTTGGGGAGTGGGA
CTTGCCTGAGGCTGTGCAGCGACTGGTGGAGCTACAGAACACGAGGGTCCCAAATGCCGAAGAAATTTTC**TGA**GC
CTTTGTACATAGATGAGGCAAAAACCTGCGAGTGCCATCAGCCTCCCTCACATGGGAGACCCCAACCCAGCTGAC
AATGTGGAGCCCCCAGAACTTCAGAACTGTGTGGAGGCACATGTCTGCTCTCCTGAAAAGAGACTTGGTTTGGGG
ACCCCACAAAAGGAGGGAAGCTGTAGCTGTTTGGATGTGAGGAGAATGAAACTACAAAAAAAAAAAAAAAAAA

FIGURE 359

MALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEELWAAQVKRLASMAQKEPRTIKISLPGGQKIDAVA
WNTTPYQLARQISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAVFWHSSTHVLGAAAEQFLGAV
LCRGPSTEYGFYHDFFLGKERTIRGSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHLIEEKVTG
PTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSSLWRSSGAPETLQRVSGISFPTTELLRVWEAWREEAELR
DHRRIGKEQELFFFHELSPGSCFFLPRGTRVYNALVAFIRAEYAHRGFSEVKTPTLFSTKLWEQSGHWEHYQEDM
FAVQPPGSDRPPSSQSDDSTRHITDTLALKPMNCPAHCLMFAHRPRSWRELPLRLADFGALHRAEASGGLGGLTR
LRCFQQDDAHIFCTTDQLEAEIQSCLDFLRSVYAVLGFSFRLALSTRPSGFLGDPCLWDQAEQVLKQALKEFGEP
WDLNSGDGAFYGPKIDVHLHDALGRPHQCGTIQLDFQLPLRFDLQYKGQAGALERPVLIHRAVLGSVERLLGVLA
ESCGGKWPLWLSPFQVVVIPVGSEQEEYAKEAQQSLRAAGLVSDLDADSGLTLSRRIRRAQLAHYNFQFVVGQKE
QSKRTVNIRTRDNRRLGEWDLPEAVQRLVELQNTRVPNAEEIF

FIGURE 360

ACCAGATCCCAGAGGCTGAACACCTCGACCTTCTCTGCACAGCAGGTCCAGCATCCTTTGAAGCATGAGTTCTTA
CCAGCAGAAGCAGACCTTTACCCCACCACCTCAGCTTCAACAGCAGCAGGTGAAACAACCCAGCCAGCCTCCACC
TCAGGAAATATTTGTTCCCACAACCAAGGAGCCATGCCACTCAAAGGTTCCACAACCTGGAAACACAAAGATTCC
AGAGCCAGGCTGTACCAAGGTCCCTGAGCCAGGCTGTACCAAGGTCCCTGAGCCAGGCTGTACCAAGGTCCCTGA
GCCAGGTTGTACCAAGGTCCCTGAGCCAGGCTGTACCAAGGTCCCTGAGCCAGGTTGTACCAAGGTCCCTGAGCC
AGGCTACACCAAGGTCCCTGAACCAGGCAGCATCAAGGTCCCTGACCAAGGCTTCATCAAGTTTCCTGAGCCAGG
TGCCATCAAAGTTCCTGAGCAAGGATACACCAAAGTTCCTGTGCCAGGCTACACAAAGCTACCAGAGCCATGTCC
TTCAACGGTCACTCCAGGCCCAGCTCAGCAGAAGACCAAGCAGAAGTAATTTGGTGCACAGACAAGCCCTTGAGA
AGCCAACCACCAGATGCTGGACACCCTCTTCCCATCTGTTTCTGTGTCTTAATTGTCTGTAGACCTTGTAATCAG
CACATTGTCACCCCAAGCCATAGTCTCTCTCTTATTTGTATCCTAAAAATACGTACTATAAAGCTTTTGTTCACA
CACACTCTGAAGAATCCTGTAAGCCCCTGAATTAAGCAGAAAGTCTTCATGGCTTTTCTGGTCTTCGGCTGCTCA
GGGTTCATCTGAAGATTCGAATGAAAAGAAATGCATGTTTCCTGCTCTTCCCTCATTAAATTGCTTTTAATTCCA

FIGURE 361

CAGTTCTAAGGGACCATACAGAGTATTCCTCTCTTCACACCAGGACCAGTCACTGTTGCAGC**ATG**AGTTCCCAGC
AGCAGAAGCAGCCTTGCACCCCACCCCCTCAGCTTCAGCAGCAGCAGGTGAAACAGCCTTGCCAGCCTCCACCTC
AGGAACCATGCATCCCCAAAACCAAGGAGCCCTGCCACCCCAAGGTGCCTGAGCCCTGCCACCCCAAAGTGCCCG
AGCCCTGCCAGCCCAAGGTTCCAGAGCCATGCCACCCCAAGGTGCCTGAGCCCTGCCCTTCAATAGTCACTCCAG
CACCAGCCCAGCAGAAGACCAAGCAGAAG**TAA**TGTGGTCCACAGCCATGCCCTTGAGGAGCCGGCCACCAGATGC
TGAATCCCCTATCCCATTCTGCGTATGAGTCCCATTTGCCTTGCAATTAGCATTCTGTCTCCCCCAAAAAAGAAT
GTGCTATGAAGCTTTCTTTCCTACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTT
TCAGCTGCTCAGAATTCATCTGAAGAGAGACTTAAGATGAAAGCAAATGATTCAGCTCCCTTATACCCCCATTAA
ATTCACTTTCAATTCCA

FIGURE 362

MSSQQQKQPCTPPPQLQQQQVKQPCQPPPQEPCIPKTKEPCHPKVPEPCHPKVPEPCQPKVPEPCHPKVPEPCPS
IVTPAPAQQKTKQK

FIGURE 363

ATGACAATTGCAAAGGTGGTAGAAGCTCATGACCAGGTGACAGACAGACACAGAACACATCAACAGAATTGTCTG
ATGGTTCCCAGGGAGAGAGCTGCTGCTCTTTCTTCCGAAGCTCTGGGAGCTGGCACAGCTGAGGACTTCCTTTTC
TTAGCTCCACCTGGACAGTGGCAGTATGGCAGCCTCAGAAAGGGAATCTTTTGCTGTCACAGATCATCACAGGCA
GGCCACAGGTTAAGGAGAAAGAAGCTCCCTGTGCATCCATGGAAGGCTTTGGTGAGAAGATGCAAGTGGAGCTGT
GGAACGAGGGAGAGAGCTGCTGCTCTTTCTTCCGAAGCTCTGGGAGCTGGCACAGCCCAGGACTTCCTTTGCTCA
GTCTCCACCTGGACAGTGGCAGTATGGCAGCCTCAGAAAAGAAACTTTTTGCTGTCAGGGATCATCATGGGCAGA
TTACTGGCTAAGGAGAAAGAAGCTCCCTGTGTATCCATGGTAGGCTTTGATGAGAAGATGAAGGTGGAGCTGTGG
AACGAGATACTTTATTCAGGGAGTGAAAGAAAAGTGACAATTGCACAGGTGGTAGAAGCTCATGCCCAGGTGAAA
GACAGACACAGAACACATCAACAGAATTCTCTGATGGTTCCCAGGCACACAGCTGCAGCTCTTTCTGCTGAAGCT
CTGGGAACTGACAAAGCCAAGGTTCCTTTGCTCAGTCTCCACCTGGACAGTGGCATCTCCACCTGGACAGTGGCA
ATATGGCAGCCTCAGAAAGGAAACCTTTTGCTATCAGGGATCATCATGGGCAGATCACTGGCTAAGAGGAAAGAA
GCTAACTGTGTATCCATGGTAGGCTTTGATGAGAAGATGCAGGTGAAGCTGTGGAACAAGTGCAGGCACCAGAGC
AGCAGCAGCCCTAGTGCCCCCAGCATCTCAGACAGGCTCACTTTACAAGTTGAGGTGATGAACTTGAAGCTAAGA
GTTCCTCACAGTCCAGGGAGTGAAAGGAAAGTGACAACTGCACAGGTGGTGGAAGCTCATGCCCAGGGGACAGAC
AGACACAGAAAACATCAACAGAATTCTCTAATGGTTCCCAGGGAGAGAGCTGCTCTTTCTTCTGAAGCTCTGGGA
GCTGGCACAGCCCAGGACTTCCTTTGCTCAGTCTCCACCTGGACAGTGGCAGTATGGCAGCCTCAAAAAGAAAAC
CTTTTGCTATCAGAGATCATCACAGGCCGATCACAGGCTAAGAGGAAAGAAGCTCCCTGTGTATCCCTGGATGGC
TTTGATGAGAAGATGCAGGTGGAGCTGTGGAACGAGCATCAAATCAACATTCATAGGATTGGATCAACCAAACTT
GCTGTATTCAGATTAAATTCAACATTTCAGGGCACAAAGAACAGAGGAACTCCAGGAAGCCGACTCACCAGGTTC
TCCAAGGCAGATCGGTGCTTAGGAGACTATAATCCGTGTGGACAGCCACCTAGAAGCAAACTTCTGGCCATGGTA
GCACAGACTGTGTCATCATTCCAGGTTCTGTGGCCAAGCCCCCCAAACAGGAATCACGTAGTGAAGTTCAAAGAA
ACTTCCAAAAGGTGCAGCAAAAGAAAGAAAAGAAAAACATAA

FIGURE 364

AAACACTCTGTGTGGCTCCTCGGCTTTGGGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCAGCTGGAACGC
AACATAGAGACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAACCAGGGG
GAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAATAAGAATGAAAAGGTCATAGAA
CACATCATGGAGGACCTGGACACAAATGCAGACAAGCAGCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGG
CTAACCTGGGCCTCCCACGAGAAGATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGG
GAGGGCACCCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGCCATGGCCACAGTCATGGTGGCCACGGC
CACAGGCCACTAATCAGGAGGCCAGGCCACCCTGCCTCTACCCAACCAGGGCCCCGGGGCCTGTTATGTCAAACT
GTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTCCTCCAA

FIGURE 365

MTCKMSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENKNEKVIEHIMEDLDTNADKQLS
FEEFIMLMARLTWASHEKMHEGDEGPGHHHKPGLGEGTP

FIGURE 366

GAGCAGCCTTCCTGAGAGAGGAGAGAGAAAGCTCAGGGAGGTCTGGAGCAAAGATACTCCTGGAGGTGGGGAGTG
AGGCAGGGATAAGGAAGGAGAGTATCCTCCAGCACCTTCCAGTGGGTGGGGCAAGTCCGTGGGCATCATGTTGAC
CGAGCTGGAGAAAGCCTTGAACTCTATCATCGACGTCTACCACAAGTACTCCCTGATAAAGGGGAATTTCCATGC
CGTCTACAGGGATGACCTGAAGAAATTGCTAGAGACCGAGTGTCCTCAGTATATCAGGAAAAAGGGTGCAGACGT
CTGGTTCAAAGAGTTGGATATCAACACTGATGGTGCAGTTAACTTCCAGGAGTTCCTCATTCTGGTGATAAAGAT
GGGCGTGGCAGCCCACAAAAAAAGCCATGAAGAAAGCCACAAAGAGTAGCTGAGTTACTGGGCCCAGAGGCTGGG
CCCCTGGACATGTACCTGCAGAATAATAAAGTCATCAATACCTC

FIGURE 367

GGGACCGCTATAAGGCCAGTCGGACTGCGACATAGCCCATCCCCTCGACCGCTCGCGTCGCATTTGGCCGCCTCC
CTACCGCTCCAAGCCCAGCCCTCAGCC**ATG**GCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATCTTC
CACAAGTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGAAGGAGCTGATCCAGAAGGAG
CTCACCATTGGCTCGAAGCTGCAGGATGCTGAAATTGCAAGGCTGATGGAAGACTTGGACCGGAACAAGGACCAG
GAGGTGAACTTCCAGGAGTATGTCACCTTCCTGGGGGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGGC**TGA**

AAATAAATAGGGAAGATGGAGACACCTCTGGGGGTCCTCTCTGAGTCAAATCCAGTGGTGGGTAATTGTACAATA
AATTTTTTTGGTCAAATTT

FIGURE 368

MACPLDQAIGLLVAIFHKYSGREGDKHTLSKKELKELIQKELTIGSKLQDAEIARLMEDLDRNKDQEVNFQEYVT
FLGALALIYNEALKG

FIGURE 369

ATTCTTCCCCTCTCTACAACCCTCTCTCCTCAGCGCTTCTTCTTTCTTGGTTTGATCCTGACTGCTGTC**ATG**GCG
TGCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAGAGGGTGACAAGTTC
AAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGCCCAGCTTCTTGGGGAAAAGGACAGATGAA
GCTGCTTTCCAGAAGCTGATGAGCAACTTGGACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTC
TTCCTGTCCTGCATCGCCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAA**TGA**

AAACTCCTCTGATGTGGTTGGGGGGTCTGCCAGCTGGGGCCCTCCCTGTCGCCAGTGGGCACTTTTTTTTTTCCA
CCCTGGCTCCTTCAGACACGTGCTTGATGCTGAGCAAGTTCAATAAAGATTCTTGGAAGTTT

FIGURE 370

MACPLEKALDVMVSTFHKYSGKEGDKFKLNKSELKELLTRELPSFLGKRTDEAAFQKLMSNLDSNRDNEVDFQEY
CVFLSCIAMMCNEFFEGFPDKQPRKK

FIGURE 371

GGTGCTTCTGAGATGTGGGCTTGCACACGCTGTTGCTATAGTACGTGTGATCCTGACTGCTGTC**ATG**GCGTGCCC
TCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAGAGGGTGACAAGTTCAAGCT
CAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGCCCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGC
TTTCCAGAAGCTGATGAGCAACTTGGACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCCT
GTCCTGCATCGCCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAA**TGA**AAACT
CCTCTGATGTGGTTGGGGGGTCTGCCAGCTGGGGCCCTCCCTGTCGCCAGTGGGCACTTTTTTTTTCCACCCTG
GCTCCTTCAGACACGTGCTTGATGCTGAGCAAGTTCAATAAAGATTCTTGGAAGTTT

FIGURE 372

MACPLEKALDVMVSTFHKYSGKEGDKFKLNKSELKELLTRELPSFLGKRTDEAAFQKLMSNLDSNRDNEVDFQEY
CVFLSCIAMMCNEFFEGFPDKQPRKK

FIGURE 373

ACACATTCCCCACCCTCTGGGAGCTCCTAGTCTGAGAGAGGAAACACTCCTGCCCAAGGGAGCTTCCAGTTAGAT
GGCAGAGAGAGATGCCTCTGGCTTCAGGAGTCCCGAGTCTAAGGAGGGAAACGACTCCTTCAGGGAGCTTCCTGC
TCCTAGGCTGTAGCCATGGCTCCTGCCAGACTGCACAGGAGCCCCCATCTGCCAGCCGGTGCATGTGGCCCTGCT
CCCCAGAGCCTGCGCAGATGCCATCAAAATGGGACTCTGGTCACCCTGTCATTTCCCTTCTGGCAGACACTAAAA
TGGGGAGCCCTGCCCTCAGGGGGGTGTCCCAAGTGCCATCAGAGGAGGCTTGGTGACTCCCAGACACAAGGGAAG
CTTTAGCGTCTGCCCTCAGGGTGAGATGGAGGTATCGCCTCCGGCCTCAGGGAACCACAGTCTGAGGGGGAGATG
CAGCCCCTGCCTTCCCATTCAGAGAGGGGTTTTGTGAGGTGGCTTGGGGGCATAGGGCAGAAGTGGATCCTACAG
GCTGAGCTAAGGCCCCAAGAGCCTCAGCAGTGTACCCATCACCTGGCACCTCTGCAGCCACAGATCCATGATGTG
CAGTTCTCTGGAGCAGGCGCTGGCTGTGCTGGTCACTACCTTCCACAAGTACTCCTGCCAAGAGGGCGACAAGTT
CAAGCTGAGTAAGGGGGAAATGAAGGAACTTCTGCACAAGGAGCTGCCCAGCTTTGTGGGGGAGAAAGTGGATGA
GGAGGGGCTGAAGAAGCTGATGGGCAGCCTGGATGAGAACAGTGACCAGCAGGTGGACTTCCAGGAGTATGCTGT
TTTCCTGGCACTCATCACTGTCATGTGCAATGACTTCTTCCAGGGCTGCCCAGACCGACCCTGAAGCAGAACTCT
TGACTTCCTGCCATGGATCTCTTGGGCCCAGGACTGTTGATGCCTTTGAGTTTTGTATTCAATAAACTTTTTTTG
TCTGTTGATAATATTTTAATTGCTCAGTGATGTTCCATAACCCGGCTGGCTCAGCTGGAGTGCTGGGAGATGAGG
GCCTCCTGGATCCTGCTCCCTTCTGGGCTCTGACTCTCCTGGAAATCTCTCCAAGGCCAGAGCTATGCTTTAGGT
CTCAATTTTGGAATTTCAAACACCAGCAAAAAATTGGAAATCGAGATAGGTTGCTGACTTTTATTTTGTCAAATA
AAGATATTAAAAAAGGC

FIGURE 374

GGACTGTTGAAGACAGGTCTCCACACACAGCTCCAGCAGCCACATTTGCAACCTTGGCCATCTGTCCAGAACCTG
CTCCCACCTCAGGCCCAGGCCAACCGTGCACTGCTGCA**ATG**GGCTCTGAGCTGGAGACGGCGATGGAGACCCTCA
TCAACGTGTTCCACGCCCACTCGGGCAAAGAGGGGGACAAGTACAAGCTGAGCAAGAAGGAGCTGAAAGAGCTGC
TGCAGACGGAGCTCTCTGGCTTCCTGGATGCCCAGAAGGATGTGGATGCTGTGGACAAGGTGATGAAGGAGCTAG
ACGAGAATGGAGACGGGGAGGTGGACTTCCAGGAGTATGTGGTGCTTGTGGCTGCTCTCACAGTGGCCTGTAACA
ATTTCTTCTGGGAGAACAGT**TGA**GCAGACAGCCACATTGGGCAGCGCCCTTCCTCTCCACCCTCCCAGACCTGCC
TCTTCCCCCTGCTTCCACCTCACCCCACTTATCCCTCTCCATAACCCCACCCTTGCCCACCCCACCCCCACCCCC
ACCAAGGGCGCAAGAGTAGCGGTCCAAGCCTGCAACTCATCTTTCATTAAAGGCTTCTCTCTCACCAGCAAAAAA
AAAAAAA

FIGURE 375

MGSELETAMETLINVFHAHSGKEGDKYKLSKKELKELLQTELSGFLDAQKDVDAVDKVMKELDENGDGEVDFQEY
VVLVAALTVACNNFFWENS

FIGURE 376

TCAGACAAGCACTGGACGTGGCGGCCATTTTGTTTTGGACACCGAGCAGGAGCTGGCGGCCGCTGCAGACGAAAG
GCAGGAAAGGGCAGGCCGGGTGAGCAGACGGATCGGCCGACTAGACAGCCAACCAGCAACAACGAACTGAGCTCG
CATACTACCGCTTACGCATCTAACCAACCGCCCATCTAGCTAACCCGAGCCCCTCCACCGTCAACTCAGGTTCGG
CCGGTCCCCGGCCCGCCTGCCGGAGCCGTGGTGGCAGCCCCGGGAGGAGCACTGGCGTCTGTTTCCTTCGATTCT
CGGGATTCGAAGATGGCTGCACAGTCAGCGCCGAAAGTTGTGCTAAAAAGCACCACCAAGATGTCTCTAAATGAG
CGCTTTACTAATATGCTGAAGAACAAACAGCCGACGCCAGTGAATATTCGGGCTTCGATGCAGCAACAACAGCAG
CTAGCCAGTGCCAGAAACAGAAGACTGGCCCAGCAGATGGAGAATAGACCCTCTGTCCAGGCAGCATTAAAACTT
AAGCAGAGCTTAAAGCAGCGCCTGGGTAAGAGTAACATCCAGGCACGGTTAGGCCGACCCATAGGGGCCCTGGCC
AGGGGAGCAATCGGAGGACGAGGCCTACCCATAATCCAGAGAGGCTTGCCCAGAGGAGGACTACGTGGGGGACGT
GCCACCAGAACCCTACTTAGGGGCGGGATGTCACTCCGAGGTCAAAACCTGCTCCGAGGTGGACGAGCCGTAGCT
CCCCGAATGGGCTTAAGAAGAGGTGGTGTTCGAGGTCGTGGAGGTCCTGGGAGAGGGGGCCTAGGGCGTGGAGCT
ATGGGTCGTGGCGGAATCGGTGGTAGAGGTCGGGGTATGATAGGTCGGGGAAGAGGGGGCTTTGGAGGCCGAGGC
CGAGGCCGTGGACGAGGGAGAGGTGCCCTTGCTCGCCCTGTATTGACCAAGGAGCAGCTGGACAACCAATTGGAT
GCATATATGTCGAAAACAAAAGGACACCTGGATGCTGAGTTGGATGCCTACATGGCGCAGACAGATCCGAAACC
AATGATTGAAGCCTGCCCATCCTCCCATGAGAGACTCTTGTTAGTCAACACATCTGTAAATAACCTTGAGATAAC
AGATGAGAAGAAATCTGATTGATGCTGGATGGACCTATCACAATAGGCTGTGGACTTACTTGCCACCAGCTTGTG
CATTTAGTGTGTTCCTTTTACTTTTTGATACTGTGTTGTATGAAACCCTTTTGTCCTTTGATTTGGTTTTTTGTT
TTTGTTTTTTTAGGGGGGAGGGGGGGTTTCCCCTCCTTTGCCCAGACTTCTCTTTGAACACAAATGCATTAGCCT
TGTGGCTAGAACACCCTCTTCCTACCTCTGTCTCCCCTCACTTGTCATATGCTCTGACATGCTAACATTTCTTTT
GTTCATCCCTGTTGCCCCCACAGAAACATCCCAGAAAAACCGGTCAGTGTTCCTTCCTCCCTGATCCTTAGGTTT
CTGAAATAGGGTTCTGTTACATCCTCTTCGATAGCCTGTTTAAAATGTTTAGAAGGTCTGGAGCTCAAAAATGCG
TTCTTCC

FIGURE 377

AGGGGTGACAGAGGCCGTGGTCGTGGTGGGCGCTTTGGTTCCAGAGGAGGCCCAGGAGGAGGGTTCAGGCCCTTT
GTACCACATATCCCATTTGACTTCTATTTGTTGTTTACTTCTGGTTTAGTGTGAAATGGCCTTTCCCCGGGTCAA
GCCAGCACCTGATGAAACTTCCTTCAGTGAGGCCTTGCTGAAGAGGAATCAGGACCTGGCTCCCAATTCTGCTGA
ACAGGCATCTATCCTTTCTCTGGTGACAAAAATAAACAATGTGATTGATAATCTGATTGTGGCTCCAGGGACATT
TGAAGTGCAAATTGAAGAAGTTCGACAGGTGGGATCCTATAAAAAGGGGACAATGACTACAGGACACAATGTGGC
TGACCTGGTGGTGATACTCAAGATTCTGCCAACGTTGGAAGCTGTTGCTGCCCTGGGGAACAAAGTCGTGGAAAG
CCTAAGAGCACAGGATCCTTCTGAAGTTTTAACCATGCTGACCAACGAAACTGGCTTTGAAATCAGTTCTTCTGA
TGCTACAGTGAAGATTCTCATTACAACAGTGCCACCCAATCTTCGAAAACTGGATCCAGAACTCCATTTGGATAT
CAAAGTATTGCAGAGTGCCTTAGCAGCCATCCGACATGCCCGCTGGTTCGAGGAAAATGCTTCTCAGTCCACAGT
TAAAGTTCTCATCAGACTACTGAAGGACTTGAGGATTCGTTTTCCTGGCTTTGAGCCCCTCACACCCTGGATCCT
TGACCTACTAGGCCATTATGCTGTGATGAACAACCCCACCAGACAGCCTTTGGCCCTAAACGTTGCATACAGGCG
CTGCTTGCAGATTCTGGCTGCAGGACTGTTCCTGCCAGGTTCAGTGGGTATCACTGACCCCTGTGAGAGTGGCAA
CTTTAGAGTACACACAGTCATGACCCTAGAACAGCAGGACATGGTCTGCTATACAGCTCAGACTCTCGTCCGAAT
CCTCTCACATGGTGGCTTTAGGAAGATCCTTGGCCAGGAGGGTGATGCCAGCTATCTTGCTTCTGAAATATCTAC
CTGGGATGGAGTGATAGTAACACCTTCAGAAAAGGCTTATGAGAAGCCACCAGAGAAGAAGGAAGGAGAGGAAGA
AGAGGAGAATACAGAAGAACCACCTCAAGGAGAGGAAGAAGAAAGCATGGAAACTCAGGAGTGACATTCCCTTCA
CTCCTTTTCCTACCCAAGGGGGAAGACTGGAGCCTAAGCTGCCTGCTACTGGGCTTTACATGGTGACAGACATTT
CCGTGGGATAGGGAAGATAGCAGGAAGAAAAGTAAACTCCATAGAAGTGTCATTCCACTGGGTTTTGATATTGGC
TTAGCTGCCAGTCTCCCATTTGTGACCTATGCCATCCATCTATAATGGAGGATACCAACATTTCTTCCTAATATT
CTATAATCTCCAACTCCTGAAAACCCCTCTCTCAACTAATACTTTGCTGTTGAAATGTTGTGAAATGTTAAGTGT
CTGGAAATTTTTTTTCTAAGAAAAACTATTAAAGTACTT

FIGURE 378

MRGDRGRGRGGRFGSRGGPGGGFRPFVPHIPFDFYLCEMAFPRVKPAPDETSFSEALLKRNQDLAPNSAEQASIL
SLVTKINNVIDNLIVAPGTFEVQIEEVRQVGSYKKGTMTTGHNVADLVVILKILPTLEAVAALGNKVVESLRAQD
PSEVLTMLTNETGFEISSSDATVKILITTVPPNLRKLDPELHLDIKVLQSALAAIRHARWFEENASQSTVKVLIR
LLKDLRIRFPGFEPLTPWILDLLGHYAVMNNPTRQPLALNVAYRRCLQILAAGLFLPGSVGITDPCESGNFRVHT
VMTLEQQDMVCYTAQTLVRILSHGGFRKILGQEGDASYLASEISTWDGVIVTPSEKAYEKPPEKKEGEEEEENTE
EPPQGEEEESMETQE

FIGURE 379

CACACCCGCACTCCTCCCGGGTTTCTGCTCTCCGCCCGTGTGGAGTGGTGGGGGCCTGGGTGGGA**ATG**GGCGTGT
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTCGGAAGGGAGGAT
CAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGCGGGCTCCATGGCTGCCCTCCTGCTGC
TGCCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGAAGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGG
ACTTGGCCTTTGCGGTGCGAGCTCTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCG
ACCCGGAAGGTCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACTGGCCCAGCAGCGCGCCGCGCACA
CCTTTCTCATTCACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAACAGGGCTGCACGCGCCT
TCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAGCGGCGAGGGGAGCGCTGGAGAAGGCGAGC
GGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCGGAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAG
GTGGAGGAGCCGCCGCCCCTCTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGT
GGCTCTGGTTCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCCACCGCCCTGCGCCGGGGCCCCCTGC
TGCACTGCCTCCGCAGCTGCGGCGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTGGAGTCCCTGGAGCCGGACC
TGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGGCCCAGGAACCCACCCTGCTGGAATTAGCGATT
TGCTGGCTGAAGTGTCCGCTGAAGTGGATGGGCCAGTGCCAGGATACCTCTCTTCCCCCCAGAGCATAACAGACA
CGTGCCTGTACATCTTCACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGC
AATGCCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCACTCTACCACA
TGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTGGTGCTGAAATCCAAGTTCTCGG
CTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGACGGTGTTCCAGTACATTGGGGAGCTGTGCCGATACC
TTGTCAACCAGCCCCCGAGCAAGGCAGAACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAG
ATACCTGGGAGCGTTTTGTGCGGCGCTTCGGGCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACG
TGGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGCATATCTTCCCCT
TCTCCTTGATTCGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCCCAGGGGCACTGTATGGCCACATCTC
CAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCAGCAGTCCCCATTCCTGGGCTATGCTGGCGGGCCAGAGC
TGGCCCAGGGGAAGTTGCTAAAGGATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCT
GCGATGACCAAGGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGCCA
CAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTGTGCCAG
GGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCCCCACGCTTTGGACCTTATGCAGCTCTACA
CCCACGTGTCTGAGAACTTGCCACCTTATGCCCGGCCCCGATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAG
AGACCTTCAAACAGCAGAAAGTTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCACTGTACG
TTCTGGACCAGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGCGCCCTCCTGGCAGGAAACCTTC
GAATC**TGA**GAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGGCCGTTGCAGGTGTACTGG
GCTGTCAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTTGTAATAAATGTGGCTGGAGCTGATCCAGCTG
TCTCTGACCTACAAAAAAAAAAAAAAAAAA

FIGURE 380

MGVCQRTRAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPLLLLKLHLWPQLRW
LPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQRAAHTFLIHGSRRFSYSEAERESNRA
ARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGP
EFLWLWFGLAKAGLRTAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAG
ISDLLAEVSAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYLALP
LYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERGHKVRLAVGSG
LRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCM
ATSPGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGE
NVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESL
ATTETFKQQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

FIGURE 381

GGCACGAGGGGGCTTCAGGACAATTCGTGATGGCGGGGGCTGGTTCCGCCGCTGTATCGGGGGCAGGGACCCCGG
TGGCGGGGCCCACAGGCCGCGACCTTTTCGCCGAAGGGCTGCTGGAGTTCCTGCGACCCGCTGTGCAGCAGCTCG
ACTCTCACGTACACGCCGTCAGAGAGAGCCAGGTAGAGCTCCGGGAACAAATTGACAACCTAGCCACAGAACTGT
GCCGCATAAATGAGGATCAGAAGGTGGCCCTGGATCTTGACCCCTATGTTAAGAAGCTACTTAATGCCCGGCGAC
GCGTTGTCTTGGTTAACAACATTCTACAGAATGCTCAGGAACGACTGAGACGGCTAAACCACAGTGTTGCCAAGG
AAACAGCCCGCAGGAGAGCAATGCTGGATTCGGGAATTTACCCCCCTGGCTCCCCAGGCAAATAACAGATGAGCC
TATGGACTCAGTAGCACAAGTACTGTTCCCCAGCTGCCTTGTTTCAACAGACATGCAAAGATCCTAGGAGACAGT
CCCCATAGACCTTCAGACATTAAAAAGGGAGCCGTACAGTTTGTTTGAAGCACTTCGTCTTACCCATTTATGTAG
GGGCCCCAGGAAACCTACACACAGCCAGAATGAGGTTCCCAAAGGACTTACATTAATTATGGCTCTTGCTTCCTT
TCACAAATGAGCTGAGGCCTCTACTTTTTTTTTTTTAAGCTGCATACTTGAGGCTTACCTTCTTCAGGACTAGTT
AACCAGAGGGGCTTCCTTTGTATGTTACATGCCTGGTTACATGGGCCTGGACAGCATGTCCTCTACCTGTGACTT
CTCATTTTCCTGTTTACACTGGGGATTTGGAGGGGGCAGGCAAAGTCAAAGTGAATGACCTCTGTCCACCCACTT
TTTTATTGCACTGGCTTGAATACAGTAGCAGTGTTGATAGAATCATTTTATTCAATAAATACTTAAAATGAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 382

MAGAGSAAVSGAGTPVAGPTGRDLFAEGLLEFLRPAVQQLDSHVHAVRESQVELREQIDNLATELCRINEDQKVA
LDLDPYVKKLLNARRRVVLVNNILQNAQERLRRLNHSVAKETARRRAMLDSGIYPPGSPGK

FIGURE 383

CTATGATAAGCTAATTATTTATGTTTGCATAATATTTATGTTTGCATGTTAGTGACATATATTTTAAAATGTGAT
ACACTCCTGTAATTTATGAGAGTATGTTCATTGCTGTGAGCTTTGAAGGTGCTCTAATCCTTCCTCATATTTGGC
CTTAGAATGCACCTCGGATCCCCCAAGGTTTAGGCTTTCTTCATTTGTCTTTGAAACTATATCTTCTGTCTCTTG
TCATATCTGCTTATTGCGTGTTTTTCATACCTTCCACCTCTCTAAAAGCCGTTACCTGAGCCCTCGTTATCACTT
TTGGTTGAATGTGCTGCACTTAGCTGCATTTCTAAGTTTCTGATTCTTGCAAGTTTGTGGAAACAGAGGAGTCTT
TAACCCACATCAGCCTTGATCTAAGTGTACCACTTTACTTAAAAGTTCGTGGGATCTGGAGCTCCTGGTCTAGCA
AGCCATGAAAATGCCAATAAATGTTTGTAATAAAGCTTTTATTTAAACATCCATTTTGTTCGACCTTGAAGCTTT
ACTAATATGCTGAAGAACAAACAGCCGACGCCAGTGAATATTCGGGCTTCGATGCAGCAACAACAGCAGCTAGCC
AGTGCCAGAAACAGAAGACTGGCCCAGCAGATGGAGAATAGACCCTCTGTCCAGGCAGCATTAAAACTTAAGCAG
AGCTTAAAGCAGCGCCTGGGTAAGAGTAACATCCAGGCACGGTTAGGCCGACCCATAGGGGCCCTGGCCAGGGGA
GCAATCGGAGGACGAGGCCTACCCATAATCCAGAGAGGCTTGCCCAGAGGAGGACTACGTGGGGGACGTGCCACC
AGAACCCTACTTAGGGGCGGGATGTCACTCCGAGGTCAAAACCTGCTCCGAGGTGGACGAGCCGTAGCTCCCCGA
ATGGGCTTAAGAAGAGGTGGTGTTCGAGGTCGTGGAGGTCCTGGGAGAGGGGGCCTAGGGCGTGGAGCTATGGGT
CGTGGCGGAATCGGTGGTAGAGGTCGGGGTATGATAGGTCGGGGAAGAGGGGGCTTTGGAGGCCGAGGCCGAGGC
CGTGGACGAGGGAGAGGTGCCCTTGCTCGCCCTGTATTGACCAAGGAGCAGCTGGACAACCAATTGGATGCATAT
ATGTCGAAAACAAAAGGACACCTGGATGCTGAGTTGGATGCCTACATGGCGCAGACAGATCCCGAAACCAATGAT
TGAAGCCTGCCCATCCTCCCATGAGAGACTCTTGTTAGTCAACACATCTGTAAATAACCTTGAGATAACAGATGA
GAAGAAATCTGATTGATGCTGGATGGACCTATCACAATAGGCTGTGGACTTACTTGCCACCAGCTTGTGCATTTA
GTGTGTTCCTTTTACTTTTTGATACTGTGTTGTATGAAACCCTTTTGTCCTTTGATTTGGTTTTTTGTTTTTGTT
TTTTTAGGGGGGAGGGGGGGTTTCCCCTCCTTTGCCCAGACTTCTCTTTGAACACAAATGCATTAGCCTTGTGGC
TAGAACACCCTCTTCCTACCTCTGTCTCCCCTCACTTGTCATATGCTCTGACATGCTAACATTTCTTTTGTTCAT
CCCTGTTGCCCCCACAGAAACATCCCAGAAAAACCGGTCAGTGTTCCTTCCTCCCTGATCCTTAGGTTTCTGAAA
TAGGGTTCTGTTACATCCTCTTCGATAGCCTGTTTAAAATGTTTAGAAGGTCTGGAGCTCAAAAATGCGTTCTTC
C

FIGURE 384

CCACAGATCCATGATGTGCAGTTCTCTGGAGCAGGCGCTGGCTGTGCTGGTCACTACCTTCCACAAGTACTCCTG
CCAAGAGGGCGACAAGTTCAAGCTGAGTAAGGGGGAAATGAAGGAACTTCTGCACAAGGAGCTGCCCAGCTTTGT
GGGGGAGAAAGTGGATGAGGAGGGGCTGAAGAAGCTGATGGGCAGCCTGGATGAGAACAGTGACCAGCAGGTGGA
CTTCCAGGAGTATGCTGTTTTCCTGGCACTCATCACTGTCATGTGCAATGACTTCTTCCAGGGCTGCCCAGACCG
ACCCTGAAGCAGAACTCTTGACTTCCTGCCATGGATCTCTTGGGCCCAGGACTGTTGATGCCTTTGAGTTTTGTA
TTCAATAAACTTTTTTTGTCTGTTGAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 385

MMCSSLEQALAVLVTTFHKYSCQEGDKFKLSKGEMKELLHKELPSFVGEKVDEEGLKKLMGSLDENSDQQVDFQE
YAVFLALITVMCNDFFQGCPDRP

FIGURE 386

GCGCCCAGACTTGCTGCCGGGCTGGACGGTCCGCACGGTGCTGGGCAGCAGCGAAAACGCGCTGGGCGTGTGCTC
CGACACCGCAGCGCCCCTGGCCGCGGTGGACCTCAAGTGGGAGCACAACCCCGCTGTGTTCCTGGCCCCGGCTG
CGTGTACGCCGCCGCCCCAGTGGGGCGCTTCACCGCGCACTGGCGGGTCCCGCTGCTGACCGCCGGCGCCCCGGC
GCTGGGCTTCGGTGTCAAGGACGAGTATGCGCTGACCACCCGCGCGGGGCCCAGCTACGCCAAGCTGGGGGACTT
CGTGGCGGCGCTGCACCGACGGCTGGGCTGGGAGCGCCAAGCGCTCATGCTCTACGCCTACCGGCCGGGTGACGA
AGAGCACTGCTTCTTCCTCGTGGAGGGGCTGTTCATGCGGGTCCGCGACCGCCTCAATATTACGGTGGACCACCT
GGAGTTCGCCGAGGACGACCTCAGCCACTACACCAGGCTGCTGCGGACCATGCCGCGCAAAGGCCGAGTTATCTA
CATCTGCAGCTCCCCTGATGCCTTCAGAACCCTCATGCTCCTGGCCCTGGAAGCTGGCTTGTGTGGGGAGGACTA
CGTTTTCTTCCACCTGGATATCTTTGGGCAAAGCCTGCAAGGTGGACAGGGCCCTGCTCCCCGCAGGCCCTGGGA
GAGAGGGGATGGGCAGGATGTCAGTGCCCGCCAGGCCTTTCAGGCTGCCAAAATCATTACATATAAAGACCCAGA
TAATCCCGAGTACTTGGAATTCCTGAAGCAGTTAAAACACCTGGCCTATGAGCAGTTCAACTTCACCATGGAGGA
TGGCCTGGTGAACACCATCCCAGCATCCTTCCACGACGGGCTCCTGCTCTATATCCAGGCAGTGACGGAGACTCT
GGCACATGGGGGAACTGTTACTGATGGGGAGAACATCACTCAGCGGATGTGGAACCGAAGCTTTCAAGGTGTGAC
AGGATACCTGAAAATTGATAGCAGTGGCGATCGGGAAACAGACTTCTCCCTCTGGGATATGGATCCCGAGAATGG
TGCCTTCAGGGTTGTACTGAACTACAATGGGACTTCCCAAGAGCTGGTGGCTGTGTCGGGGCGCAAACTGAACTG
GCCCCTGGGGTACCCTCCTCCTGACATCCCCAAATGTGGCTTTGACAACGAAGACCCAGCATGCAACCAAGATCA
CCTTTCCACCCTGGAGGTGCTGGCTTTGGTGGGCAGCCTCTCCTTGCTCGGCATTCTGATTGTCTCCTTCTTCAT
ATACAGGAAGATGCAGCTGGAGAAGGAACTGGCCTCGGAGCTGTGGCGGGTGCGCTGGGAGGACGTTGAGCCCAG
TAGCCTTGAGAGGCACCTGCGGAGTGCAGGCAGCCGGCTGACCCTGAGCGGGAGAGGCTCCAATTACGGCTCCCT
GCTAACCACAGAGGGCCAGTTCCAAGTCTTTGCCAAGACAGCATATTATAAGGGCAACCTCGTGGCTGTGAAACG
TGTGAACCGTAAACGCATTGAGCTGACACGAAAAGTCCTGTTTGAACTGAAGCATATGCGGGATGTGCAGAATGA
ACACCTGACCAGGTTTGTGGGAGCCTGCACCGACCCCCCCAATATCTGCATCCTCACAGAGTACTGTCCCCGTGG
GAGCCTGCAGGACATTCTGGAGAATGAGAGCATCACCCTGGACTGGATGTTCCGGTACTCACTCACCAATGACAT
CGTCAAGGGCATGCTGTTTCTACACAATGGGGCTATCTGTTCCCATGGGAACCTCAAGTCATCCAACTGCGTGGT
AGATGGGCGCTTTGTGCTCAAGATCACCGACTATGGGCTGGAGAGCTTCAGGGACCTGGACCCAGAGCAAGGACA
CACCGTTTATGCCAAAAAGCTGTGGACGGCCCCTGAGCTCCTGCGAATGGCTTCACCCCCTGTGCGGGGCTCCCA
GGCTGGTGACGTATACAGCTTTGGGATCATCCTTCAGGAGATTGCCCTGAGGAGTGGGGTCTTCCACGTGGAAGG
TTTGGACCTGAGCCCCAAAGAGATCATCGAGCGGGTGACTCGGGGTGAGCAGCCCCCCTTCCGGCCCTCCCTGGC
CCTGCAGAGTCACCTGGAGGAGTTGGGGCTGCTCATGCAGCGGTGCTGGGCTGAGGACCCACAGGAGAGGCCACC
ATTCCAGCAGATCCGCCTGACGTTGCGCAAATTTAACAGGGAGAACAGCAGCAACATCCTGGACAACCTGCTGTC
CCGCATGGAGCAGTACGCGAACAATCTGGAGGAACTGGTGGAGGAGCGGACCCAGGCATACCTGGAGGAGAAGCG
CAAGGCTGAGGCCCTGCTCTACCAGATCCTGCCTCACTCAGTGGCTGAGCAGCTGAAGCGTGGGGAGACGGTGCA
GGCCGAAGCCTTTGACAGTGTTACCATCTACTTCAGTGACATTGTGGGTTTCACAGCGCTGTCGGCGGAGAGCAC
ACCCATGCAGGTGGTGACCCTGCTCAATGACCTGTACACTTGCTTTGATGCTGTCATAGACAACTTTGATGTGTA
CAAGGTGGAGACAATTGGCGATGCCTACATGGTGGTGTCAGGGCTCCCTGTGCGGAACGGGCGGCTACACGCCTG
CGAGGTAGCCCGCATGGCCCTGGCACTGCTGGATGCTGTGCGCTCCTTCCGAATCCGCCACCGGCCCCAGGAGCA
GCTGCGCTTGCGCATTGGCATCCACACAGGACCTGTGTGTGCTGGAGTGGTGGGACTGAAGATGCCCCGTTACTG
TCTCTTTGGGGATACAGTCAACACAGCCTCAAGAATGGAGTCTAATGGGGAAGCCCTGAAGATCCACTTGTCTTC
TGAGACCAAGGCTGTCCTGGAGGAGTTTGGTGGTTTCGAGCTGGAGCTTCGAGGGGATGTAGAAATGAAGGGCAA
AGGCAAGGTTCGGACCTACTGGCTCCTTGGGGAGAGGGGGAGTAGCACCCGAGGCTGACCTGCCTCCTCTCCTAT
CCCTCCACACCTCCCTACCCTGTGCCAGAAGCAACAGAGGTGCCAGGCCTCAGCCTCACCCACAGCAGCCCCATC
GCCAAAGGATGGAAGTAATTTGAATAGCTCAGGTGTGCTGACCCCAGTGAAGACACCAGATAGGACCTCTGAGAG
GGGACTGGCATGGGGGGATCTCAGAGCTTACAGGCTGAGCCAAGCCCACGGCCATGCACAGGGACACTCACACAG
GCACACGCACCTGCTCTCCACCTGGACTCAGGCCGGGCTGGGCTGTGGATTCCTGATCCCCTCCCCTCCCCATGC
TCTCCTCCCTCAGCCTTGCTACCCTGTGACTTACTGGGAGGAGAAAGAGTCACCTGAAGGGGAACATGAAAAGAG
ACTAGGTGAAGAGAGGGCAGGGGAGCCCACATCTGGGGCTGGCCCACAATACCTGCTCCCCCGACCCCCTCCACC
CAGCAGTAGACACAGTGCACAGGGGAGAAGAGGGGTGGCGCAGAAGGGTTGGGGGCCTGTATGCCTTGCTTCTAC
CATGAGCAGAGACAATTAAAATCTTTATTCCAGTG

FIGURE 387

MPGPRRPAGSRLRLLLLLLLPPLLLLLRGSHAGNLTVAVVLPLANTSYPWSWARVGPAVELALAQVKARPDLLPG
WTVRTVLGSSENALGVCSDTAAPLAAVDLKWEHNPAVFLGPGCVYAAAPVGRFTAHWRVPLLTAGAPALGFGVKD
EYALTTRAGPSYAKLGDFVAALHRRLGWERQALMLYAYRPGDEEHCFFLVEGLFMRVRDRLNITVDHLEFAEDDL
SHYTRLLRTMPRKGRVIYICSSPDAFRTLMLLALEAGLCGEDYVFFHLDIFGQSLQGGQGPAPRRPWERGDGQDV
SARQAFQAAKIITYKDPDNPEYLEFLKQLKHLAYEQFNFTMEDGLVNTIPASFHDGLLLYIQAVTETLAHGGTVT
DGENITQRMWNRSFQGVTGYLKIDSSGDRETDFSLWDMDPENGAFRVVLNYNGTSQELVAVSGRKLNWPLGYPPP
DIPKCGFDNEDPACNQDHLSTLEVLALVGSLSLLGILIVSFFIYRKMQLEKELASELWRVRWEDVEPSSLERHLR
SAGSRLTLSGRGSNYGSLLTTEGQFQVFAKTAYYKGNLVAVKRVNRKRIELTRKVLFELKHMRDVQNEHLTRFVG
ACTDPPNICILTEYCPRGSLQDILENESITLDWMFRYSLTNDIVKGMLFLHNGAICSHGNLKSSNCVVDGRFVLK
ITDYGLESFRDLDPEQGHTVYAKKLWTAPELLRMASPPVRGSQAGDVYSFGIILQEIALRSGVFHVEGLDLSPKE
IIERVTRGEQPPFRPSLALQSHLEELGLLMQRCWAEDPQERPPFQQIRLTLRKFNRENSSNILDNLLSRMEQYAN
NLEELVEERTQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAESTPMQVVTL
LNDLYTCFDAVIDNFDVYKVETIGDAYMVVSGLPVRNGRLHACEVARMALALLDAVRSFRIRHRPQEQLRLRIGI
HTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGEALKIHLSSETKAVLEEFGGFELELRGDVEMKGKGKVRTYW
LLGERGSSTRG

FIGURE 388

CTGGGTGGCGGTTATGGTGGGGCCAGCGGCATGGGAGGCATCACCGCAGTCATGGTCAACCAGAACCTGCTGAGC
CCCCTTGTCCTGGAGGTGGACCCCAACATCCAGGCCGTGTGCACCCAGGAGAAGGAGCCGATCAAGACCCTCAAC
AACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCCTGGAGCAGCAGAACAAGATGCCGGAGACCAAGTGGAGC
CTCCTGCAGCAGCAGAAGACGGCTCGGAGCAACATGGACAAGTTCGAGAGCTACATCAACAACCTTAGGCAGCAG
CTGGAGATTCTGGGCCAGGAGAAGCTGAAGCTGGAGGCGGAGCTTGGCAACATGCAGGGGCTGGTGGAGGACTTC
AAGAACAAGTATGAGGATGAGATCAATAAGCGTACAGAGATGGAGAATGAATTTGTGCTCACCAAGAAGGATGTG
GATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTTACTGAAGAGATCAGCTTCCTCAGG
CAGCTGTATGAAGAGGAGATCCGGGAGCTGCAGTCCCAGATCTCAGACACATCATTGCTGAGGTCAAGGCACAGT
ACGAGGACCGCCAGCCGCAGCCAGGCTGAGGCTGAGAGCATGTACCAGATCAAGAATGAGGAGCTGCAAGAGCCT
GGCTGGGAAGCACGGGGATGA

FIGURE 389

TTGCCCGGGACTAGGAGCTTAAGTGAAGAGGTACGCCTTGTTCGGTGGAAATCAGCCGTAGCCATGAGTTTCTGC
CGGGGCTAGCCCTAGAGTACGGAGCAGGCGGACTTTTCGGTTCCCCGCCCCGCCAGGTGGCGGGGCCTACTAGGC
CTCCGGGCATCCCCGGTCTCAAGTAGGCCTCATCTGCCGGCAAGGGCGCCCGAAACGCGGGAGGCGCC**ATG**TCGC
TGGTTGCTTACGCCAGCAGCGATGAGAGCGAGCCGGATGAGGCTGAGCCCGAGCCGGAGGAAGAGGAGGCGGTGG
CTCCTACATCTGGGCCCGCTTTAGGGGGCTTGTTCGCTTCTCTCCCTGCGCCCAAGGGTCCGGCCTTGCTGCCTC
CGCCCCCTCAGATGCTGGCGCCAGCCTTTCCCCCGCCGCTGTTGCTTCCCCCACCCACCGGAGACCCCAGGCTTC
AGCCTCCTCCCCCCTTGCCCTTCGGCCTGGGAGGCTTCCCCCCACCTCCAGGCGTGAGCCCGGCTGAAGCGGCGG
GAGTTGGGGAGGGACTGGGATTGGGGTTGCCCTCGCCCCGAGGCCCTGGCCTCAATCTGCCCCCTCCAATTGGCG
GTGCCGGTCCCCCGCTGGGGCTTCCCAAGCCAAAGAAGAGGAAAGAGCCCGTGAAGATCGCGGCGCCGGAGTTGC
ATAAGGGAGATTCAGATTCTGAGGAAGATGAACCCACAAAGAAGAAAACTATCCTTCAGGGATCCAGTGAGGGGA
CTGGTTTGTCTGCCTTGCTTCCCCAACCTAAAAACCTGACTGTGAAAGAGACTAACAGGTTGCTCCTGCCCCATG
CCTTCTCCCGCAAACCCTCGGATGGCTCCCCTGATACTAAGCCCTCCAGACTGGCTTCTAAGACCAAGACTTCCT
CTCTTGCCCCTGTTGTGGGCACCACAACCACCACTCCGTCGCCCTCTGCTATCAAGGCTGCTGCCAAGAGTGCTG
CCCTGCAGGTGACAAAGCAGATCACGCAGGAAGAAGACGACAGTGATGAGGAAGTAGCCCCCGAAAACTTTTTCT
CCCTCCCTGAAAAGGCTGAGCCACCTGGAGTTGAGCCATACCCTTACCCCATCCCCACTGTCCCTGAAGAGCTGC
CTCCAGGCACGGAACCAGAGCCGGCTTTCCAGGACGATGCAGCCAATGCCCCCCTTGAATTCAAGATGGCAGCAG
GTTCAAGTGGGGCCCCTTGGATGCCTAAGCCTGGGGACGACTACAGCTACAATCAGTTTTCCACATATGGCGATG
CCAATGCCGCTGGTGCTTATTATCAGGATTATTACAGTGGTGGCTACTATCCTGCACAGGACCCGGCCCTGGTCC
CCACCCAGGAAATTGCCCCAGATGCCTCCTTCATCGATGACGAAGCATTTAAGCGGCTGCAGGGCAAGAGGAACC
GAGGGAGAGAAGAAATCAACTTTGTGGAGATCAAAGGTGATGACCAGCTCAGTGGGGCCCAGCAATGGATGACTA
AGTCATTGACAGAAGAGAAAACCATGAAGTCATTCAGCAAAAAGAAAGGTGAGCAGCCAACAGGCCAGCAGCGGC
GGAAACACCAGATCACATATCTTATTCATCAGGCCAAGGAGCGGGAGCTGGAACTGAAGAACACCTGGTCAGAGA
ACAAGCTCAGCCGCCGTCAGACCCAAGCCAAATATGGATTC**TAG**GGCTCTGGAACTGATTGCTCCCAGGATCTCC
TGCCAGCCCAGCTGGCCTGGCCCCCAGCTTCACCTCTGGGACCCCAGCTGCTCTAAGCCCAGGATCTCTTTCCCC
AAGGACCCAGCCCTCGCCTCTGCGAGAATGAACATATTTGATAGATTTTTCTTAACAAGTTAGAAAATTCAGCTC
CTTTCTGTCCTGGAGCTAGCAAAGACTTGTGTGATGCCTCCGAAGGGGCTCTGAGTTCTGGGGTGGGAGTTTTGC
TCTCTGTCAGGTGTGATAAAATGTTGAACCCTCCCCACCACCACTTTTTTTTTTTTTAAACCAGGGATGTCTGTT
GAAATAAAACATTCAGTCTGACAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 390

MSLVAYASSDESEPDEAEPEPEEEEAVAPTSGPALGGLFASLPAPKGPALLPPPPQMLAPAFPPPLLLPPPTGDP
RLQPPPPLPFGLGGFPPPPGVSPAEAAGVGEGLGLGLPSPRGPGLNLPPPIGGAGPPLGLPKPKKRKEPVKIAAP
ELHKGDSDSEEDEPTKKKTILQGSSEGTGLSALLPQPKNLTVKETNRLLLPHAFSRKPSDGSPDTKPSRLASKTK
TSSLAPVVGTTTTTPSPSAIKAAAKSAALQVTKQITQEEDDSDEEVAPENFFSLPEKAEPPGVEPYPYPIPTVPE
ELPPGTEPEPAFQDDAANAPLEFKMAAGSSGAPWMPKPGDDYSYNQFSTYGDANAAGAYYQDYYSGGYYPAQDPA
LVPTQEIAPDASFIDDEAFKRLQGKRNRGREEINFVEIKGDDQLSGAQQWMTKSLTEEKTMKSFSKKKGEQPTGQ
QRRKHQITYLIHQAKERELELKNTWSENKLSRRQTQAKYGF

FIGURE 391

GAGGAGGAGTGGGGACCGGGCGGGGGGTGGAGGAAGAGGCCTCGCGCAGAGGAGGGAGCAATTGAATTTCAAACA
CAAACAACTGCACGAGCGCGCACCCACCGCGCCGGAGCCTTGCCCCGATCCGCGCCCGCCCCGTCCGTGCGGCGC
GCGGGCGGAGACGCCGTGGCCGCGCCGGAGCTCGGGCCGGGGGCCACCATCGAGGCGGGGGCCGCGCGAGGGCCG
GAGCGGAGCGGCGCCGCCACCGCCGCACGCGCAAACTTGGGCTCGCGCTTCCCGGCCCGGCGCGGAGCCCGGGGC
GCCCGGAGCCCCGCCATGTCGCGATCCAACCGGCAGAAGGAGTACAAATGCGGGGACCTGGTGTTCGCCAAGATG
AAGGGCTACCCACACTGGCCGGCCCGGATTGACGAGATGCCTGAGGCTGCCGTGAAATCAACAGCCAACAAATAC
CAAGTCTTTTTTTTCGGGACCCACGAGACGGCATTCCTGGGCCCCAAAGACCTCTTCCCTTACGAGGAATCCAAG
GAGAAGTTTGGCAAGCCCAACAAGAGGAAAGGGTTCAGCGAGGGGCTGTGGGAGATCGAGAACAACCCTACTGTC
AAGGCTTCCGGCTATCAGTCCTCCCAGAAAAAGAGCTGTGTGGAAGAGCCTGAACCAGAGCCCGAAGCTGCAGAG
GGTGACGGTGATAAGAAGGGGAATGCAGAGGGCAGCAGCGACGAGGAAGGGAAGCTGGTCATTGATGAGCCAGCC
AAGGAGAAGAACGAGAAAGGAGCGTTGAAGAGGAGAGCAGGGGACTTGCTGGAGGACTCTCCTAAACGTCCCAAG
GAGGCAGAAAACCCTGAAGGAGAGGAGAAGGAGGCAGCCACCTTGGAGGTTGAGAGGCCCCTTCCTATGGAGGTG
GAAAAGAATAGCACCCCCTCTGAGCCCGGCTCTGGCCGGGGGCCTCCCCAAGAGGAAGAAGAGGAGGAGGATGAA
GAGGAAGAGGCTACCAAGGAAGATGCTGAGGCCCCAGGCATCAGAGATCATGAGAGCCTGTAGCCACCAATGTTT
CAAGAGGAGCCCCCACCCTGTTCCTGCTGCTGTCTGGGTGCTACTGGGGAAACTGGCCATGGCCTGCAAACTGGG
AACCCCTTTCCCACCCCAACCTGCTCTCCTCTTCTACTCACTTTTCCCACTCCAAGCCCAGCCCATGGAGATTGA
CCTGGATGGGGCAGGCCACCTGGCTCTCACCTCTAGGTCCCCATACTCCTATGATCTGAGTCAGAGCCATGTCTT
CTCCCTGGAATGAGTTGAGGCCACTGTGTTCCTTCCGCTTGGGAGGGGCAATCCTCAAATGCGGGGTGGGGGCAG
CACAGGAGGGCGGCCTCCTTCTGAGCTCCTGTCCCCTGCTACACCTATTATCCCAGCTGCCTAGATTCAGGGAAA
GTGGGACAGCTTGTAGGGGAGGGGCTCCTTTCCATAAATCCTTGATGATTGACAACACCCATTTTTCCTTTTGCC
GACCCCAAGAGTTTTGGGAGTTGTAGTTAATCATCAAGAGAATTTGGGGCTTCCAAGTTGTTCGGGCCAAGGACC
TGAGACCTGAAGGGTTGACTTTACCCATTTGGGTGGGAGTGTTGAGCATCTGTCCCCCTTTAGATCTCTGAAGCC
ACAAATAGGATGCTTGGGAAGACTCCTAGCTGTCCTTTTTCCTCTCCACACAGTGCTCAAGGCCAGCTTATAGTC
ATATATATCACCCAGACATAAAGGAAAAGACACATTTTTTAGGAAATGTTTTTAATAAAAGAAAATTACAAAAAA
AAATTTTAAAGACCCCTAACCCTTTGTGTGCTCTCCATTCTGCTCCTTCCCCATCGTTGCCCCCATTTCTGAGGT
GCACTGGGAGGCTCCCCTTCTATTTGGGGCTTGATGACTTTCTTTTTGTAGCTGGGGCTTTGATGTTCCTTCCAG
TGTCATTTCTCATCCACATACCCTGACCTGGCCCCCTCAGTGTTGTCACCAGATCTGATTTGTAACCCACTGAGA
GGACAGAGAGAAATAAGTGCCCTCTCCCACCCTCTTCCTACTGGTCTCTCTATGCCTCTCTACAGTCTCGTCTCT
TTTACCCTGGCCCCTCTCCCTTGGGCTCTGATGAAAAATTGCTGACTGTAGCTTTGGAAGTTTAGCTCTGAGAAC
CGTAGATGATTTCAGTTCTAGGAAAATAAAACCCGTTGATTACT

FIGURE 392

AGCTTTGGGGTTGTCCCTGGACTTGTCTTGGTTCCAGAACCTGACGACCCGGCGACGGCGACGTCTCTTTTGACT
AAAAGACAGTGTCCAGTGCTCCAGCCTAGGAGTCTACGGGGACCGCCTCCCGCGCCGCCACC**ATG**CCCAACTTCT
CTGGCAACTGGAAAATCATCCGATCGGAAAACTTCGAGGAATTGCTCAAAGTGCTGGGGGTGAATGTGATGCTGA
GGAAGATTGCTGTGGCTGCAGCGTCCAAGCCAGCAGTGGAGATCAAACAGGAGGGAGACACTTTCTACATCAAAA
CCTCCACCACCGTGCGCACCACAGAGATTAACTTCAAGGTTGGGGAGGAGTTTGAGGAGCAGACTGTGGATGGGA
GGCCCTGTAAGAGCCTGGTGAAATGGGAGAGTGAGAATAAAATGGTCTGTGAGCAGAAGCTCCTGAAGGGAGAGG
GCCCCAAGACCTCGTGGACCAGAGAACTGACCAACGATGGGGAACTGATCCTGACCATGACGGCGGATGACGTTG
TGTGCACCAGGGTCTACGTCCGAGAG**TGA**GTGGCCACAGGTAGAACCGCGGCCGAAGCCCACCACTGGCCATGCT
CACCGCCCTGCTTCACTGCCCCCTCCGTCCCACCCCCTCCTTCTAGGATAGCGCTCCCCTTACCCCAGTCACTTC
TGGGGGTCACTGGGATGCCTCTTGCAGGGTCTTGCTTTCTTTGACCTCTTCTCTCCTCCCCTACACCAACAAAGA
GGAATGGCTGCAAGAGCCCAGATCACCCATTCCGGGTTCACTCCCCGCCTCCCCAAGTCAGCAGTCCTAGCCCCA
AACCAGCCCAGAGCAGGGTCTCTCTAAAGGGGACTTGAGGGCCTGAGCAGGAAAGACTGGCCCTCTAGCTTCTAC
CCTTTGTCCCTGTAGCCTATACAGTTTAGAATATTTATTTGTTAATTTTATTAAAATGCTTTAAAAAAA

FIGURE 393

MPNFSGNWKIIRSENFEELLKVLGVNVMLRKIAVAAASKPAVEIKQEGDTFYIKTSTTVRTTEINFKVGEEFEEQ
TVDGRPCKSLVKWESENKMVCEQKLLKGEGPKTSWTRELTNDGELILTMTADDVVCTRVYVRE

FIGURE 394

GCAGTCTCCGCCGCAGTCTCAGCTGCAGCTGCAGGACTGAGCCGTGCACCCGGAGGAGACCCCCGGAGGAGGCGA
CAAACTTCGCAGTGCCGCGACCCAACCCCAGCCCTGGGTAGCCTGCAGC**ATG**GCCCAGCTGTTCCTGCCCCTGCT
GGCAGCCCTGGTCCTGGCCCAGGCTCCTGCAGCTTTAGCAGATGTTCTGGAAGGAGACAGCTCAGAGGACCGCGC
TTTTCGCGTGCGCATCGCGGGCGACGCGCCACTGCAGGGCGTGCTCGGCGGCGCCCTCACCATCCCTTGCCACGT
CCACTACCTGCGGCCACCGCCGAGCCGGCGGGCTGTGCTGGGCTCTCCGCGGGTCAAGTGGACTTTCCTGTCCCG
GGGCCGGGAGGCAGAGGTGCTGGTGGCGCGGGGAGTGCGCGTCAAGGTGAACGAGGCCTACCGGTTCCGCGTGGC
ACTGCCTGCGTACCCAGCGTCGCTCACCGACGTCTCCCTGGCGCTGAGCGAGCTGCGCCCCAACGACTCGGGTAT
CTATCGCTGTGAGGTCCAGCACGGCATCGATGACAGCAGCGACGCTGTGGAGGTCAAGGTCAAAGGGGTCGTCTT
TCTCTACCGAGAGGGCTCTGCCCGCTATGCTTTCTCCTTTTCTGGGGCCCAGGAGGCCTGTGCCCGCATTGGAGC
CCACATCGCCACCCCGGAGCAGCTCTATGCCGCCTACCTTGGGGGCTATGAGCAATGTGATGCTGGCTGGCTGTC
GGATCAGACCGTGAGGTATCCCATCCAGACCCCACGAGAGGCCTGTTACGGAGACATGGATGGCTTCCCCGGGGT
CCGGAACTATGGTGTGGTGGACCCGGATGACCTCTATGATGTGTACTGTTATGCTGAAGACCTAAATGGAGAACT
GTTCCTGGGTGACCCTCCAGAGAAGCTGACATTGGAGGAAGCACGGGCGTACTGCCAGGAGCGGGGTGCAGAGAT
TGCCACCACGGGCCAACTGTATGCAGCCTGGGATGGTGGCCTGGACCACTGCAGCCCAGGGTGGCTAGCTGATGG
CAGTGTGCGCTACCCCATCGTCACACCCAGCCAGCGCTGTGGTGGGGGCTTGCCTGGTGTCAAGACTCTCTTCCT
CTTCCCCAACCAGACTGGCTTCCCCAATAAGCACAGCCGCTTCAACGTCTACTGCTTCCGAGACTCGGCCCAGCC
TTCTGCCATCCCTGAGGCCTCCAACCCAGCCTCCAACCCAGCCTCTGATGGACTAGAGGCTATCGTCACAGTGAC
AGAGACCCTGGAGGAACTGCAGCTGCCTCAGGAAGCCACAGAGAGTGAATCCCGTGGGGCCATCTACTCCATCCC
CATCATGGAGGACGGAGGAGGTGGAAGCTCCACTCCAGAAGACCCAGCAGAGGCCCCTAGGACGCTCCTAGAATT
TGAAACACAATCCATGGTACCGCCCACGGGGTTCTCAGAAGAGGAAGGTAAGGCATTGGAGGAAGAAGAGAAATA
TGAAGATGAAGAAGAGAAAGAGGAGGAAGAAGAAGAGGAGGAGGTGGAGGATGAGGCTCTGTGGGCATGGCCCAG
CGAGCTCAGCAGCCCGGGCCCTGAGGCCTCTCTCCCCACTGAGCCAGCAGCCCAGGAGAAGTCACTCTCCCAGGC
GCCAGCAAGGGCAGTCCTGCAGCCTGGTGCATCACCACTTCCTGATGGAGAGTCAGAAGCTTCCAGGCCTCCAAG
GGTCCATGGACCACCTACTGAGACTCTGCCCACTCCCAGGGAGAGGAACCTAGCATCCCCATCACCTTCCACTCT
GGTTGAGGCAAGAGAGGTGGGGGAGGCAACTGGTGGTCCTGAGCTATCTGGGGTCCCTCGAGGAGAGAGCGAGGA
GACAGGAAGCTCCGAGGGTGCCCCTTCCCTGCTTCCAGCCACACGGGCCCCTGAGGGTACCAGGGAGCTGGAGGC
CCCCTCTGAAGATAATTCTGGAAGAACTGCCCCAGCAGGGACCTCAGTGCAGGCCCAGCCAGTGCTGCCCACTGA
CAGCGCCAGCCGAGGTGGAGTGGCCGTGGTCCCCGCATCAGGTGACTGTGTCCCCAGCCCCTGCCACAATGGTGG
GACATGCTTGGAGGAGGAGGAAGGGGTCCGCTGCCTATGTCTGCCTGGCTATGGGGGGGACCTGTGCGATGTTGG
CCTCCGCTTCTGCAACCCCGGCTGGGACGCCTTCCAGGGCGCCTGCTACAAGCACTTTTCCACACGAAGGAGCTG
GGAGGAGGCAGAGACCCAGTGCCGGATGTACGGCGCGCATCTGGCCAGCATCAGCACACCCGAGGAACAGGACTT
CATCAACAACCGGTACCGGGAGTACCAGTGGATCGGACTCAACGACAGGACCATCGAAGGCGACTTCTTGTGGTC
GGATGGCGTCCCCCTGCTCTATGAGAACTGGAACCCTGGGCAGCCTGACAGCTACTTCCTGTCTGGAGAGAACTG
CGTGGTCATGGTGTGGCATGATCAGGGACAATGGAGTGACGTGCCCTGCAACTACCACCTGTCCTACACCTGCAA
GATGGGGCTGGTGTCCTGTGGGCCGCCACCGGAGCTGCCCCTGGCTCAAGTGTTCGGCCGCCCACGGCTGCGCTA
TGAGGTGGACACTGTGCTTCGCTACCGGTGCCGGGAAGGACTGGCCCAGCGCAATCTGCCGCTGATCCGATGCCA
AGAGAACGGTCGTTGGGAGGCCCCCCAGATCTCCTGTGTGCCCAGAAGACCTGCCCGAGCTCTGCACCCAGAGGA
GGACCCAGAAGGACGTCAGGGGAGGCTACTGGGACGCTGGAAGGCGCTGTTGATCCCCCCTTCCAGCCCCATGCC
AGGTCCC**TAG**GGGGCAAGGCCTTGAACACTGCCGGCCACAGCACTGCCCTGTCACCCAAATTTTCCCTCACACCC
TGCGCTCCCGCCACCACAGGAAGTGACAACATGACGAGGGGTGGTGCTGGAGTCCAGGTGACAGTTCCTGAAGGG
GCTTCTGGGAAATACCTAGGAGGCTCCAGCCCAGCCCAGGCCCTCTCCCCCTACCCTGGGCACCAGATCTTCCAT
CAGGGCCGGAGTAAATCCCTAAGTGCCTCAACTGCCCTCTCCCTGGCAGCCATCTTGTCCCCTCTATTCCTCTAG
GGAGCACTGTGCCCACTCTTTCTGGGTTTTCCAAGGGAATGGGCTTGCAGGATGGAGTGTCTGTAAAATCAACAG
GAAATAAAACTGTGTATGAGCCCAGGCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 395

MAQLFLPLLAALVLAQAPAALADVLEGDSSEDRAFRVRIAGDAPLQGVLGGALTIPCHVHYLRPPPSRRAVLGSP
RVKWTFLSRGREAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQHGIDDSSDAV
EVKVKGVVFLYREGSARYAFSFSGAQEACARIGAHIATPEQLYAAYLGGYEQCDAGWLSDQTVRYPIQTPREACY
GDMDGFPGVRNYGVVDPDDLYDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQERGAEIATTGQLYAAWDGGLDH
CSPGWLADGSVRYPIVTPSQRCGGGLPGVKTLFLFPNQTGFPNKHSRFNVYCFRDSAQPSAIPEASNPASNPASD
GLEAIVTVTETLEELQLPQEATESESRGAIYSIPIMEDGGGGSSTPEDPAEAPRTLLEFETQSMVPPTGFSEEEG
KALEEEEKYEDEEEKEEEEEEEEVEDEALWAWPSELSSPGPEASLPTEPAAQEKSLSQAPARAVLQPGASPLPDG
ESEASRPPRVHGPPTETLPTPRERNLASPSPSTLVEAREVGEATGGPELSGVPRGESEETGSSEGAPSLLPATRA
PEGTRELEAPSEDNSGRTAPAGTSVQAQPVLPTDSASRGGVAVVPASGDCVPSPCHNGGTCLEEEEGVRCLCLPG
YGGDLCDVGLRFCNPGWDAFQGACYKHFSTRRSWEEAETQCRMYGAHLASISTPEEQDFINNRYREYQWIGLNDR
TIEGDFLWSDGVPLLYENWNPGQPDSYFLSGENCVVMVWHDQGQWSDVPCNYHLSYTCKMGLVSCGPPPELPLAQ
VFGRPRLRYEVDTVLRYRCREGLAQRNLPLIRCQENGRWEAPQISCVPRRPARALHPEEDPEGRQGRLLGRWKAL
LIPPSSPMPGP

FIGURE 396

CTCCTCACAGAAGCCTGGAGCTGGGCATCCAAGAAGAAGCAGCCTCATTTGTTTTCTGGTGTCATCGTAGGTGGC
CACCTATGGCTTTTGGGAATGTAAAAAGGGCAGCTCTCTGGC**ATG**TTCCTGACTGAGGATCTCATAACATTTAAC
TTGAGGAACTTCCTCCTTTTCCAGCTTTGGGAGTCAAGCTTCTCACCTGGGGCGGGTGGGTTCTGCACCACCCTC
CCACCCTCCTTCCTCCGTGTGGACGATAGAGCCACATCCAGCACCACGGACAGCTCCCGGGCGCCTTCATCTCCT
CGTCCTCCAGGCAGCACAAGCCATTGTGGAATCTCCACCAGGTGTACAGAACGGTGCCTCTGCGTCCTGCCACTC
AGGACCTCTCAAGTCCCCGATGTGATGGCTCCTCAGCATGATCAGGAGAAATTCCATGATCTTGCTTATTCCTGT
CTTGGGAAGTCCTTCTCCATGTCTAACCAAGATCTATATGGCTATAGCACCAGCTCTTTGGCTCTTGGCTTGGCA
TGGCTAAGTTGGGAGACCAAAAAGAAGAATGTACTTCATCTGGTTGGGCTGGATTCCCTC**TGA**TAAGCCTTCCCA
GTTGACTGAAAGATGAGGCTAGGCTCTAGCAAGTTGAAGTCAAACCAGCTCCTTCAAGAAGCTTTGAGCAGAATG
AAGTGGGGAGGACCCAGCTTCCAGCCCAGGAAGCCCACTGTACCTGGAGCCATCTGGGATAAGACTTTGACCCAT
GACTCCCATATCCACAGCCTGTCCATCCTAGCCCATCCCAGTTTATCCTGTATCATTTGAGCTGGGATTCCCACA
TCCTCTGAGTTGGAAGTCCCATCTCAAGTCTTCAATAAAGACTCTTGAATATTG

FIGURE 397

MFLTEDLITFNLRNFLLFQLWESSFSPGAGGFCTTLPPSFLRVDDRATSSTTDSSRAPSSPRPPGSTSHCGISTR
CTERCLCVLPLRTSQVPDVMAPQHDQEKFHDLAYSCLGKSFSMSNQDLYGYSTSSLALGLAWLSWETKKKNVLHL
VGLDSL

FIGURE 398

TTGCGTAGGGGGCGGGACTAAGGCTGTCAATTGGTCTGTTTTTGTGCCGATCAATGAGATGGGTGCGGTGATTGG
CGACTACCTTGAGAGTAGCGGGTTGAGGTGTAAGCCCTGAGGAGGCAGCGTTTTCTGGGCTTCTGTCTGGTTCTC
TCTCTCCAGAAGGTTCTGCCGGTTCCCCCAGCTCTGGGTACCCGGCTCTGCATCGCGTCGCCATGATGGGCCATC
GTCCAGTGCTCGTGCTCAGCCAGAACACAAAGCGTGAATCCGGAAGAAAAGTTCAATCTGGAAACATCAATGCTG
CCAAGACTATTGCAGATATCATCCGAACATGTTTGGGACCCAAGTCCATGATGAAGATGCTTTTGGACCCAATGG
GAGGCATTGTGATGACCAATGATGGCAATGCCATTCTTCGAGAGATTCAAGTCCAGCATCCAGCGGCCAAGTCCA
TGATCGAAATTAGCCGGACCCAGGATGAAGAGGTTGGAGATGGGACCACATCAGTAATTATTCTTGCAGGGGAAA
TGCTGTCTGTAGCTGAGCACTTCCTGGAGCAGCAGATGCACCCAACAGTGGTGATCAGTGCTTACCGCAAGGCAT
TGGATGATATGATCAGCACCCTAAAGAAAATAAGTATCCCAGTCGACATCAGTGACAGTGATATGATGCTGAACA
TCATCAACAGCTCTATTACTACCAAAGCCATCAGTCGGTGGTCATCTTTGGCTTGCAACATTGCCCTGGATGCTG
TCAAGATGGTACAGTTTGAGGAGAATGGTCGGAAAGAGATTGACATAAAAAAATATGCAAGAGTGGAAAAGATAC
CTGGAGGCATCATTGAAGACTCCTGTGTCTTGCGTGGAGTCATGATTAACAAGGATGTGACCCATCCACGTATGC
GGCGCTATATCAAGAACCCTCGCATTGTGCTGCTGGATTCTTCTCTGGAATACAAGAAAGGAGAAAGCCAGACTG
ACATTGAGATTACACGAGAGGAGGACTTCACCCGAATTCTCCAGATGGAGGAAGAGTACATCCAGCAGCTCTGTG
AGGACATTATCCAACTGAAGCCCGATGTGGTCATCACTGAAAAGGGCATCTCAGATTTAGCTCAGCACTACCTTA
TGCGGGCCAATATCACAGCCATCCGCAGAGTCCGGAAGACAGACAATAATCGCATTGCTAGAGCCTGTGGGGCCC
GGATAGTCAGCCGACCAGAGGAACTGAGAGAAGATGATGTTGGAACAGGAGCAGGCCTGTTGGAAATCAAGAAAA
TTGGAGATGAATACTTTACTTTCATCACTGACTGCAAAGACCCCAAGGCCTGCACCATTCTCCTCCGGGGGGCTA
GCAAAGAGATTCTCTCGGAAGTAGAACGCAACCTCCAGGATGCCATGCAAGTGTGTCGCAATGTTCTCCTGGACC
CTCAGCTGGTGCCAGGGGGTGGGGCCTCCGAGATGGCTGTGGCCCATGCCTTGACAGAAAAATCCAAGGCCATGA
CTGGTGTGGAACAATGGCCATACAGGGCTGTTGCCCAGGCCCTAGAGGTCATTCCTCGTACCCTGATCCAGAACT
GTGGGGCCAGCACCATCCGTCTACTTACCTCCCTTCGGGCCAAGCACACCCAGGAGAACTGTGAGACCTGGGGTG
TAAATGGTGAGACGGGTACTTTGGTGGACATGAAGGAACTGGGCATATGGGAGCCATTGGCTGTGAAGCTGCAGA
CTTATAAGACAGCAGTGGAGACGGCAGTTCTGCTACTGCGAATTGATGACATCGTTTCAGGCCACAAAAAGAAAG
GCGATGACCAGAGCCGGCAAGGCGGGGCTCCTGATGCTGGCCAGGAGTGAGTGCTAGGCAAGGCTACTTCAATGC
ACAGAACCAGCAGAGTCTCCCCTTTTCCTGAGCCAGAGTGCCAGGAACACTGTGGACGTCTTTGTTCAGAAGGGA
TCAGGTTGGGGGGCAGCCCCCAGTCCCTTTCTGTCCCAGCTCAGTTTTCCAAAAGACACTGACATGTAATTCTTC
TCTATTGTAAGGTTTCCATTTAGTTTGCTTCCGATGATTAAATCTAAGTCATTTG

FIGURE 399

MGHRPVLVLSQNTKRESGRKVQSGNINAAKTIADIIRTCLGPKSMMKMLLDPMGGIVMTNDGNAILREIQVQHPA
AKSMIEISRTQDEEVGDGTTSVIILAGEMLSVAEHFLEQQMHPTVVISAYRKALDDMISTLKKISIPVDISDSDM
MLNIINSSITTKAISRWSSLACNIALDAVKMVQFEENGRKEIDIKKYARVEKIPGGIIEDSCVLRGVMINKDVTH
PRMRRYIKNPRIVLLDSSLEYKKGESQTDIEITREEDFTRILQMEEEYIQQLCEDIIQLKPDVVITEKGISDLAQ
HYLMRANITAIRRVRKTDNNRIARACGARIVSRPEELREDDVGTGAGLLEIKKIGDEYFTFITDCKDPKACTILL
RGASKEILSEVERNLQDAMQVCRNVLLDPQLVPGGGASEMAVAHALTEKSKAMTGVEQWPYRAVAQALEVIPRTL
IQNCGASTIRLLTSLRAKHTQENCETWGVNGETGTLVDMKELGIWEPLAVKLQTYKTAVETAVLLLRIDDIVSGH
KKKGDDQSRQGGAPDAGQE

FIGURE 400

GAATTGCGGCCGT<u>**ATG**</u>CGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCCCCAGCCCCCTGCTCCT
TTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGAAGACCCGCCAGGTGTCTCTGGAGGTCAT
CCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTCATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGT
GTGGAGCAGCCTGGGGCCTCTGGCAGTGGTAATGGTGGCCACCAACACCCCCCACAGCACCCTGAGCGTCAACTG
GAGCCTCCTGCTATCCCCTGAGCCCGATGGGGGCCTGATGGTGCTCCCTAAGGACAGCATTCAGTTTTCTTCTGC
CCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGCCTTTGGGAAGACC
ATATCCTCCATACTCCTTGGCCGATTTCTCTTGGAACAACATCACTGATTCATTGGATCCTGCCACCCTGAGTGC
CACATTTCAAGGCCACCCCATGAACGACCCTACCAGGACTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGC
CTTTTCCAGGTCCAGCCGACCAGCCCAACCCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGC
CCTGATTGGAGCCTCTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGA
CTGCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGGACCAGCTACT
GTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCCAGAAGCCGGGGGGCCGAGAATC
AGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAGCATACTCTCTTCCCCAGTCACCCATTGTCCGAGC
CTTCTTTGGGTCCCAGAATAACTTCTGTGCCTTCAATCTGACGTTCGGGGCTTCCACAGGCCCTGGCTATTGGGA
CCAACACTACCTCAGCTGGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCACTAGTCCT
GGGCATCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGCTGCACCA
CAAGAAGTACTCAGAGTACCAGTCCATAAAT<u>**TAA**</u>GGCCCGCTCTCTGGAGGGAAGGACATTACTGAACCTGTCTT
GCTGTGCCTCGAAACTCTGGAGGTTGGAGCATCAAGTTCCAGCCGGCCCCTTCACTCCCCCATCTTGCTTTTCTG
TGGAACCTCAGAGGCCAGCCTCGACTTCCTGGAGACCCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTT
TGGAGGCGGGCAGGGGACAGGGCTATTGATAAGGTCCCCTTGGTGTTGCCTTCTTGCATCTCCACACATTTCCCT
TGGATGGGACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGATTTA
TTTTTTTTC

FIGURE 401

MRGSVECTWGWGHCAPSPLLLWTLLLFAAPFGLLGEKTRQVSLEVIPNWLGPLQNLLHIRAVGTNSTLHYVWSSL
GPLAVVMVATNTPHSTLSVNWSLLLSPEPDGGLMVLPKDSIQFSSALVFTRLLEFDSTNVSDTAAKPLGRPYPPY
SLADFSWNNITDSLDPATLSATFQGHPMNDPTRTFANGSLAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGA
SPRGNRSLFGLEVATLGQGPDCPSMQEQHSIDDEYAPAVFQLDQLLWGSLPSGFAQWRPVAYSQKPGGRESALPC
QASPLHPALAYSLPQSPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPPVDGLSPLVLGIMA
VALGAPGLMLLGGGLVLLLHHKKYSEYQSIN

FIGURE 402

GGCAGCATGGCGTCTTTCCGGCTTCTCCAAACCCTTGCGAAAAACTTTATTGGCAAAGCTATCAGAGAACGGACA
GTGTACCCACTGAGGCGGCCAAAGCTTAACTGGATCAGGGCAGGATGACATGACCTTGTGGTAGATCCCAGAACT
GAGGCCCCAGG**ATG**ACAGAACAGGAGACCCTGGCCCTACTGGAAGTGAAGAGGTCTGATTCCCCAGAGAAGAGCT
CACCCCAGGCCTTGGTTCCCAATGGCCGGCAGCCAGAAGGGGAAGGTGGGGCCGAATCCCCGGGAGCTGAGTCCC
TCAGAGTGGGGTCTTCAGCTGGATCTCCCACAGCCATAGAGGGGGCTGAGGATGGTCTAGACAGCACAGTAAGTG
AGGCTGCCACCTTGCCCTGGGGGACTGGCCCTCAGCCCAGTGCTCCGTTCCCGGATCCCCCTGGCTGGCGGGACA
TTGAACCAGAGCCCCCTGAGTCAGAACCACTTACCAAGCTAGAGGAGCTGCCCGAAGACGATGCCAACCTGCTGC
CTGAGAAAGCGGCCCGTGCCTTCGTGCCTATTGACCTACAGTGCATTGAGCGGCAGCCCCAAGAAGACCTTATCG
TGCGCTGTGAGGCAGGCGAGGGCGAGTGCCGAACCTTCATGCCCCCCCGGGTCACCCACCCCGACCCCACTGAGC
GCAAGTGGGCTGAGGCAGTGGTGAGGCCGCCTGGCTGTTCCTGTGGGGGCTGCGGGAGCTGTGGAGACCGTGAGT
GGCTAAGGGCTGTGGCCTCCGTGGGAGCCGCACTCATTCTCTTCCCTTGCCTACTATACGGGGCATATGCCTTCC
TGCCGTTTGATGTCCCACGGCTGCCCACCATGAGTTCCCGCCTGATCTACACACTGCGCTGCGGGGTCTTTGCCA
CCTTCCCCATTGTGCTGGGGATCCTGGTGTACGGGCTGAGCCTGTTATGCTTTTCTGCCCTTCGGCCCTTTGGGG
AGCCACGGCGGGAGGTGGAGATCCACCGGCGATATGTGGCCCAGTCGGTCCAGCTCTTTATTCTCTACTTCTTCA
ACCTGGCCGTGCTTTCCACTTACCTGCCCCAGGATACCCTCAAACTGCTCCCTCTGCTCACTGGTCTCTTTGCCG
TCTCCCGGCTGATCTACTGGCTGACCTTTGCCGTGGGCCGCTCCTTCCGAGGCTTCGGCTACGGCCTGACGTTTC
TGCCACTGCTGTCGATGCTGATGTGGAACCTCTACTACATGTTCGTGGTGGAGCCGGAGCGCATGCTCACTGCCA
CCGAGAGCCGCCTGGACTACCCGGACCACGCCCGCTCGGCCTCCGACTACAGGCCCCGCCCCTGGGGC**TGA**GCCT
CTCCGCCCTCGCCCTCGGAGTAGGGGGTAGCGGCTTGGGTCTGACACATCTTTGAACCTTGTGGCCAGGCCTGGA
CTTCGCCCCCAGGCCTAGGACCGCGGTGGGTGGAACCCTGCTACTGCCCCAACAGGGACTCCAATCAATCGGAGT
TCTCCCCTTGCCGGAGCTGCCCTTCACCTTTGGGGCCCGAGACAGTCATAAGGGATGGACTTAGTTTTCTTGCAG
GGAAAAAGGTGGACAGCCGTGTTTCTTAAGGATGCTGAGGGCATGGGGCCAGGACCAGGGGAGAGGCACAGCTCC
TTCCTGAGCAGCCTCTCACCACTGCCACAAGGCTCCCTAATGCTGGTCTCTGCTCCACTCCCCGGCTTCCCGTGA
GGCAGGAGGCAGAGCCACAGCCAAGGCCCTGACCACTTCTGTGCCAGTTGTCTAAGCAGAGCGCCTCAGGGACGC
TGGAAATGCCTTAAGGATAGAGGCTGGGCATCACATCAAATGGGACTGTGGTGTTTGGTGAAAACCTTCCTGAGG
ATCTGGATTCAGGACCCTCCATGACTGGCCTATTTACTGTTTACAGCTGGCCAGTGCAGAGCTGCTGCTCTTTTA
CCTTTTTAGGCCCCTGTAACTTCCCACCTTTAAACTGCCCAGAAGGCATGCCTCTCCCACAGGAAGAGGGGAGCA
GACAGGGAAATCTGCCTACCAAGAGGGGTGTGTGTGTCTTTGTGCCCACACGTGGTGGCTGGGGAGTGCCTGGAT
GGTGCGGTGGTTGATGTTAACCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAACAATAAATTACTACCAG
TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 403

MTEQETLALLEVKRSDSPEKSSPQALVPNGRQPEGEGGAESPGAESLRVGSSAGSPTAIEGAEDGLDSTVSEAAT
LPWGTGPQPSAPFPDPPGWRDIEPEPPESEPLTKLEELPEDDANLLPEKAARAFVPIDLQCIERQPQEDLIVRCE
AGEGECRTFMPPRVTHPDPTERKWAEAVVRPPGCSCGGCGSCGDREWLRAVASVGAALILFPCLLYGAYAFLPFD
VPRLPTMSSRLIYTLRCGVFATFPIVLGILVYGLSLLCFSALRPFGEPRREVEIHRRYVAQSVQLFILYFFNLAV
LSTYLPQDTLKLLPLLTGLFAVSRLIYWLTFAVGRSFRGFGYGLTFLPLLSMLMWNLYYMFVVEPERMLTATESR
LDYPDHARSASDYRPRPWG

FIGURE 404

ACTCAGTGTTCGCGGGAGCCGCACCTACACCAGCCAACCCAGATCCCGAGGTCCGACAGCGCCCGGCCCAGATCC
CCACGCCTGCCAGGAGCAAGCCGAGAGCCAGCCGGCCGGCGCACTCCGACTCCGAGCAGTCTCTGTCCTTCGACC
CGAGCCCCGCGCCCTTTCCGGGACCCCTGCCCCGCGGGCAGCGCTGCCAACCTGCCGGCC**ATG**GAGACCCCGTCC
CAGCGGCGCGCCACCCGCAGCGGGGCGCAGGCCAGCTCCACTCCGCTGTCGCCCACCCGCATCACCCGGCTGCAG
GAGAAGGAGGACCTGCAGGAGCTCAATGATCGCTTGGCGGTCTACATCGACCGTGTGCGCTCGCTGGAAACGGAG
AACGCAGGGCTGCGCCTTCGCATCACCGAGTCTGAAGAGGTGGTCAGCCGCGAGGTGTCCGGCATCAAGGCCGCC
TACGAGGCCGAGCTCGGGGATGCCCGCAAGACCCTTGACTCAGTAGCCAAGGAGCGCGCCCGCCTGCAGCTGGAG
CTGAGCAAAGTGCGTGAGGAGTTTAAGGAGCTGAAAGCGCGCAATACCAAGAAGGAGGGTGACCTGATAGCTGCT
CAGGCTCGGCTGAAGGACCTGGAGGCTCTGCTGAACTCCAAGGAGGCCGCACTGAGCACTGCTCTCAGTGAGAAG
CGCACGCTGGAGGGCGAGCTGCATGATCTGCGGGGCCAGGTGGCCAAGCTTGAGGCAGCCCTAGGTGAGGCCAAG
AAGCAACTTCAGGATGAGATGCTGCGGCGGGTGGATGCTGAGAACAGGCTGCAGACCATGAAGGAGGAACTGGAC
TTCCAGAAGAACATCTACAGTGAGGAGCTGCGTGAGACCAAGCGCCGTCATGAGACCCGACTGGTGGAGATTGAC
AATGGGAAGCAGCGTGAGTTTGAGAGCCGGCTGGCGGATGCGCTGCAGGAACTGCGGGCCCAGCATGAGGACCAG
GTGGAGCAGTATAAGAAGGAGCTGGAGAAGACTTATTCTGCCAAGCTGGACAATGCCAGGCAGTCTGCTGAGAGG
AACAGCAACCTGGTGGGGGCTGCCCACGAGGAGCTGCAGCAGTCGCGCATCCGCATCGACAGCCTCTCTGCCCAG
CTCAGCCAGCTCCAGAAGCAGCTGGCAGCCAAGGAGGCGAAGCTTCGAGACCTGGAGGACTCACTGGCCCGTGAG
CGGGACACCAGCCGGCGGCTGCTGGCGGAAAAGGAGCGGGAGATGGCCGAGATGCGGGCAAGGATGCAGCAGCAG
CTGGACGAGTACCAGGAGCTTCTGGACATCAAGCTGGCCCTGGACATGGAGATCCACGCCTACCGCAAGCTCTTG
GAGGGCGAGGAGGAGAGGCTACGCCTGTCCCCCAGCCCTACCTCGCAGCGCAGCCGTGGCCGTGCTTCCTCTCAC
TCATCCCAGACACAGGGTGGGGGCAGCGTCACCAAAAAGCGCAAACTGGAGTCCACTGAGAGCCGCAGCAGCTTC
TCACAGCACGCACGCACTAGCGGGCGCGTGGCCGTGGAGGAGGTGGATGAGGAGGGCAAGTTTGTCCGGCTGCGC
AACAAGTCCAATGAGGACCAGTCCATGGGCAATTGGCAGATCAAGCGCCAGAATGGAGATGATCCCTTGCTGACT
TACCGGTTCCCACCAAAGTTCACCCTGAAGGCTGGGCAGGTGGTGACGATCTGGGCTGCAGGAGCTGGGGCCACC
CACAGCCCCCCTACCGACCTGGTGTGGAAGGCACAGAACACCTGGGGCTGCGGGAACAGCCTGCGTACGGCTCTC
ATCAACTCCACTGGGGAAGAAGTGGCCATGCGCAAGCTGGTGCGCTCAGTGACTGTGGTTGAGGACGACGAGGAT
GAGGATGGAGATGACCTGCTCCATCACCACCATGTGAGTGGTAGCCGCCGC**TGA**GGCCGAGCCTGCACTGGGGCC
ACCCAGCCAGGCCTGGGGGCAGCCTCTCCCCAGCCTCCCCGTGCCAAAAATCTTTTCATTAAAGAATGTTTGGAA
CTTT

FIGURE 405

METPSQRRATRSGAQASSTPLSPTRITRLQEKEDLQELNDRLAVYIDRVRSLETENAGLRLRITESEEVVSREVS
GIKAAYEAELGDARKTLDSVAKERARLQLELSKVREEFKELKARNTKKEGDLIAAQARLKDLEALLNSKEAALST
ALSEKRTLEGELHDLRGQVAKLEAALGEAKKQLQDEMLRRVDAENRLQTMKEELDFQKNIYSEELRETKRRHETR
LVEIDNGKQREFESRLADALQELRAQHEDQVEQYKKELEKTYSAKLDNARQSAERNSNLVGAAHEELQQSRIRID
SLSAQLSQLQKQLAAKEAKLRDLEDSLARERDTSRRLLAEKEREMAEMRARMQQQLDEYQELLDIKLALDMEIHA
YRKLLEGEEERLRLSPSPTSQRSRGRASSHSSQTQGGGSVTKKRKLESTESRSSFSQHARTSGRVAVEEVDEEGK
FVRLRNKSNEDQSMGNWQIKRQNGDDPLLTYRFPPKFTLKAGQVVTIWAAGAGATHSPPTDLVWKAQNTWGCGNS
LRTALINSTGEEVAMRKLVRSVTVVEDDEDEDGDDLLHHHHVSGSRR

FIGURE 406

GCGCAGACGCCCCAGCCCCCCACCGCCCCCAAAGGGGCGAGCGACGCCAAGCTCTGCGCTCTCTACAAAGAGGCC
GAGCTGCGCCTGAAGGGCAGCAGCAACACCACGGAGTGTGTTCCCGTGCCCACCTCCGAGCACGTGGCCGAGATC
GTGGGCAGGCAAGGCTGCAAGATTAAGGCCTTGAGGGCCAAGACCAACACCTACATCAAGACACCGGTGAGGGGC
GAGGAACCAGTGTTCATGGTGACAGGGCGACGGGAGGACGTGGCCACAGCCCGGCGGGAAATCATCTCAGCAGCG
GAGCACTTCTCCATGATCCGTGCCTCCCGCAACAAGTCAGGCGCCGCCTTTGGTGTGGCTCCTGCTCTGCCCGGC
CAGGTGACCATCCGTGTGCGGGTGCCCTACCGCGTGGTGGGGCTGGTGGTGGGCCCCAAAGGGGCAACCATCAAG
CGCATCCAGCAGCAAACCAACACATACATTATCACACCAAGCCGTGACCGCGACCCCGTGTTCGAGATCACGGGT
GCCCCAGGCAACGTGGAGCGTGCGCGCGAGGAGATCGAGACGCACATCGCGGTGCGCACTGGCAAGATCCTCGAG
TACAACAATGAAAACGACTTCCTGGCGGGGAGCCCCGACGCAGCAATCGATAGCCGCTACTCCGACGCCTGGCGG
GTGCACCAGCCCGGCTGCAAGCCCCTCTCCACCTTCCGGCAGAACAGCCTGGGCTGCATCGGCGAGTGCGGAGTG
GACTCTGGCTTTGAGGCCCCACGCCTGGGTGAGCAGGGCGGGGACTTTGGCTACGGCGGGTACCTCTTTCCGGGC
TATGGCGTGGGCAAGCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCCCGCTGTGGGCGGGCCAGGAGAAC
GCCACGCCCACCTCCGTGCTCTTCTCCTCTGCCTCCTCCTCCTCCTCTTCCGCCAAGGCCCGCGCTGGGCCC
CCGGGCGCACACCGCTCCCCTGCCACTTCCGCGGGACCCGAGCTGGCCGGACTCCCGAGGCGCCCCCGGGAGAG
CCGCTCCAGGGCTTCTCTAAACTTGGTGGGGGCGGCCTGCGGAGCCCCGGCGGCGGGCGGGATTGCATGGTCTGC
TTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCTGCGGACACAACCTGTTCTGCATGGAGTGTGCAGTACGCATC
TGCGAGAGGACGGACCCAGAGTGTCCCGTCTGCCACATCACAGCCACGCAAGCCATCCGAATATTCTCCTAAGCC
CCGTGCCCCATGCCTCCGGGGCCCACTCCACTGGGCCCACCCTGGACCTGTTTTCCACTAAAGCCTTTTGGAAAG
CGGTGATTTGAGGGGCAAGGTGCTTAGAGATACTCGCTCGCTGGGGAAGGGGGGAGGGAGGCAGTGGTGGCTGGA
GGGTGCGCCACTTTCAGAGCCTCTGGTCACCCTGTCCTGGAAAGATTGGGAGGGGGCCAGACTGAAAATTTTACT
AGAGTTACAACTCTGATACCTCAACACACCCTTAAATCTGGAAGCAGCTAAGAGAAACTTTTGTTTTGCCAGAGG
TGGCCACTAAGGCATTCTGACGCCCTCTGCCCACCTCCCCCGCTGTGTGTCACTCCACCCCTTCTTCCGAGGAGG
GGGTGGGTAAAAGGGAGAGGGAGAATTACCACCTGTATCTAGAGGTGCTCTTTGCAATCCCTAAGCCCTCTGGTC
CTGACCTCCGACCTCCCAGCTCTGTCTTGTTCCTTGTCTTTGTCTTTCTTCCCTTCCCCCTGCCCCTGCCCCTAC
CAGCCCAGCTTTGGGGACACCATCCTTCTGGGGAGAAGTAGGGGGAGGAATATTTGGATGGTCCCTCCATTCCTC
TTCAGGCATCTGGAGGCCCTCTCCCCCACTCCTCCAAAGAAACATCTCAAATTATTGATGGAATGTATCCCCATT
CTCAGTGAAAATGTGAGGAGGGGACTAATACTGGGGTAAAGGGTCAAACCCCCACCTTCATCACTATGGGCATTA
TATTTAGGGAGTAGTTCTTGGGCTGGATTTTCTGGTTGTGGAAGTGGGGGCGCCAGAGTAGTGTGTCTGCTATTT
AAAGGAGCAGGAAAGGGCGTGAGGCAGGAGGAGAGACTGGTGGAGGGAAGAGCTGCTCCTCCCATGCAGTGCCCG
ACTCCCTGCACCCCTCTCAACCTGACCTGAACCTTTATTGAATCCTTATTAGCTTGAATCCTTATTAGCTTGAAT
CCTCCATGCAAATCATGGAGTCTGTGTCCCACCTGATGTGGTTGAGGAGAAGCCAGGTCTTCAAAGAGGGGTCAG
CCTGGGGCAAAGCAGGACTGGGGGGAGGTGGGCAGCAGGGCCTATTCTGAGAATCACATATTGTTACAGGCCTTG
CACCCCCTTTGCTGCTTCCCTCCTGCTCATTTGGGGCTGCCACCAGCTCTCCACCCTCCTGGTTCCGCTGGCCGG
GCCAAGAGAGGATGGAGGGATGGGAGTCCCAGGAGATCCTTGTAAATAGTGGGGTGGGACTGTTCTGAGTGATCA
CCCGAGCACTTAAAGCTCCAGAGTCCCATTCTTCCTGGATGGAGCAGGTGGAGGTGCAGAGGGGATTTCCTCCTC
TCCTTCCTCCTGTCGAGAATTAACACCTCTCCACAGCCTTCCCCTCCAGAACACCAGCCAGGGAGGGGTGGGGAA
GGAGGTCACAGCCAAGAAAACTGCCCTGTGACGACTTCCCTCCTTCCCGCCTATGTGAGCCATCCTGAGATGTCT
GTACAATAGAAACCAAACCAAATGGGCACCCTCGGTTGCCGGGGGGCAGGTGGGGAGGGGGGTGGGAAGAAGGGA
TGTCTGTCTGTCGTCCCCCTCCCCCTCTCCACTCTTTACCCACAAAGGCAGAAGACTGTTACACTAGGGGGCTCA
GCAAATTCAATCCCACCCTTACCAATTGAGCCAAACCTAGAAACAAACACAAAACACGAATAGTGAGAGACAAAA
TAGAGGAGAGAAAGAGAGCATGAGAGGGAGCGAGACAGGCGACCAACACAGAGGAGAGAAAACAAAAATAGC

FIGURE 407

LRLKGSSNTTECVPVPTSEHVAEIVGRQGCKIKALRAKTNTYIKTPVRGEEPVFMVTGRREDVATARREIISAAE
HFSMIRASRNKSGAAFGVAPALPGQVTIRVRVPYRVVGLVVGPKGATIKRIQQQTNTYIITPSRDRDPVFEITGA
PGNVERAREEIETHIAVRTGKILEYNNENDFLAGSPDAAIDSRYSDAWRVHQPGCKPLSTFRQNSLGCIGECGVD
SGFEAPRLGEQGGDFGYGGYLFPGYGVGKQDVYYGVAETSPPLWAGQENATPTSVLFSSASSSSSSSAKARAGPP
GAHRSPATSAGPELAGLPRRPPG

FIGURE 408

GGAGGAGCCGGGCGGGCTGGCGGGCGGCCGGGTGGCGGCGGCGGCATGGCGGAGCCGAGCGGGGCCGAGACGAGG
CCCCCCATTCGGGTCACCGTCAAGACCCCCAAGGACAAGGAGGAAATTGTGATCTGCGATCGAGCCTCGGTCAAG
GAGTTCAAAGAGGAAATCTCCCGGAGGTTTAAGGCTCAGCAGGATCAGCTGGTCCTGATCTTCGCAGGCAAGATC
CTCAAGGATGGGGACACACTGAACCAGCACGGAATCAAGGACGGGCTCACTGTCCATCTGGTCATCAAGACCCCT
CAGAAGGCTCAAGATCCAGCTGCTGCCACTGCTTCTTCCCCCTCCACACCTGACCCTGCCTCAGCACCCTCCACC
ACGCCTGCTTCACCCGCCACCCCTGCCCAGCCCTCCACCTCTGGCAGTGCCTCTTCAGATGCTGGCAGTGGAAGC
CGGAGGAGCAGTGGTGGGGGGCCCTCTCCGGGGGCTGGGGAGGGATCCCCCAGTGCTACTGCGTCCATACTCTCT
GGCTTTGGGGGCATCCTGGGGCTGGGCAGCCTAGGCCTGGGCTCTGCCAACTTCATGGAGCTGCAGCAGCAGATG
CAGCGGCAGCTGATGTCCAATCCTGAGATGCTGTCACAGATCATGGAGAACCCCCTGGTCCAGGATATGATGTCT
AACCCTGATCTGATGCGTCACATGATTATGGCCAACCCCCAGATGCAGCAGTTGATGGAGCGGAACCCTGAGATC
AGCCACATGCTCAATAACCCTGAACTCATGAGGCAGACAATGGAGCTTGCTCGGAATCCAGCCATGATGCAAGAG
ATGATGCGGAACCAGGACCGGGCCCTGAGCAACCTTGAGAGCATCCCTGGAGGGTATAATGCCCTCCGCCGCATG
TACACGGACATCCAGGAGCCCATGTTCAGTGCTGCCCGGGAACAGTTTGGCAACAATCCCTTCTCTTCCCTGGCC
GGGAACTCCGACAGCTCATCCTCCCAGCCTCTGCGGACTGAGAATCGAGAGCCCCTCCCTAACCCCTGGAGCCCC
TCGCCCCCCACCTCCCAGGCCCCCGGGTCCGGTGGGGAGGGCACCGGAGGATCGGGGACCAGCCAGGTGCACCCG
ACAGTCTCGAACCCCTTTGGGATCAATGCGGCTAGCCTGGGGTCAGGGATGTTCAATAGCCCAGAAATGCAAGCC
CTCCTCCAGCAGATCTCTGAGAACCCCCAGCTGATGCAGAATGTGATCTCAGCACCCTACATGCGCAGCATGATG
CAGACGCTTGCCCAGAACCCCGACTTTGCTGCTCAGATGATGGTGAATGTGCCGCTCTTCGCGGGGAACCCCCAA
CTGCAGGAGCAGCTCCGCCTGCAGCTCCCAGTCTTCCTGCAGCAGATGCAGAACCCAGAGTCACTCTCCATCCTT
ACCAATCCCCGAGCCATGCAGGCATTGCTGCAGATCCAGCAGGGACTACAGACCTTGCAGACCGAGGCCCCTGGG
CTGGTACCCAGCCTTGGCTCCTTTGGGATATCCCGGACCCCAGCACCCTCAGCAGGCAGCAACGCAGGGTCTACG
CCCGAGGCCCCCACTTCCTCACCAGCCACGCCAGCCACATCTTCTCCAACAGGGGCTTCCAGCGCCCAGCAGCAA
CTCATGCAGCAGATGATCCAGCTTTTGGCTGGAAGTGGAAACTCACAGGTGCAGACGCCAGAAGTGAGATTTCAG
CAGCAGCTGGAGCAGCTCAACTCCATGGGCTTCATCAATCGTGAGGCTAACCTGCAGGCCCTGATTGCCACAGGA
GGGGACATCAACGCAGCTATCGAGAGACTGCTGGGCTCCCAGCTCTCCTAATCCCTCGGCCCATGCCTCCTGCCT
CTCCCCTCCCTCGATGTCAGCATTCGGTTCTTCTGTCAATCCTTACCCTCTGCAGCTTGTCCTCCCTTCCGTCTT
CTCCCTCATCCTTTCCAAACAGCAGGGTGACTTTAGAGGCATGGGCTCCAACCCCTTAGCTCTGTCTGAGAATTA
TGGTTTTACTGCTACGTCTCTAACAGACTCTTCTCTCCTGGTCTCCTTGAGCAGTGCTACTTAAACAGTTTTCAC
AGTTTCATTGATTGACTCTACCTCCTTGCCCCACACCACTTTTGCAATCTTTAAACTTTCAGTGGCTGTGCAGAG
TCGAGGGAGGAACCAGCTCTCTGGTTTACTGGAACATAGTCTTCCATCTATACCACTAGGGTTTTGTCTTATGTT
TACTTTTGGTAACTCTCTTCCTTCTTTTTCTCCCTACCCCCCAACCCCTAGCCCAACCAATGCTAGAATTTCTTG
CTCTGAAGGAGGAGCAGGTGAAACAGGTGGTAATTTTCCTTCTCGGCCCCTATTCTGGTTCATTCAGCACTTTTT
GGTGGGAACTGTTGGAAATTCCAGGGTAAGGAGGAAGATGCCTGTTCTCCCTGTCTGAAGAGGGAGATGAGACAG
CTCTCTGGACAGGAATTAACAAACGCTGGAGCAGCCCAGAGGAAATTCGTGTGAAAGAGGAGGGAATGAGATTAT
TCGGAGGAAGGGAATGGGGGAGACAGCCTGAGTAAAAGGCTTGGAAGTTGGAATTAACAGTGGGGAGCAGAAGCA
CTCATAGCTCTTTTAGGCAGAAGAATCCAGGCCCGAGCTGGCAGAAGAGACTTAGAGATGCTAATGGAATTTAAA
CTGAAAAAAGGAGCCCAATGAAGCTAAGCGCCACGCCCCACAAGGGGTCATATTGGCTTTAGTTCCTCAAGCATA
TGTGCTTATATGCACACACACACACATTTCCATGGACCCAGGTCTTGCTTGTGTCCCCAGGCACCAGTAGTTTGA
GCCCCCCTCAAAAGACATGAAGGGGGTTGGGGTCTGTGTGAGTAGTGGGGAGGTGCATGTGTATCCACATGTGTG
CATACACTCTTAAGTTGGGTGGGAAGTGGATTCCTTGTTGGTTTCTGGTTCAGAGTGCTCTCCCACCACCAGAGA
CAAGTGGGTAAAAAGGTCAGTCCATTGCAGGAATATATATCCGGGAGAGCTAGGTCCCTTGGGGCTCTGGATGCT
GGGTAACCCAGAGGTAATGTGGGTACCCTTTCTGAAGCTGTCAGGGCTGTGACTAGCACCCTTATCACCCCTCAC
TGCCTTGTGGGAATAGTAGAGGGTTTTTTCCTCCAGAGCCCCTGGCCTTTCAGTTCTTAACTATTTCCCTCCAG
GCCAGAAAGTTTTCTTTGAGGAAGGAGAGGAGAGGGTGGCAATGATGCCTTTGATCTGGAATTGGACATTTCTCT
GTCAGAGCACAGAGGAGGCTCATATCACCTCTTCCCTCTCCTACTTGGCCCAGCTGCTTGGAGGACCGACCCCAT
GGCTGAGAATATGACGGCAAGAGGAACAGAGTTTGCTCCAAGTGGGAAAGGGTCCCAAGCAGTCCAGAGAAGATG
TCTGTGTGGCTTTCCCTCCCTGCCTCCCCCAGCTCCCACACTGGCCTTTGTAAATAAATGGCGTGGTCTTTGTTG
TG

FIGURE 409

GGCTCTCTTCCTGTCTTTGTGGCTCCGGAAAGGCGTTTGGGATGCCAACG**ATG**AGGCTGCTGTCATTTGTGGTGT
TGGCTCTATTTGCTGTCACTCAAGCAGAGGAAGGAGCCAGGCTTTTGGCTTCCAAATCACTGCTGAACAGATACG
CCGTGGAGGGACGAGACCTGACCTTGCAGTACAACATCTACAATGTTGGCTCAAGTGCTGCATTAGACGTGGAAC
TATCTGATGATTCCTTCCCTCCAGAAGACTTTGGCATTGTGTCTGGAATGCTCAATGTCAAATGGGACCGGATTG
CCCCTGCTAGCAATGTCTCCCACACTGTGGTCCTGCGCCCTCTCAAGGCTGGTTATTTCAACTTCACCTCGGCAA
CAATTACTTACCTGGCCCAGGAGGATGGGCCCGTTGTGATTGGCTCTACCAGTGCACCTGGACAGGGAGGAATCC
TGGCTCAGCGGGAGTTTGACAGGCGATTCTCCCCTCATTTTCTGGACTGGGCAGCCTTTGGGGTCATGACCCTTC
CCTCCATCGGCATCCCCCTGCTATTGTGGTACTCCAGCAAGAGGAAATATGACACTCCCAAAACGAAGAAGAAC**T**
GATTGGGGCTTCCACAGCCCTCCTCTCCCAAGAAATCCAGGCTCCTCTCCCAAGAAATCCAGGTGCTTTCCAGAC
TCCAAAGGGTATCTTAAATGCAATCTCTTCTCTCTTAGCCCTTGGCCACTTTCTCCTGGATCCTGCCCTGCTCTC
AGCCATAGTGAAGGACCAGCCCTAGGAGTCTGCGAGAGCCTCCTTGGTTCCATCGTGAAGCCATAAACAGGAATG
CCTTTGGCAATAGCCTTGAGCCTAGAGGGCCCTCTGATGCCCCACTGAGGTGCTGTTGGTTTATTGCTGGCAACG
TGAATTCTCTCAGGGGTCTAGGAGGGGCATTTTGGAGACTGCCTGACACCACCCCTATCCCCTGCCTCCCCCTCT
CAGAAGAGGGTGGAAGATGAAATGAAAGCTATGGGACTCTTGGAGGATACCCAGTGTCTATTCTGGGTTAGAGAA
GTGCTTACTAAGGGGTTTTCTAATAAAAACAAATGCCAATTGC

FIGURE 410

MRLLSFVVLALFAVTQAEEGARLLASKSLLNRYAVEGRDLTLQYNIYNVGSSAALDVELSDDSFPPEDFGIVSGM
LNVKWDRIAPASNVSHTVVLRPLKAGYFNFTSATITYLAQEDGPVVIGSTSAPGQGGILAQREFDRRFSPHFLDW
AAFGVMTLPSIGIPLLLWYSSKRKYDTPKTKKN

FIGURE 411A

GAGACCAACGCGTGCGGGCCGAACCCCTCCCCCGCCTTCCCCCAACAATACAGGACGCCGGGGTCCGCGCCGCG
TCCTCCCTGGTCCCCCCGTCCGATTATGTCTCGGATCGAATCCCTCACGCGGGCGCGGATCGACCGGAGCAGAGA
GCTGGCGAGCAAGACCCGGGAAAAGGAGAAAATGAAGAAAGCCAAGGATGCCCGCTATACAAATGGGCACCTCTT
CACCACCATTTCAGTTTCAGGCATGACCATGTGCTATGCCTGTAACAAGAGCATCACAGCCAAGGAAGCCCTCAT
CTGCCCAACCTGCAATGTGACTATCCACAACCGCTGTAAAGACACCCTCGCCAACTGTACCAAGGTCAAGCAGAA
GCAACAGAAAGCGGCCCTGCTGAAGAACAACACCGCCTTGCAGTCCGTTTCTCTTCGAAGTAAGACAACCATCCG
GGAGCGGCCAAGCTCGGCCATCTACCCCTCCGACAGCTTCCGGCAGTCCCTCCTGGGCTCCCGCCGTGGCCGCTC
CTCCTTGTCTTTAGCCAAGAGTGTTTCTACCACCAACATTGCTGGACATTTCAATGATGAGTCTCCCCTGGGGCT
GCGCCGGATCCTCTCACAGTCCACAGACTCCCTCAACATGCGGAACCGAACCCTATCCGTGGAATCCCTCATTGA
CGAAGAGGTAATCTACAGTGAGCTGATGAGTGACTTTGAGATGGATGAGAAGGACTTTGCAGCTGACTCTTGGAG
TCTTGCTGTGGACAGCAGCTTCCTGCAGCAGCATAAAAAGGAGGTGATGAAGCAGCAAGATGTCATCTATGAGCT
AATCCAGACAGAGCTGCACCATGTGAGGACACTGAAGATCATGACCCGCCTCTTCCGCACGGGGATGCTGGAAGA
GCTACACTTGGAGCCAGGAGTGGTCCAGGGCCTGTTCCCCTGCGTGGACGAGCTCAGTGACATCCATACACGCTT
CCTCAGCCAGCTATTAGAACGCCGACGCCAGGCCCTGTGCCCTGGCAGCACCCGGAACTTTGTCATCCATCGCTT
GGGTGATCTGCTCATCAGCCAGTTCTCAGGTCCTAGTGCGGAGCAGATGTGTAAGACCTACTCGGAGTTCTGCAG
CCGCCACAGCAAGGCCTTAAAGCTCTATAAGGAGCTGTACGCCCGAGACAAACGCTTCCAGCAATTCATCCGGAA
AGTGACCCGCCCCGCCGTGCTCAAGCGGCACGGGGTACAGGAGTGCATCCTGCTGGTGACTCAGCGCATCACCAA
GTACCCGTTACTCATCAGCCGCATCCTGCAGCATTCCCACGGGATCGAGGAGGAGCGCCAGGACCTGACCACAGC
ACTGGGGCTAGTGAAGGAGCTGCTGTCCAATGTGGACGAGGGTATTTATCAGCTGGAGAAAGGGGCCCGTCTGCA
GGAGATCTACAACCGCATGGACCCTCGGGCCCAAACCCCAGTGCCTGGCAAGGGCCCCTTTGGCCGAGAGGAACT
TCTGAGGCGCAAACTCATCCACGATGGCTGCCTGCTCTGGAAGACAGCGACGGGGCGCTTCAAAGATGTGCTAGT
GCTGCTGATGACAGATGTACTGGTGTTTCTCCAGGAAAAGGACCAGAAGTACATCTTTCCTACCCTGGACAAGCC
TTCAGTGGTATCGCTGCAGAATCTAATCGTACGAGACATTGCCAACCAGGAGAAAGGGATGTTTCTGATCAGCGC
AGCCCCACCTGAGATGTACGAGGTGCACACAGCATCCCGGGATGACCGGAGCACCTGGATCCGGGTCATTCAGCA
GAGCGTGCGCACATGCCCATCCAGGGAGGACTTCCCCCTGATTGAGACAGAGGATGAGGCTTACCTGCGGCGAAT
TAAGATGGAGTTGCAGCAGAAGGACCGGGCACTGGTGGAGCTGCTGCGAGAGAAGGTCGGGCTGTTTGCTGAGAT
GACCCATTTCCAGGCCGAAGAGGATGGTGGCAGTGGGATGGCCCTGCCCACCCTGCCCAGGGGCCTTTTCCGCTC
TGAGTCCCTTGAGTCCCCTCGTGGCGAGCGGCTGCTGCAGGATGCCATCCGTGAGGTGGAGGGTCTGAAAGACCT
GCTGGTGGGGCCAGGAGTGGAACTGCTCTTGACACCCCGAGAGCCAGCCCTGCCCTTGGAACCAGACAGCGGTGG
TAACACGAGTCCTGGGGTCACTGCCAATGGTGAGGCCAGAACCTTCAATGGCTCCATTGAACTCTGCAGAGCTGA
CTCAGACTCTAGCCAGAGGGATCGAAATGGAAATCAGCTGAGATCACCGCAAGAGGAGGCGTTACAGCGATTGGT
CAATCTCTATGGACTTCTACATGGCCTACAGGCAGCTGTGGCCCAGCAGGACACTCTGATGGAAGCCCGGTTCCC
TGAGGGCCCTGAGCGGCGGGAGAAGCTGTGCCGAGCCAACTCTCGGGATGGGGAGGCTGGCAGGGCTGGGGCTGC
CCCTGTGGCCCCTGAAAAGCAGGCCACGGAACTGGCATTACTGCAGCGGCAACATGCGCTGCTGCAGGAGGAGCT
ACGGCGCTGCCGGCGGCTAGGTGAAGAACGGGCAACCGAAGCTGGCAGCCTGGAGGCCCGGCTCCGGGAGAGTGA
GCAGGCCCGGGCACTGCTGGAGCGTGAGGCCGAAGAGGCTCGAAGGCAGCTGGCCGCCCTGGGCCAGACCGAGCC
ACTCCCAGCTGAGGCCCCCTGGGCCCGCAGACCTGTGGATCCTCGGCGGCGCAGCCTCCCCGCAGGCGATGCCCT
GTACTTGAGTTTCAACCCCCCACAGCCCAGCCGAGGCACTGACCGCCTGGATCTACCTGTCACTACTCGCTCTGT
CCATCGAAACTTTGAGGACCGAGAGAGGCAGGAACTGGGGAGCCCCGAAGAGCGGCTGCAAGACAGCAGTGACCC
TGACACTGGCAGCGAGGAGGAAGGTAGCAGCCGTCTGTCTCCGCCCCACAGTCCACGAGACTTTACCAGAATGCA
GGACATCCCGGAGGAGACGGAGAGCCGCGACGGGGAGGCTGTAGCCTCCGAGAGCTAAGGGGGCCCCTCCCCCCT
GCCCCGTGCCCCACTGAAGAACATTACTGAGGGGGCTAACCTTGGGGACTCCAATTTGCCAATGATGAGGGAACA
TTTGAAAGAACTGCAAATTGTCCTTGCCAGCTCTTGGGATCCTTGGATACCTGGGGCCATTTAAGAAGCTAGGGG
AATTAGGCCACAACACCCCCTGGGACATCCGAAAGCTACACCACAGATGCCAGTGGTTCATGCCTTCTTCCCGCA
ACTTTAGGAAAATTTATTTATTTATTGTTTATTAGTTATGGGGGGAGAGGGGAGATTTAAAGGACCAGGGACATG
GGAACCAAGCCATAGGGATCAGAGGGCCTTGTCCTTGAACACTACTGGGGTATATTCAGGCTCATCCACGCAGCT
GCTGGGTTCTTGCCCTAACGGCCCTCCCCTGCAACATCCGTCTTGGAGGAGAGGCTGCAGCCACAGCACCCTACT
GCCCTTTAAATAAAGGAGGGCTGTGGCAGGGCCATGTCCCTTTCTCCTCTCCCCTCAACCTCTTACTGCTGTTC

FIGURE 411B

TCCCTTTCTCCGTCCTTCATGGAAGCCCTGGGAGATAACCTGGCTTCCTGGAGTTGATGGAATAAAGGTTGGGGT
GGCCATAATGGTTTGTTGGGGGTGAGGGAAAAAACCCACAGGGACCAGAATGTTTTGTTGTTCTTTTGTTTTCTT
TTTTGTACCAAAGTCAACTGCACGTGTTTTATATTTTTAAGAGATCGTAGGCAATTAGAGATCGAAGCCTCCTAT
CTCCACATCTCTGAAGAAGTTGAGGGGTGGGGGAGAGAATGACTTCTGCCTTCATCTGCAGTAACGGGGGGACCT
ATACTGACCTCTTCCCCAGCCATTTAGAAACAAGTTCTAGGGTGGGTTGGAAAATCTCCAAGAGCCCTGACCTCA
TCTTCCACCTCAGCAACCATGACCTGAAACCTCAGCGTGAATTTGGGGGATTTTTCAGTGGAACCCTTGCCCCCA
AATGTCGACCAGCCCCCAAATGTCGAAGAATTTTCTTCTTGCCAATTTTGTTGTTTAAAAAAAAAATTCAGGGAA
AATTAAAAACCTGGAACTCCA

FIGURE 412

ATGCAGCAGCACGTTCAGCTCTTGACCCAAATCCACCTTCTTGCCACCTGCAACCCCAACCTCAATCCGGAGGCC
ACTACCACCAGGATATTTCTTAAAGAGCTGGGAACCTTTGCTCAAAGCTCCATCGCCCTTCACCATCAGTACAAC
CCCAAGTTTCAGACCCTGTTCCAACCCTGTAACTTGATGGGAGCTATGCAGCTGATTGAAGACTTCAGCACACAT
GTCAGCATTGACTGCAGCCCTCATAAAACTGTCAAGAAGACTGCGAATGAATTTCCCTGTTTGCCAAAGCAAGTG
GCTTGGATTCTGGCCACAAGCAAGGTTTTCATGTATCCAGAGTTACTTCCAGTGTGTTCCCTGAAGGCAAAGAAT
CCCCAGGATAAGATCGTCTTCACCAAGGCTGAGGACAATTTGTTAGCTTTAGGACTGAAGCATTTTGAAGGAACT
GAGTTTCCTAATCCTCTAATCAGCAAGTACCTTCTAACCTGCAAAACTGCCCACCAACTGACAGTGAGAATCAAG
AACCTCAACATGAACAGAGCTCCTGACAACATCATTAAATTTTATAAGAAGACCAAACAGCTGCCAGTCCTAGGA
AAATGCTGTGAAGAGATCCAGCCACATCAGTGGAAGCCACCTATAGAGAGAGAAGAACACCGGCTCCCATTCTGG
TTAAAGGCCAGTCTGCCATCCATCCAGGAAGAACTGCGGCACATGGCTGATGGTGCTAGAGAGGTAGGAAATATG
ACTGGAACCACTGAGATCAACTCAGATCGAAGCCTAGAAAAAGACAATTTGGAGTTGGGGAGTGAATCTCGGTAC
CCACTGCTATTGCCTAAGGGTGTAGTCCTGAAACTGAAGCCAGTTGCCACCCGTTTCCCCAGGAAGGCTTGGAGA
CAGAAGCGTTCATCAGTCCTGAAGCCCCTCCTTATCCAACCCAGCCCCTCTCTCCAGCCCAGCTTCAACCCTGGG
AAAACACCAGCCCGATCAACTCATTCAGAAGCCCCTCCGAGCAAAATGGTGCTCCGGATTCCTCACCCAATACAG
CCAGCCACTGTTTTACAGACAGTTCCAGGTGTCCCTCCACTGGGGGTCAGTGGAGGTGAGAGTTTTGAGTCTCCT
GCAGCACTGCCTGCTGTGCCCCCTGAGGCCAGGACAAGCTTCCCTCTGTCTGAGTCCCAGACTTTGCTCTCTTCT
GCCCCTGTGCCCAAGGTAATGCTGCCCTCCCTTGCCCCTTCTAAGTTTCGAAAGCCATATGTGAGACGGAGACCC
TCAAAGAGAAGAGGAGTCAAGGCCTCTCCCTGTATGAAACCTGCCCCTGTTATCCACCACCCTGCATCTGTTATC
TTCACTGTTCCTGCTACCACTGTGAAGATTGTGAGCCTTGGCGGTGGCTGTAACATGATCCAGCCTGTCAATGCG
GCTGTGGCCCAGAGTCCCCAGACTATTCCCATCACTACCCTCTTGGTTAACCCTACTTCCTTCCCCTGTCCATTG
AACCAGTCCCTTGTGGCCTCCTCTGTCTCACCCTTAATTGTTTCTGGCAATTCTGTGAATCTTCCTATACCATCC
ACCCCTGAAGATAAGGCCCACGTGAATGTGGACATTGCTTGTGCTGTGGCTGATGGGAAAATGCCTTTCAGGGC
CTAGAACCCAAATTAGAGCCCCAGGAACTATCTCCTCTCTCTGCTACTGTTTTCCCGAAAGTGGAACATAGCCCA
GGGCCTCCACTAGCAGATGCAGAGTGCCAAGAAGGATTGTCAGAGAATAGTGCCTGTCGCTGGACCGTTGTGAAA
ACAGAGGAGGGGAGGCAAGCTCTGGAGCCGCTCCCTCAGGGCATCCAGGAGTCTCTAAACAACCCTACCCCTGGG
GATTTAGAGGAAATTGTCAAGATGGAACCTGAAGAAGCTAGAGAGGAAATCAGTGGATCCCCTGAGCGTGATATT
TGTGATGACATCAAAGTGGAACATGCTGTGGAATTGGACACTGGTGCCCCAAGCGAGGAGTTGAGCAGTGCTGGA
GAAGTAACGAAACAGACAGTCTTACAGAAGGAAGAGGAGAGGAGTCAGCCAACTAAAACCCCTTCATCTTCTCAA
GAGCCCCCTGATGAAGGAACCTCAGGGACAGATGTGAACAAAGGATCATCAAAGAATGCTTTGTCCTCAATGGAT
CCTGAAGTGAGGCTTAGTAGCCCCCCAGGGAAGCCAGAAGATTCATCCAGTGTTGATGGTCAGTCAGTGGGGACT
CCAGTTGGGCCAGAAACTGGAGGAGAGAAGAATGGGCCAGAAGAAGAGGAAGAAGAGGACTTTGATGACCTCACC
CAAGATGAGGAAGATGAAATGTCATCAGCTTCTGAGGAATCTGTGCTTTCTGTCCCAGAACTCCAGGTGAGAGCT
GGAGAATATTCTCAAGTATTTCGTGGACTCAGTAATATGTATCACTTATTGATATGCCACCTGCTTGCTTGCTGC
ACTATGGATAGTCCTAAAATCATTTGTATT**TGA**

FIGURE 413

MQQHVQLLTQIHLLATCNPNLNPEATTTRIFLKELGTFAQSSIALHHQYNPKFQTLFQPCNLMGAMQLIEDFSTH
VSIDCSPHKTVKKTANEFPCLPKQVAWILATSKVFMYPELLPVCSLKAKNPQDKIVFTKAEDNLLALGLKHFEGT
EFPNPLISKYLLTCKTAHQLTVRIKNLNMNRAPDNIIKFYKKTKQLPVLGKCCEEIQPHQWKPPIEREEHRLPFW
LKASLPSIQEELRHMADGAREVGNMTGTTEINSDRSLEKDNLELGSESRYPLLLPKGVVLKLKPVATRFPRKAWR
QKRSSVLKPLLIQPSPSLQPSFNPGKTPARSTHSEAPPSKMVLRIPHPIQPATVLQTVPGVPPLGVSGGESFESP
AALPAVPPEARTSFPLSESQTLLSSAPVPKVMLPSLAPSKFRKPYVRRRPSKRRGVKASPCMKPAPVIHHPASVI
FTVPATTVKIVSLGGGCNMIQPVNAAVAQSPQTIPITTLLVNPTSFPCPLNQSLVASSVSPLIVSGNSVNLPIPS
TPEDKAHVNVDIACAVADGENAFQGLEPKLEPQELSPLSATVFPKVEHSPGPPLADAECQEGLSENSACRWTVVK
TEEGRQALEPLPQGIQESLNNPTPGDLEEIVKMEPEEAREEISGSPERDICDDIKVEHAVELDTGAPSEELSSAG
EVTKQTVLQKEEERSQPTKTPSSSQEPPDEGTSGTDVNKGSSKNALSSMDPEVRLSSPPGKPEDSSSVDGQSVGT
PVGPETGGEKNGPEEEEEEDFDDLTQDEEDEMSSASEESVLSVPELQVRAGEYSQVFRGLSNMYHLLICHLLACC
TMDSPKIICI

FIGURE 414

GCCTTTTTTGCAGTCTCAGGACGGGCGCTTTGGAGCCGGCCCCAGGCAGCGTGTGTCGGTCGCCTAGTCTGGAGA
ACTAGTCCTCGACTCACGTGCAAGG**ATG**ATGCTGAAAGGAATAACAAGGCTTATCTCTAGGATCCATAAGTTGGA
CCCTGGGCGTTTTTTACACATGGGGACCCAGGCTCGCCAAAGCATTGCTGCTCACCTAGATAACCAGGTTCCAGT
TGAGAGTCCGAGAGCTATTTCCCGCACCAATGAGAATGACCCGGCCAAGCATGGGGATCAGCACGAGGGTCAGCA
CTACAACATCTCCCCCCAGGATTTGGAGACTGTATTTCCCCATGGCCTTCCTCCTCGCTTTGTGATGCAGGTGAA
GACATTCAGTGAAGCTTGCCTGATGGTAAGGAAACCAGCCCTAGAACTTCTGCATTACCTGAAAAACACCAGTTT
TGCTTATCCAGCTATACGATATCTTCTGTATGGAGAGAAGGGAACAGGAAAAACCCTAAGTCTTTGCCATGTTAT
TCATTTCTGTGCAAAACAGGACTGGCTGATACTACATATTCCAGATGCTCATCTTTGGGTGAAAAATTGTCGGGA
TCTTCTGCAGTCCAGCTACAACAAACAGCGCTTTGATCAACCTTTAGAGGCTTCAACCTGGCTGAAGAATTTCAA
AACTACAAATGAGCGCTTCCTGAACCAGATAAAAGTTCAAGAGAAGTATGTCTGGAATAAGAGAGAAAGCACTGA
GAAAGGGAGTCCTCTGGGAGAAGTGGTTGAACAGGGCATAACACGGGTGAGGAACGCCACAGATGCAGTTGGAAT
TGTGCTGAAAGAGCTAAAGAGGCAAAGTTCTTTGGGTATGTTTCACCTCCTAGTGGCCGTGGATGGAATCAATGC
TCTTTGGGGAAGAACCACTCTGAAAAGAGAAGATAAAAGCCCGATTGCCCCCGAGGAATTAGCACTTGTTCACAA
CTTGAGGAAAATGATGAAAAATGATTGGCATGGAGGCGCCATTGTGTCGGCTTTGAGCCAGACTGGGTCTCTCTT
TAAGCCCCGGAAAGCCTATCTGCCCCAGGAGTTGCTGGGAAAGGAAGGATTTGATGCCCTGGATCCCTTTATTCC
CATCCTGGTTTCCAACTATAACCCAAAGGAATTTGAAAGTTGTATTCAGTATTATTTGGAAAACAATTGGCTTCA
ACATGAGAAAGCTCCTACAGAAGAAGGGAAAAAAGAGCTGCTGTTCCTAAGTAACGCGAACCCCTCGCTGCTGGA
GCGGCACTGTGCCTACCTC**TAA**GCCAAGATCACAGCATGTGAGGAAGACAGTGGACATCTGCTTTATGCTGGACC
CAGTAAGATGAGGAAGTCGGGCAGTACACAGGAAGAGGAGCCAGGCCCTTGTACCTATGGGATTGGACAGGACTG
CAGTTGGCTCTGGACCTGCATTAAAATGGGTTTCACTGTGAATGCGTGACAATAAGATATTCCCTTGTTCCTAAA
ACTTTATATCAGTTTATTGGATGTGGTTTTTCACATTTAAGATAATTATGGCTCTTTTCCTAAAAAATAAAATAT
CTTTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 415

MMLKGITRLISRIHKLDPGRFLHMGTQARQSIAAHLDNQVPVESPRAISRTNENDPAKHGDQHEGQHYNISPQDL
ETVFPHGLPPRFVMQVKTFSEACLMVRKPALELLHYLKNTSFAYPAIRYLLYGEKGTGKTLSLCHVIHFCAKQDW
LILHIPDAHLWVKNCRDLLQSSYNKQRFDQPLEASTWLKNFKTTNERFLNQIKVQEKYVWNKRESTEKGSPLGEV
VEQGITRVRNATDAVGIVLKELKRQSSLGMFHLLVAVDGINALWGRTTLKREDKSPIAPEELALVHNLRKMMKND
WHGGAIVSALSQTGSLFKPRKAYLPQELLGKEGFDALDPFIPILVSNYNPKEFESCIQYYLENNWLQHEKAPTEE
GKKELLFLSNANPSLLERHCAYL

FIGURE 416

TCTTCACCACTGCTCTCCCAGAGGTCCAGGTCCGGGAGATGACAGTGGCTCCCAGAAAGCCCAGGATTCAATCGC
TGAGAGAGTGCTTAGGCCCGAATGCCGGCCCAAATCGTTCTACTCACCGTGTCGGAGGCCGAGAGCGATGAGAGT
ACAGGGAAGTGAGGAAGAGGGGGTGGCCGCCAGGCTCCTCCGCTTCCCTGGGTCCACCGCGGATCCCTCCCGCTT
GTCAGGAGGCGGCCAGCGGGTAAGCCGACTGGCGGAAATGCGAGAGAGGAGAAGGGAAAGGTGGAGGGCTAAAGG
GGCAAACTGAGAGGAGGCGGATCCCGCAACCGACACTGGGATCGTTTCCCCTCGCAAAGCGAACCCAAAATGGCG
GCGGCAGCGGCGGCAGCAGAGTGGCCGCGGCAGCTCCTCCAGAGGGAGGGAGCTAAGGGCGCCTAGCGACACCCC
CAACCTCCCACTCCTCCCTCCTCGCGTTCTTCCCCACGGTCCCCCGCTTCGCCCGACTCCGGCCATGTAGCGCGC
ACGTCAGCCCGCACGCGTACGAGTGTCTACGGGCTCGTCGCTGGCTGCTCCCACCAACCACCACCTTCGGCCGTC
CTGCGAGCCAGCCATCCCGTACGCGCTCACCCACGGGAACCTCCTCGCCCAGTTCTCCACTCCCCCTCAGACCCT
GTCAAGCCGGCTCCAGCGCAGGCCCTCACGCGTACCTTCAGCGGCGCGAGCCCAAGCCTTCTCCACCTCCTCTTC
TCTCCTCCCCCTCCCTCCCCGCCCGCACGGCCACCAACCGCCGCCAAAGCAGCCGCCGCCAGCACCCCCACCCTA
CACTCCTCGCGCGTGCGCCTCCCACAGTCCCCACCGCGGGACTGTTCCATTCCTGGCGGCTGCAGGGGCAGGAGA
GGAAGGGACCGGCAAAGCGAGTCTGGCTTGCCGTTTGACTGGAATTGCCAGGGTGGCCGGCCGAGTCCCATGACA
ACCTACCTCCCTGGGTTCGTCGCCCGCGGCGCTGCGGCTCGCCTCCTCCTCCATGGGACCGCGGCGAGGGGATCGA
GGGCGGCCTAGCGCCCCTCTGCCGGCCGGTGGTTGGAGGCCGCGGCGGCTGCGCGTTGAGTCGTTTCCTGCCGGA
TGACCCGACCCTTTTTGCAGTCTCAGGACGGGCGCTTTGGAGCCGGCCCCAGGCAGCGTGTGTCGGTCGCCTAG
TCTGGAGAACTAGTCCTCGACTCACGGTGAGGGAATGGACCGACACGGGTATTGTACCGCTGAGGGAAAGGAGCG
GGACTCCGGACCTCCAGGAGGTAGGGAGTGAGGCCGGTAGACCGGCGCGCCTCCGGGGGGGATTCCTCCCGGGCG
TTGAGTTGCCAACCTGGGACCCGAGGAAGTTCGGCGTGGTGGTGTGCTTTTTGTTGTTGTTAACCCTCCTCGGAT
TTCTCGAATTTCACACCACTGTCCATATGCGATGATGTTTGTTTGCCCTTGACGCACTTACTCATGGATGGTACT
TCAGCCTCGTTAGACAGCCTGGTGATGGAGGATGAAGAAACCATGTGCTTCTCATTCAGTTCTGGACTCAGTTTC
CCTTGTCTTCAGCAAGTTATTTTTGTTAGTTCCTTATCAAAAAGTGTACATAAAAATTAGGCAACTCCAAACATG
CCTCCAGGGTTGGTGTGTGAAATAATAAGATAGGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGG
GAGGCCGAGGCAGGTGGATGACAAGGTGAAGAGATCGAGACAATCCTGGCCAACATGGTGAAACCCCGTCTCTAC
TAAAAATACAAATATTAGCCGGCCGTGGTGGCGGGCGCCTGTAGCCCCAGCTACTCGGGAGGCTGAGGCAGGAGA
ATTGCTTGAACCCGGGCGGCGGAAGTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTGGCGACAAAGCG
AGACTCCGTCACACACACACACACACACACACGAAATAATAATATATGTAAAGTGGAATTAGCTCCAAGTCGTTAAT
AAAACAAAGCAGGCCGGGCGTCTTGTTAAATAGTTGTATCAATGACTTGATTTAGATTAATGAGGATATATTTTT
CAAATTTATGCCTTTTACAAAATTTTTAAAGAGTAGGTAATGTCGGTGATAGATATAAAGAAAGGAAAAGATCTC
CAGATGTGGAATCTTCTACTGGATCCTGTAACAGAAAGAAGACATTAGGCTGGGCGCAGTGGCTCACACCTGTAA
TCTCAGCACTTTGGGAGGCGGAGGAGGGCGCATTGCTTGAGCCTAGGAGTTCGAGACCAGCTTAGGCAACACGGT
GAAACCCCATCTCTACAAAAAGACACAAAAATTAGACAGGTGTGGCACACGCTTGTAGTCTGAGCTACTTGGGAG
GCTGAAGCAGGAGGATTGAGGAAGAGGTTGCAAAGTTAGCCGAGATCACGCCATCACACTGCAGCCTAGGTGACA
GAGCGAGACCCTGTCTCAAAAAAAGAAAGAAGACATTAGCAGAAAAGCTGAGGAAATGCAAATAAAGTCTGCAAT
TTTTAAAT

FIGURE 417

MTRPFFAVSGRALWSRPQAACVGRLVWRTSPRLTVREWTDTGIVPLRERSGTPDLQEVGSEAGRPARLRGGFLPG
VELPTWDPRKFGVVVCFLLLLTLLGFLEFHTTVHMR

FIGURE 418

GAGAGAAGAGGAGGTGGAGAAGGCTTGGGCTCGCGCCGCTGAAGTCGGCTTACCCGCTGGCCGCCTCCTGACAAG
CGGGAGGGATCCGCGGTGGACCCAGGGAAGCGGAGGAGCCTGGCGGCCACCCCCTCTTCCTCACTTCCCTGTACT
CTCATCGCTCTCGGCCTCCGACACGAAAAGGAAGCAAATGAGCTGATGGAAGATCTGTTTGAAACTAGACAGGGT
CTTGCCATGTTCTGGAACTCATAGGCTCAAGTAATCTTCCTGCCTCAACCTCCCAAAGTGCTGGAATTACAGTTC
CAAGATGAG**ATG**GGATTCTCCAACATGGAAGATGATGGCCCAGAAGAGGAGGAGCGTGTGGCTGAGCCTCAAGCT
AACTTTAACACCCCTCAAGCTCTACGGTTTGAGGAACTACTGGCCAACCTACTAAATGAACAACATCAGATAGCG
AAGGAACTATTTGAACAGCTGAAGATGAAGAAACCTTCAGCCAAACAGCAGAAGGAGGTAGAGAAGGTTAAACCC
CAGTGTAAGGAAGTTCATCAGACCCTGATTCTGGACCCAGCACAAAGGAAGAGACTCCAGCAGCAGATGCAGCAG
CATGTTCAGCTCTTGACACAAATCCACCTTCTTGCCACCTGCAACCCCAATCTCAATCCGGAGGCCAGTAGCACC
AGGATATGTCTTAAAGAGCTGGGAACCTTTGCTCAAAGCTCCATCGCCCTTCACCATCAGTACAACCCCAAGTTT
CAGACCCTGTTCCAACCCTGTAACTTGATGGGAGCTATGCAGCTGATTGAAGACTTCAGCACACATGTCAGCATT
GACTGCAGCCCTCATAAAACTGTCAAGAAGACTGCCAATGAATTTCCCTGTTTGCCAAAGCAAGTGGCTTGGATC
CTGGCCACAAGCAAGGTTTTCATGTATCCAGAGTTACTTCCAGTGTGTTCCCTGAAGGCAAAGAATCCCCAGGAT
AAGATCCTCTTCACCAAGGCTGAGGACAATTTGTTAGCTTTAGGACTGAAGCATTTTGAAGGGACTGAGTTTCTT
AACCCTCTAATCAGCAAGTACCTTCTAACCTGCAAGACTGCCCGCCAACTGACAGTGAGAATCAAGAACCTCAAC
ATGAACAGAGCTCCTGACAACATCATTAAATTTTATAAGAAGACCAAACAGCTGCCAGTCCTAGGAAAATGCTGT
GAAGAGATCCAGCCACATCAGTGGAAGCCACCTATAGAGAGAGAAGAACACCGGCTCCCATTCTGGTTAAAGGCC
AGTCTGCCATCCATCCAGGAAGAACTGCGGCACATGGCTGATGGTGCTAGAGAGGTAGGAAATATGACTGGAACC
ACTGAGATCAACTCAGATCAAGGCCTAGAAAAAGACAACTCAGAGTTGGGGAGTGAAACTCGGTACCCACTGCTA
TTGCCTAAGGGTGTAGTCCTGAAACTGAAGCCAGTTGCCGACCGTTTCCCCAAGAAGGCTTGGAGACAGAAGCGT
TCATCAGTCCTGAAACCCCTCCTTATCCAACCCAGCCCCTCTCTCCAGCCCAGCTTCAACCCTGGGAAAACACCA
GCCCAATCAACTCATTCAGAAGCCCCTCCGAGCAAAATGGTGCTCCGGATTCCTCACCCAATACAGCCAGCCACT
GTTTTACAGACAGTTCCAGGTGTCCCTCCACTGGGGGTCAGTGGAGGTGAGAGTTTTGAGTCTCCTGCAGCACTG
CCTGCTATGCCCCCTGAGGCCAGGACAAGCTTCCCTCTGTCTGAGTCCCAGACTTTGCTCTCTTCTGCCCCTGTG
CCCAAGGTAATGATGCCCTCCCCTGCCTCTTCCATGTTTCGAAAGCCATATGTGAGACGGAGACCCTCAAAAAGA
AGGGGAGCCAGGGCCTTTCGCTGTATCAAACCTGCCCCTGTTATCCACCCTGCATCTGTTATCTTCACTGTTCCT
GCTACCACTGTGAAGATTGTGAGCCTTGGCGGTGGCTGTAACATGATCCAGCCTGTCAATGCGGCTGTGGCCCAG
AGTCCCCAGACTATTCCCATCGCCACCCTCTTGGTTAACCCTACTTCCTTCCCCTGTCCATTGAACCAGCCCCTT
GTGGCCTCCTCTGTCTCACCCTTAATTGTTTCTGGCAATTCTGTGAATCTTCCTATACCATCCACCCCTGAAGAT
AAGGCCCACATGAATGTGGACATTGCTTGTGCTGTGGCTGATGGGGAAAATGCCTTTCAGGGCCTAGAACCCAAA
TTAGAGCCCCAGGAACTATCTCCTCTCTCTGCTACTGTTTTCCCCAAAGTGGAACATAGCCCAGGGCCTCCACCA
GTCGATAAACAGTGCCAAGAAGGATTGTCAGAGAACAGTGCCTATCGCTGGACCGTTGTGAAAACAGAGGAGGGA
AGGCAAGCTCTGGAGCCGCTCCCTCAGGGCATCCAGGAGTCTCTAAACAACTCTTCCCCTGGGGATTTAGAGGAA
GTTGTCAAGATGGAACCTGAAGATGCTACAGAGGAAATCAGTGGATTTCTT**TGA**GCTAGGAGAATAAGAGTCTGG
AGACTGGGAGCCTTCACTTCGGCCTCCGATTGGTGGCGCATAGGGTGTAACCAATAGGAAACCCCTAAAGGGTAC
TTAAACCCCAGATTTTGCAACTGGGGCTCTTGAGCAGCTTGCTTTAGCCTGCTCCCACTCTGTGGAATATACTTT
TGCTTCAATAAATCTGTGCTTTTATTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAA

FIGURE 419

MGFSNMEDDGPEEEERVAEPQANFNTPQALRFEELLANLLNEQHQIAKELFEQLKMKKPSAKQQKEVEKVKPQCK
EVHQTLILDPAQRKRLQQQMQQHVQLLTQIHLLATCNPNLNPEASSTRICLKELGTFAQSSIALHHQYNPKFQTL
FQPCNLMGAMQLIEDFSTHVSIDCSPHKTVKKTANEFPCLPKQVAWILATSKVFMYPELLPVCSLKAKNPQDKIL
FTKAEDNLLALGLKHFEGTEFLNPLISKYLLTCKTARQLTVRIKNLNMNRAPDNIIKFYKKTKQLPVLGKCCEEI
QPHQWKPPIEREEHRLPFWLKASLPSIQEELRHMADGAREVGNMTGTTEINSDQGLEKDNSELGSETRYPLLLPK
GVVLKLKPVADRFPKKAWRQKRSSVLKPLLIQPSPSLQPSFNPGKTPAQSTHSEAPPSKMVLRIPHPIQPATVLQ
TVPGVPPLGVSGGESFESPAALPAMPPEARTSFPLSESQTLLSSAPVPKVMMPSPASSMFRKPYVRRRPSKRRGA
RAFRCIKPAPVIHPASVIFTVPATTVKIVSLGGGCNMIQPVNAAVAQSPQTIPIATLLVNPTSFPCPLNQPLVAS
SVSPLIVSGNSVNLPIPSTPEDKAHMNVDIACAVADGENAFQGLEPKLEPQELSPLSATVFPKVEHSPGPPPVDK
QCQEGLSENSAYRWTVVKTEEGRQALEPLPQGIQESLNNSSPGDLEEVVKMEPEDATEEISGFL

FIGURE 420

AGCGCAGT**ATG**GCGGGCGGGGCCCGGGAGGTGCTCACACTGCAGTTGGGACATTTTGCCGGTTTCGTGGGCGCGC
ACTGGTGGAACCAGCAGGATGCTGCGCTGGGCCGAGCGACCGATTCCAAGGAGCCCCCGGGAGAGCTGTGCCCCG
ACGTCCTGTATCGTACGGGCCGGACGCTGCACGGCCAGGAGACCTACACGCCGCGACTCATCCTCATGGATCTGA
AGGGTAGTTTGAGCTCCCTAAAAGAGGAAGGTGGACTCTACAGGGACAAACAGTTGGATGCTGCAATAGCATGGC
AGGGGAAGCTCACCACACACAAAGAGGAACTCTATCCCAAGAACCCTTATCTCCAAGACTTTCTGAGTGCAGAGG
GAGTGCTGAGTAGTGATGGTGTCTGGAGGGTCAAATCCATTCCCAATGGCAAAGGTTCCTCACCACTCCCCACCG
CTACAACTCCAAAACCACTTATCCCTACAGAGGCCAGCATCAGGGTCTGGTCAGACTTCCTCAGAGTCCATCTCC
ATCCCCGGAGCATCTGTATGATTCAGAAGTACAACCACGATGGGGAAGCAGGTCGGCTGGAGGCTTTTGGCCAAG
GGGAAAGTGTCCTAAAGGAACCCAAGTACCAGGAAGAGCTGGAGGACAGGCTGCATTTCTACGTGGAGGAATGTG
ACTACTTGCAGGGCTTCCAGATCCTGTGTGACCTGCACGATGGCTTCTCTGGGGTAGGCGCGAAGGCGGCAGAGC
TGCTACAAGATGAATATTCAGGGCGGGGAATAATAACCTGGGGCCTGCTACCTGGTCCCTACCATCGTGGGGAGG
CCCAGAGAAACATCTATCGTCTATTAAACACAGCTTTTGGTCTCGTGCACCTGACTGCTCACAGCTCTCTTGTCT
GCCCCTTGTCCTTGGGTGGGAGCCTGGGCCTGCGACCCGAGCCACCTGTCAGCTTCCCTTACCTGCATTATGATG
CCACTCTGCCCTTCCACTGCAGTGCCATCCTGGCTACAGCCCTGGACACAGTCACTGTTCCTTATCGCCTGTGTT
CCTCTCCAGTTTCCATGGTTCATCTGGCTGACATGCTGAGCTTCTGTGGGAAAAAGGTGGTGACAGCAGGAGCAA
TCATCCCTTTCCCCTTGGCTCCAGGCCAGTCCCTTCCTGATTCCCTGGTGCAGTTTGGAGGAGCCACCCCATGGA
CCCCACTGTCTGCATGTGGGGAGCCTTCTGGAACACGTTGCTTTGCCCAGTCAGTGGTGCTGAGGGGTATAGACA
GAGCATGCCACACAAGCCAGCTCACCCCAGGGACACCTCCACCCTCTGCCCTTCATGCATGTACCACTGGGGAAG
AAATCTTGGCTCAGTATTTACAACAGCAGCAGCCTGGAGTCATGAGTTCTTCCCATCTGCTGCTGACTCCCTGCA
GGGTGGCTCCTCCTTACCCCCACCTCTTCTCAAGCTGCAGTCCACCGGGTATGGTTCTGGATGGTTCCCCCAAGG
GAGCAGCAGTGGAGAGCATCCCAGTGTTTGGGGCACTGTGTTCCTCTTCGTCCCTGCACCAGACCCTGGAAGCCT
TGGCCAGAGACCTCACCAAACTCGACTTGCGGCGCTGGGCCAGCTTCATGGATGCTGGAGTGGAGCACGATGACG
TAGCAGAGCTGCTGCAGGAGCTACAAAGCCTGGCCCAGTGCTACCAGGGTGGTGACAGCCTCGTGGAC**TAA**AGTT
CCCAGTGTGGGAGAAAGGAGCTAGTTTGCAATAAAAACAGCTGGATGCAGGAGCCCAGTGTCTTCATGCAGAGGA
GCTCAATGTCGCGGGACTAGCTACACCAACATATGCACTTTTTACATTTAGAAACACTGTGATTAGACCACAGAA
CAATAAATATGTGCCATCAGACC

FIGURE 421

MAGGAREVLTLQLGHFAGFVGAHWWNQQDAALGRATDSKEPPGELCPDVLYRTGRTLHGQETYTPRLILMDLKGS
LSSLKEEGGLYRDKQLDAAIAWQGKLTTHKEELYPKNPYLQDFLSAEGVLSSDGVWRVKSIPNGKGSSPLPTATT
PKPLIPTEASIRVWSDFLRVHLHPRSICMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEECDYL
QGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLPGPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPL
SLGGSLGLRPEPPVSFPYLHYDATLPFHCSAILATALDTVTVPYRLCSSPVSMVHLADMLSFCGKKVVTAGAIIP
FPLAPGQSLPDSLVQFGGATPWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSALHACTTGEEIL
AQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFSSCSPPGMVLDGSPKGAAVESIPVFGALCSSSSLHQTLEALAR
DLTKLDLRRWASFMDAGVEHDDVAELLQELQSLAQCYQGGDSLVD

FIGURE 422

AGGTGAGAGAGGATGTGTGCTGGGCCTTGGAGGAAGGGGGCCGAGACCGGGCCTTACTTCTGTAACGATACTGTG
AGGCATCGGAAGGCCAGCCTGTTGTGTCCGTTTTGAAGG**ATG**CCCCTGTCCCGCTGGTTGAGATCTGTGGGGGTC
TTCCTGCTGCCAGCCCCCTACTGGGCACCCCGGGAGAGGTGGCTGGGTTCCCTACGGCGGCCCTCCCTGGTGCAC
GGGTACCCAGTCCTGGCCTGGCACAGTGCCCGCTGCTGGTGCCAAGCGTGGACAGAGGAACCTCGAGCCCTTTGC
TCCTCCCTCAGAATGAACGGAGACCAGAATTCAGATGTTTATGCCCAAGAAAAGCAGGATTTCGTTCAGCACTTC
TCCCAGATCGTTAGGGTGCTGACTGAGGATGAGATGGGGCACCCAGAGATAGGAGATGCTATTGCCCGGCTCAAG
GAGGTCCTGGAGTACAATGCCATTGGAGGCAAGTATAACCGGGGTTTGACGGTGGTAGTAGCATTCCGGGAGCTG
GTGGAGCCAAGGAAACAGGATGCTGATAGTCTCCAGCGGGCCTGGACTGTGGGCTGGTGTGTGGAACTGCTGCAA
GCTTTCTTCCTGGTGGCAGATGACATCATGGATTCATCCCTTACCCGCCGGGGACAGATCTGCTGGTATCAGAAG
CCGGGCGTGGGTTTGGATGCCATCAATGATGCTAACCTCCTGGAAGCATGTATCTACCGCCTGCTGAAGCTCTAT
TGCCGGGAGCAGCCCTATTACCTGAACCTGATCGAGCTCTTCCTGCAGAGTTCCTATCAGACTGAGATTGGGCAG
ACCCTGGACCTCCTCACAGCCCCCCAGGGCAATGTGGATCTTGTCAGATTCACTGAAAAGAGGTACAAATCTATT
GTCAAGTACAAGACAGCTTTCTACTCCTTCTACCTTCCTATAGCTGCAGCCATGTACATGGCAGGAATTGATGGC
GAGAAGGAGCACGCCAATGCCAAGAAGATCCTGCTGGAGATGGGGGAGTTCTTTCAGATTCAGGATGATTACCTT
GACCTCTTTGGGGACCCCAGTGTGACCGGCAAAATTGGCACTGACATCCAGGACAACAAATGCAGCTGGCTGGTG
GTTCAGTGTCTGCAACGGGCCACTCCAGAACAGTACCAGATCCTGAAGGAAAATTACGGGCAGAAGGAGGCTGAG
AAAGTGGCCCGGGTGAAGGCGCTATATGAGGAGCTGGATCTGCCAGCAGTGTTCTTGCAATATGAGGAAGACAGT
TACAGCCACATTATGGCTCTCATTGAACAGTACGCAGCACCCCTGCCCCCAGCCGTCTTTCTGGGGCTTGCGCGC
AAAATCTACAAGCGGAGAAAG**TGA**CCTAGAGATTGCAAGGGCGGGGAGAGGAGGCTCTCAATAAATAATCGTGTA
ACCTT

FIGURE 423

MPLSRWLRSVGVFLLPAPYWAPRERWLGSLRRPSLVHGYPVLAWHSARCWCQAWTEEPRALCSSLRMNGDQNSDV
YAQEKQDFVQHFSQIVRVLTEDEMGHPEIGDAIARLKEVLEYNAIGGKYNRGLTVVVAFRELVEPRKQDADSLQR
AWTVGWCVELLQAFFLVADDIMDSSLTRRGQICWYQKPGVGLDAINDANLLEACIYRLLKLYCREQPYYLNLIEL
FLQSSYQTEIGQTLDLLTAPQGNVDLVRFTEKRYKSIVKYKTAFYSFYLPIAAAMYMAGIDGEKEHANAKKILLE
MGEFFQIQDDYLDLFGDPSVTGKIGTDIQDNKCSWLVVQCLQRATPEQYQILKENYGQKEAEKVARVKALYEELD
LPAVFLQYEEDSYSHIMALIEQYAAPLPPAVFLGLARKIYKRRK

FIGURE 424

GGTAGTTGGTTGTGGGCACTGGGTTAGAGGTATCACGTGGGGGCACTTTCGTCTTAGCTTTTGGACAAGACGCAG
GCGCAACCCACGGCTGCTGCGGGGATCCTTGTGGCCCTTCCGGTCGGTGGAACCAATCCGTGCACAGAGAAGCGG
GGCGAACTGAGGCGAGTGAAGTGGACTCTGAGGGCTACCGCTACCGCCACTGCTGCGGCAGGGGCGTGGAGGGCA
GAGGGCCGCGGAGGCCGCAGTTGCAAAC**ATG**GCTCAGAGCAGAGACGGCGGAAACCCGTTCGCCGAGCCCAGCGA
GCTTGACAACCCCTTTCAGGACCCAGCTGTGATCCAGCACCGACCCAGCCGGCAGTATGCCACGCTTGACGTCTA
CAACCCTTTTGAGACCCGGGAGCCACCACCAGCCTATGAGCCTCCAGCCCCTGCCCCATTGCCTCCACCCTCAGC
TCCCTCCTTGCAGCCCTCGAGAAAGCTCAGCCCCACAGAACCTAAGAACTATGGCTCATACAGCACTCAGGCCTC
AGCTGCAGCAGCCACAGCTGAGCTGCTGAAGAAACAGGAGGAGCTCAACCGGAAGGCAGAGGAGTTGGACCGAAG
GGAGCGAGAGCTGCAGCATGCTGCCCTGGGGGGCACAGCTACTCGACAGAACAATTGGCCCCCTCTACCTTCTTT
TTGTCCAGTTCAGCCCTGCTTTTCCAGGACATCTCCATGGAGATCCCCCAAGAATTTCAGAAGACTGTATCCAC
CATGTACTACCTCTGGATGTGCAGCACGCTGGCTCTTCTCCTGAACTTCCTCGCCTGCCTGGCCAGCTTCTGTGT
GGAAACCAACAATGGCGCAGGCTTTGGGCTTTCTATCCTCTGGGTCCTCCTTTTCACTCCCTGCTCCTTTGTCTG
CTGGTACCGCCCCATGTATAAGGCTTTCCGGAGTGACAGTTCATTCAATTTCTTCGTTTTCTTCTTCATTTTCTT
CGTCCAGGATGTGCTCTTTGTCCTCCAGGCCATTGGTATCCCAGGTTGGGGATTCAGTGGCTGGATCTCTGCTCT
GGTGGTGCCGAAGGGCAACACAGCAGTATCCGTGCTCATGCTGCTGGTCGCCCTGCTCTTCACTGGCATTGCTGT
GCTAGGAATTGTCATGCTGAAACGGATCCACTCCTTATACCGCCGCACAGGTGCCAGCTTTCAGAAGGCCCAGCA
AGAATTTGCTGCTGGTGTCTTCTCCAACCCTGCGGTGCGAACCGCAGCTGCCAATGCAGCCGCTGGGGCTGCTGA
AAATGCCTTCCGGGCCCCG**TGA**CCCCTGACTGGGATGCCCTGGCCCTGCTACTTGAGGGAGCTGACTTAGCTCCC
GTCCCTAAGGTCTCTGGGACTTGGAGAGACATCACTAACTGATGGCTCCTCCGTAGTGCTCCCAATCCTATGGCC
ATGACTGCTGAACCTGACAGGCGTGTGGGGAGTTCACTGTGACCTAGTCCCCCCATCAGGCCACACTGCTGCCAC
CTCTCACACGCCCCAACCCAGCTTCCCTCTGCTGTGCCACGGCTGTTGCTTCGGTTATTTAAATAAAAAGAAAGT
GGAACTGGAACTGACAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 425

MAQSRDGGNPFAEPSELDNPFQDPAVIQHRPSRQYATLDVYNPFETREPPPAYEPPAPAPLPPPSAPSLQPSRKL
SPTEPKNYGSYSTQASAAAATAELLKKQEELNRKAEELDRRERELQHAALGGTATRQNNWPPLPSFCPVQPCFFQ
DISMEIPQEFQKTVSTMYYLWMCSTLALLLNFLACLASFCVETNNGAGFGLSILWVLLFTPCSFVCWYRPMYKAF
RSDSSFNFFVFFFIFFVQDVLFVLQAIGIPGWGFSGWISALVVPKGNTAVSVLMLLVALLFTGIAVLGIVMLKRI
HSLYRRTGASFQKAQQEFAAGVFSNPAVRTAAANAAAGAAENAFRAP

FIGURE 426

GGTAGTTGGTTGTGGGCACTGGGTTAGAGGTATCACGTGGGGGCACTTTCGTCTTAGCTTTTGGACAAGACGCAG
GCGCAACCCACGGCTGCTGCGGGGATCCTTGTGGCCCTTCCGGTCGGTGGAACCAATCCGTGCACAGAGAAGCGG
GGCGAACTGAGGCGAGTGAAGTGGACTCTGAGGGCTACCGCTACCGCCACTGCTGCGGCAGGGGCGTGGAGGGCA
GAGGGCCGCGGAGGCCGCAGTTGCAAAC<u>ATG</u>GCTCAGAGCAGAGACGGCGGAAACCCGTTCGCCGAGCCCAGCGA
GCTTGACAACCCCTTTCAGCCACCACCAGCCTATGAGCCTCCAGCCCCTGCCCCATTGCCTCCACCCTCAGCTCC
CTCCTTGCAGCCCTCGAGAAAGCTCAGCCCCACAGAACCTAAGAACTATGGCTCATACAGCACTCAGGCCTCAGC
TGCAGCAGCCACAGCTGAGCTGCTGAAGAAACAGGAGGAGCTCAACCGGAAGGCAGAGGAGTTGGACCGAAGGGA
GCGAGAGCTGCAGCATGCTGCCCTGGGGGGCACAGCTACTCGACAGAACAATTGGCCCCCTCTACCTTCTTTTTG
TCCAGTTCAGCCCTGCTTTTTCCAGGACATCTCCATGGAGATCCCCCAAGAATTTCAGAAGACTGTATCCACCAT
GTACTACCTCTGGATGTGCAGCACGCTGGCTCTTCTCCTGAACTTCCTCGCCTGCCTGGCCAGCTTCTGTGTGGA
AACCAACAATGGCGCAGGCTTTGGGCTTTCTATCCTCTGGGTCCTCCTTTTCACTCCCTGCTCCTTTGTCTGCTG
GTACCGCCCCATGTATAAGGCTTTCCGGAGTGACAGTTCATTCAATTTCTTCGTTTTCTTCTTCATTTTCTTCGT
CCAGGATGTGCTCTTTGTCCTCCAGGCCATTGGTATCCCAGGTTGGGGATTCAGTGGCTGGATCTCTGCTCTGGT
GGTGCCGAAGGGCAACACAGCAGTATCCGTGCTCATGCTGCTGGTCGCCCTGCTCTTCACTGGCATTGCTGTGCT
AGGAATTGTCATGCTGAAACGGATCCACTCCTTATACCGCCGCACAGGTGCCAGCTTTCAGAAGGCCCAGCAAGA
ATTTGCTGCTGGTGTCTTCTCCAACCCTGCGGTGCGAACCGCAGCTGCCAATGCAGCCGCTGGGGCTGCTGAAAA
TGCCTTCCGGGCCCCG<u>TGA</u>CCCCTGACTGGGATGCCCTGGCCCTGCTACTTGAGGGAGCTGACTTAGCTCCCGTC
CCTAAGGTCTCTGGGACTTGGAGAGACATCACTAACTGATGGCTCCTCCGTAGTGCTCCCAATCCTATGGCCATG
ACTGCTGAACCTGACAGGCGTGTGGGGAGTTCACTGTGACCTAGTCCCCCCATCAGGCCACACTGCTGCCACCTC
TCACACGCCCCAACCCAGCTTCCCTCTGCTGTGCCACGGCTGTTGCTTCGGTTATTTAAATAAAAAGAAAGTGGA
ACTGGAACTGAAAAAAAAAAAAAAA

FIGURE 427

MAQSRDGGNPFAEPSELDNPFQPPPAYEPPAPAPLPPPSAPSLQPSRKLSPTEPKNYGSYSTQASAAAATAELLK
KQEELNRKAEELDRRERELQHAALGGTATRQNNWPPLPSFCPVQPCFFQDISMEIPQEFQKTVSTMYYLWMCSTL
ALLLNFLACLASFCVETNNGAGFGLSILWVLLFTPCSFVCWYRPMYKAFRSDSSFNFFVFFFIFFVQDVLFVLQA
IGIPGWGFSGWISALVVPKGNTAVSVLMLLVALLFTGIAVLGIVMLKRIHSLYRRTGASFQKAQQEFAAGVFSNP
AVRTAAANAAAGAAENAFRAP

FIGURE 428

CCTGCGGCAGCCGGAGCTCGGGGAGCGGAGCGTGGTGGGGAGGGGAGCGGGACAGGCGACACAGGAGACAGCGGC
GCCGCGGCCTCTCCCCACCAGGCGGCCCCGGATCCTACTGGACGCCCTGAGGGCACACCGACCGCGCCTCTAGAG
TCACCCCACGCCGACCCCTCCCCTCTTCTCTAGACTTATTTCCATCCTTCCCGCTTTTACCCTCCCCACCCGTCC
CTGGGCTCCAGGCCGCCGCCCCCTCCTCACTCCTGGACCGGCCCTTCTCGGTGCCCCTCTTCCCTAGGGAGATGC
GATGAGCCGGTGCCCCCGCGTCCTCATCGTCGCCCCGGGCACGGTGCCCGTCCAGTGCCCGTGGTGGGGAGGGAG
CACTCCGCGGTCCCTCCGTGACGCCCCTCGCTTGGCCCCCCCACAGCTGGCGTCCCTCGGCCATGCCCCAGGGG
ACCCAGCCAGGGGGTGGGCTCTAGAGCGAGTGGGGTGGAGAGGAGAAAGGACGGGGCCTTGGGGGCCTCTGAGAT
GCTCCCAAGTGCCAGGGAGGGCCGAGCGAGGCGCAGGCAACCGGGCAGCAGGC**ATG**ATGCCCTCGCCTAGTGACT
CCAGCCGCTCGCTGACCAGCCGGCCCAGCACCAGGGGCCTTACCCACCTCCGCCTCCACCGACCCTGGCTGCAGG
CCCTGCTTACGCTGGGGCTGGTCCAAGTGCTCCTGGGCATCCTGGTGGTCACCTTCAGCATGGTGGCCTCTTCCG
TCACCACCACCGAGAGCATCAAGAGGTCCTGCCCGTCTTGGGCTGGGTTCTCGCTGGCGTTCTCCGGGGTGGTTG
GCATTGTGTCCTGGAAGCGGCCATTCACTCTAGTGATCTCCTTCTTCTCCTTGCTTTCGGTGCTCTGTGTCATGC
TTAGCATGGCTGGCTCTGTTCTCTCCTGTAAGAATGCTCAACTGGCCCGAGACTTCCAACAGTGCTCTCTGGAAG
GAAAGGTCTGTGTGTGCTGTCCCTCTGTTCCCCTCCTCCGGCCCTGTCCAGAGTCGGGGCAGGAACTGAAAGTTG
CCCCTAACTCCACCTGTGATGAAGCCCGAGGGGCCCTCAAGAACCTGCTCTTCAGCGTCTGTGGGCTCACCATTT
GTGCCGCTATAATCTGTACACTCTCTGCTATTGTCTGCTGCATCCAAATCTTCTCCCTGGACCTCGTGCATACGC
AGCTGGCCCCTGAGCGGTCAGTCTCAGGCCCACTGGGACCTCTGGGCTGCACGTCCCCGCCCCCAGCCCCTCTCC
TACACACCATGCTGGACCTGGAGGAATTTGTCCCGCCTGTGCCCCCACCGCCCTACTATCCCCCAGAGTATACCT
GCAGCTCAGAAACAGATGCACAGAGCATCACGTACAATGGCTCCATGGACAGCCCAGTGCCCTTGTACCCTACCG
ATTGCCCCCCTTCTTATGAGGCAGTCATGGGACTACGAGGAGACAGCCAGGCCACTCTCTTTGACCCTCAGCTTC
ACGATGGCTCGTGCATCTGTGAACGAGTGGCCTCCATTGTAGACGTGTCCATGGACAGCGGGTCTCTGGTGCTGT
CAGCCATTGGTGACCTCCCTGGGGGCTCTAGCCCGTCGGAGGACTCGTGCCTGCTGGAGCTGCAGGGCTCCGTGC
GCTCCGTGGACTACGTTCTCTTTCGCTCCATCCAGCGCAGCCGTGCCGGCTACTGCCTCAGCCTGGACTGTGGCC
TGCGGGGCCCCTTCGAGGAAAGCCCCCTGCCACGGCGCCCCCCACGGGCTGCCCGCTCCTATTCCTGCTCTGCCC
CTGAAGCTCCACCCCCACTGGGTGCCCCCACAGCTGCCCGCAGCTGCCACCGGTTGGAGGGCTGGCCGCCCTGGG
TGGGACCCTGCTTCCCCGAGCTGAGGCGGCGGGTCCCCCGGGGAGGGGGCCGCCCAGCCGCAGCCCCGCCCACCC
GAGCCCCGACTCGTCGCTTCAGCGATAGCTCAGGTTCCCTCACCCCACCGGGGCACCGGCCTCCTCATCCGGCAT
CCCCACCACCGCTGCTGCTGCCACGGTCCCACAGCGACCCAGGCATCACGACCTCCAGTGACACTGCTGACTTCA
GGGACCTTTATACCAAAGTGCTTGAGGAAGAAGCTGCTTCTGTTTCCTCTGCAGATACAGGGCTCTGCTCTGAAG
CCTGCCTCTTCCGCCTAGCCCGCTGCCCTTCCCCCAAGTTGCTACGTGCCCGGTCAGCCGAGAAACGGCGCCCTG
TGCCCACCTTCCAAAAAGTTCCCCTGCCCTCGGGCCCTGCACCTGCCCACTCCCTGGGGGACCTAAAGGGCAGCT
GGCCAGGTCGGGGCCTGGTCACTCGTTTCCTCCAGATATCCAGGAAAGCCCCAGACCCCAGTGGGACTGGAGCTC
ATGGACATAAGCAGGTGCCCCGGAGCCTGTGGGGCCGGCCTGGCCGAGAGAGCCTCCACCTTCGCAGCTGCGGAG
ATCTGAGCTCTAGCTCTTCCCTGCGGCGTCTCCTGTCTGGCCGCAGGCTGGAGCGTGGTACCCGCCCCCACAGCC
TCAGCCTCAACGGGGGCAGCCGGGAGACTGGGCTC**TGA**CCTAGGCTTCTTGTCACACTGAACACATCCAGCCACA
GGCACCAGCTGGTTGGGACCAGCAGCCCCCAGCATCCTCTTGCACTGGCTGGCACAAAAAGAAACCTGCTGTATA
CCCCCCAAAGTGTCCCTTTCCCTCCTACCTCTGGGGTCTCTTGCTGCTTGCCTCTGCTGCTCTGGTCTGGGAGAG
CTTCTGTCCTGTGCTGCATGGGTATTTAGACTGTGGGGGAGATGCCCCTTCTTATAGCACTGGAGGAGGAAAACA
AATTCTTGTCCCCCCTCAGAATGAGAGTGGCTCTTTCTGATTTGCAAGGGCACTATGGTCAGGGCAAAGGCATGGC
CCAGGTGTTTAAGTACAGGGTGACGTGTGCCTATGCAATGGGGTGGTAAGGCAGGCACGAAGAGTCCAAAAAATC
TAGGTGGCCTCTCAGCTCTGCCACCTCTAGCTGCATGACCTTGGGCAAGCTATGTAACCCCAATTGCCTGCTCCA
TTAAAGACTGTGAAGGTAGAATGTTTGTAAAGCTCTTAACAGTATGTAAGCCTTCAATAAATTTCAGTTTTCCCC
TT

FIGURE 429

MMPSPSDSSRSLTSRPSTRGLTHLRLHRPWLQALLTLGLVQVLLGILVVTFSMVASSVTTTESIKRSCPSWAGFS
LAFSGVVGIVSWKRPFTLVISFFSLLSVLCVMLSMAGSVLSCKNAQLARDFQQCSLEGKVCVCCPSVPLLRPCPE
SGQELKVAPNSTCDEARGALKNLLFSVCGLTICAAIICTLSAIVCCIQIFSLDLVHTQLAPERSVSGPLGPLGCT
SPPPAPLLHTMLDLEEFVPPVPPPPYYPPEYTCSSETDAQSITYNGSMDSPVPLYPTDCPPSYEAVMGLRGDSQA
TLFDPQLHDGSCICERVASIVDVSMDSGSLVLSAIGDLPGGSSPSEDSCLLELQGSVRSVDYVLFRSIQRSRAGY
CLSLDCGLRGPFEESPLPRRPPRAARSYSCSAPEAPPPLGAPTAARSCHRLEGWPPWVGPCFPELRRRVPRGGGR
PAAAPPTRAPTRRFSDSSGSLTPPGHRPPHPASPPPLLLPRSHSDPGITTSSDTADFRDLYTKVLEEEAASVSSA
DTGLCSEACLFRLARCPSPKLLRARSAEKRRPVPTFQKVPLPSGPAPAHSLGDLKGSWPGRGLVTRFLQISRKAP
DPSGTGAHGHKQVPRSLWGRPGRESLHLRSCGDLSSSSSLRRLLSGRRLERGTRPHSLSLNGGSRETGL

FIGURE 430

CAGTGCCCCACAGCTCTTCAGGCCCTTCCTGTGCCTGGCTGCCCTCCCACCCTACCCTTTTGTACCTCTGAGAAG
GCTCTGGCCCCACGCACAGCCCCACTGTCACCAGGGCCAGTATCTGTCTCAGGGACCTCCTATCCAGAGCCTGAG
CCAGCCCCAGCCCCAGCCCCAGCTCCAGCTGCTCCATCTGAACCTGTATCTTCTTCCAAGCCACCCATTACCCTC
TTGGAGTCAGACTCACGCATCTCCAAAGAAGAACTTTTGAGAGCCCAGGCGCTGAGAGAGCAGGGTCAGACACTC
CCGAGCCTCTCGGTACAGCTGTAGGGGCGACACAGGTAGGCTTGCAGCTGCGGGAACAGTGCCACCTCCGCACCT
AAGCACTCCCATTCCTGGCCAGCATCCTTGGGGCTCATCTCATACAATAGCCCCCGGTCTCAGAGCTACCTCCTT
CTCCAGCTCTTCCTCGTCCTCAGGCCTGTGCTCCCCAGTCAGCAGCTGTAGCCGTTCCATGTACTGCCGCTGCAT
GCGGCCAGGCAGGAAGAAGTTGAGGGGAAAGGGCATAGCCTCTGCATACCACTTCCGGGTCACTTCTACGTAGTT
CTTGGTGTCTATCCAAAAAGTATGTACCTGGATTGGGTGGCAGGAAGAAACAGGCAGGTCTGAGCCAGTGCACC
TGTCTGATTCAAGGTGGGCTTCTGACCTCCATGCTCTCCTGAGTCTCTGTGTGGGTCTGTGTGTTCCCGTCCCCT
CCCCGGCTGGCCATGGATGCTGGGAGGTCTGGGCACACTCACCAGCACCGGGATCAACTTCTCCTCCAGGAGAGA
CATGAAGGCCAGGGTGTCTGCCCCTTGCTGAGCTGACAGATCATAATCAGCATTGTACTTCTGTGGAGGAAATAT
CC**ATG**GCGTGGACGCTGGGGAGCTGCAAGGGCACTTCACCAGGGAGGAAGGAGTCCTGTCTGGTACCCCCCTCAC
TGGCCTCTGAGTGCAGTGGAGGTACAGCAAGGAACTTTTCCTGCCAAGGCCCCCTTGCCTGGGCCCAGCCAGTAG
CCTGTTGCTGTTGGCAAAAAGCCTGGGCCTTGGAGCCCGCTGGCCGTCAAGGTCCTGGGCCCATTGAGAAGAAGG
AAGAAAGGTTGGGCCGCAAACTAGGAGCAGCTCCCAGAATTTCCATGGAAAGCTGGAACAATGCCTGC**TGA**CAGC
AACTTTCTAACAGTAACTTTCCCGACCCAGACACCACAAAGCTAGCACAACGGAGCTCAGATGCAGGCTAGGACT
CGGTCCATGCCTCAGGAACCAGGGAAAGCCATCCTCACACTCCCTGGATCCAGGGAACCCACGCCCAGGGCCCCC
CAGCTTGTTCCCTCAGTGCCCAGCTCTTGGCTATTTCTTTCACTTCATTCCATCGCCCAGACACCATTACCACAT
ACACATTCCATCCATACCCCCAGGTCTCAGCCTGCCCTACCTTCCCAGGCTCCAGTCCCTGTTCCTCAGCATCCC
CCACCACATCCTGAGTAAGCTTTGTCCCCAGATAACCTCTTCAGCATGATCCTTAAATCTCCCTAAGCCTCAGTT
TCTCCCCTGTGGAATGGGGGTAAGAATCTCTTTCTCTGAATGCCCCTGTGTTAGGAAATAATTTAGAATACTTCG
GAAACAAAAAGCTCTGTTCACACCTAAGCAATCAGGGCAGTGGCCCTGGCCTTGCCAGGAACTTAGGCTTTTATC
TGGATCCTCTTTCCAGGCCTCTCAATTAATTCCCCAGGTCCTTAACCTTTGGGAAATTAGAAATTAGGAAGAGTG
TCCCACTTCTGACACTGTGTTCCCTCTTGGAACCTGACCGTCAATGCTAGAAGAACCCTTGGAAAACATGCTGGC
CCAGCCCTCTAGTTTTACAAATAAGGGAGTGCACAGCCCTGAGAGGTTACATGGCCTGCCCAAGATCACGCAGTC
AATGGCAGAGTAAAGAGCATAGCCTAGGCCTCCCCACTCCTCTAGTAATGCTCTTTCATCTTCTCCAACCTGGCT
CTAAGCCTTGTCCATCCTGAGCCCCATATCTAGCCCAACCTAGTCCCTGAAAACAAGAAGTGGCCCTTAGAAATC
TCTCTCCAGTCCCACTATCAGAGGCCAACTGCTGTCTTCCAGTCTCCTTCAGCCTGTGCTCCTCTCCCTCCCTGA
CTGACAGGCAGAAGGTACCGTGCCTCTGGATATCCCCACAGTGCCCTGAGCTGCATCTCTTGCCGACTGCTTTAA
TACATCACAGTGACATTGTGTGTGTCTCTGCCACCAGACTATTGCTCCTTGATGCTCTGGGTCACCTGCATCTAG
CATGGCATATATCTAGTGCTCAATAAATGTGTATTGTACGG

FIGURE 431

MAWTLGSCKGTSPGRKESCLVPPSLASECSGGTARNFSCQGPLAWAQPVACCCWQKAWALEPAGRQGPGPIEKKE
ERLGRKLGAAPRISMESWNNAC

FIGURE 432

AAGCCCCAGCCCGGCCTCCGCTCCGGCCGCCGCCACCGCCCCTGTTTTGTTTCCATGGCGACAGGCGGCGCAGGG
CCCGCTCCAAACATAACGCGCTGTGGAAAACATGCTGCTCGGGGGACCCCCCCGCAGTCCCCGCTCGGGGACGAG
CCCCAAGGGGCCCTGGAGCAGTACAGGCCACGTGCAGTTTGGCAAGAGCCCCCAGACCTGGCCCAGGCGCACAAG
ACCCCGCTCTCCAGAGCCTGCCGCGCCTTCAAGGGTTCGGGGCTCCACTTGGACGAGGCGCCGTGACTCTCCGAG
GCGCGCCGGGCCGACAGCGCTGTCCCGCTACGTGGGCCACCTCTGGATGGGCCGGCGGCCGCCCTCCCCCGAGGC
CCGCGGCCCAGTCCCCCGCAGTTCAGCTGCCAGTCGGGCCAGAAGAAGCCTCGCCTCCCCGGGGATCTCCCCAGG
CCCCCTGACCGCAACGATCGGAGGGGCGGTGGCGGGGGGCGGGCCCAGGCAGGGGAGGGCAGAAGCACACAAGGA
AGTGTTTCCGGGACAGAGGGTGGGCAAGATGGCGGCGCCCATGGAGCTGTTCTGCTGGTCAGGGGGCTGGGGGCT
GCCGTCAGTGGACCTGGACAGCCTGGCCGTGCTGACCTATGCCAGATTTACTGGTGCTCCACTGAAGGTACACAA
GATCAGCAACCCCTGGCAGAGCCCTTCAGGAACTCTGCCTGCCCTTCGGACCAGTCATGGAGAGGTCATCTCAGT
TCCACACAAGATCATCACCCACCTTCGAAAAGAGGTACATACTTTTTGGATAGACACCAAGAACTACGTGGAAGT
GACCCGGAAGTGGTATGCAGAGGCTATGCCCTTTCCCCTCAACTTCTTCCTGCCTGGCCGCATGCAGCGGCAGTA
CATGGAACGGCTACAGCTGCTGACTGGGGAGCACAGGCCTGAGGACGAGGAAGAGCTGGAGAAGGAGCTGTACCG
AGAGGCTCGGGAGTGTCTGACCCTGCTCTCTCAGCGCCTGGGCTCTCAAAAGTTCTTCTTTGGAGATGCCCCTGC
CTCCTTGGACGCCTTCGTCTTCAGCTACTTGGCCCTGCTGCTGCAGGCAAAGCTGCCCAGTGGGAAGCTGCAGGT
CCACCTGCGTGGGCTGCACAACCTCTGTGCCTATTGTACCCACATTCTCAGTCTCTACTTCCCCTGGGATGGAGC
TGAGGTACCACCGCAACGCCAGACACCAGCAGGCCCAGAGACTGAGTGAGTGAGCCATACCGGCGCCGGAACCAG
ATCCTATCTGTGCTGGCAGTGACTGGCAGCCATGGTGGGCTACGCCTTGCTCAGCGGCATTGTCTCCATCCAGCG
GGCAACGCCTGCTCGTGGCCCCAGGCACCCGGACCCTGGGCATGGCTGAGGAGGATGAAGAGGAATGATTTGTCC
TCACGCTCCCAAGACTGGTTTTTCTACTCTCATGCATTCCAGAGGCCCCCGTGCCTCCTCGTTGTTGGTACAGCC
GGACACGGGGTGTGCCACCCAGAATAAAGCCACTCACACTG

FIGURE 433

GCCGGAAGCGCGCGGAGACCATGTAGTGAGACCCTCGCGAGGTCTGAGAGTCACTGGAGCTACCAGAAGCATCAT
GGGGCCCTGGGGAGAGCCAGAGCTCCTGGTGTGGCGCCCCGAGGCGGTAGCTTCAGAGCCTCCAGTGCCTGTGGG
GCTGGAGGTGAAGTTGGGGGCCCTGGTGCTGCTGCTGGTGCTCACCCTCCTCTGCAGCCTGGTGCCCATCTGTGT
GCTGCGCCGGCCAGGAGCTAACCATGAAGGCTCAGCTTCCCGCCAGAAAGCCCTGAGCCTAGTAAGCTGTTTCGC
GGGGGGCGTCTTTTTGGCCACTTGTCTCCTGGACCTGCTGCCTGACTACCTGGCTGCCATAGATGAGGCCCTGGC
AGCCTTGCACGTGACGCTCCAGTTCCCACTGCAAGAGTTCATCCTGGCCATGGGCTTCTTCCTGGTCCTGGTGAT
GGAGCAGATCACACTGGCTTACAAGGAGCAGTCAGGGCCGTCACCTCTGGAGGAAACAAGGGCTCTGCTGGGAAC
AGTGAATGGTGGGCCGCAGCATTGGCATGATGGGCCAGGGGTCCCACAGGCGAGTGGAGCCCCAGCAACCCCCTC
AGCCTTGCGTGCCTGTGTACTGGTGTTCTCCCTGGCCCTCCACTCCGTGTTCGAGGGGCTGGCGGTAGGGCTGCA
GCGAGACCGGGCTCGGGCCATGGAGCTGTGCCTGGCTTTGCTGCTCCACAAGGGCATCCTGGCTGTCAGCCTGTC
CCTGCGGCTGTTGCAGAGCCACCTTAGGGCACAGGTGGTGGCTGGCTGTGGGATCCTCTTCTCATGCATGACACC
TCTAGGCATCGGGCTGGGTGCAGCTCTGGCAGAGTCGGCAGGACCTCTGCACCAGCTGGCCCAGTCTGTGCTAGA
GGGCATGGCAGCTGGCACCTTTCTCTATATCACCTTTCTGGAAATCCTGCCCCAGGAGCTGGCCAGTTCTGAGCA
AAGGATCCTCAAGGTCATTCTGCTCCTAGCAGGCTTTGCCCTGCTCACTGGCCTGCTCTTCATCCAAATCTAGGG
GGCTTCAAGAGAGGGGCAGGGGAGATTGATGATCAGGTGCCCCTGTTCTCCCTTCCCTCCCCCAGTTGTGGGGAA
TAGGAAGGAAAGGGGAAGGGAAATACTGAGGACCAAAAAGTTCTCTGGGAGCTAAAGATAGAGCCTTTGGGGCTA
TCTGACTAATGAGAGGGAAGTGGGCAGACAAGAGGCTGGCCCCAGTCCCAAGGAACAAGAGATGGTCAAGTCGCT
AGAGACATATCAGGGGACATTAGGATTGGGGAAGACACTTGACTGCTAGAATCAGAGGTTGGACACTATACATAA
GGACAGGCTCACATGGGAGGCTGGAGGTGGGTACCCAGCTGCTGTGGAACGGGTATGGACAGGTCATAAACCTAG
AGTCAGTGTCCTGTTGGTCCTAGCCCATTTCAGCACCCTGCCACTTGGAGTGGACCCCTCCTACTCTTCTTAGCG
CCTACCCTCATACCTATCTCCCTCCTCCCATCTCCTAGGGGACTGGCGCCAAATGGTCTCTCCCTGCCAATTTTG
GTATCTTCTCTGGCCTCTCCAGTCCTGCTTACTCCTCTATTTTTAAAGTGCCAAACAAATCCCCTTCCTCTTTCT
CAAAGCACAGTAATGTGGCACTGAGCCCTACCCAGCACCTCAGTGAAGGGGGCCTGCTTGCTCTTTATTTTGGTC
CCGGATCCTGGGGTGGGGCAGAAATATTTTCTGGGCTGGGGTAGGAGGAAGGTTGTTGCAGCCATCTACTGCTGC
TGTACCCTAGGAATATGGGGACATGGACATGGTGTCCCATGCCCAGATGATAAACACTGAGCTGCCAAAACATTT
TTTTAAATACACCCGAGGAGCCCAAGGGGGAAGGGCAATGCCTACCCCCAGCGTTATTTTTGGGGAGGGAGGGCT
GTGCATAGGGACATATTCTTTAGAATCTATTTTATTAACTGACCTGTTTTGGGACCTGTTACCCAAATAAAAGAT
GTTTCTAG

FIGURE 434

AGAAAGAAAAGGTGTAGTGTTTGGGGAGGTCAACGGGCTATGCTGGCTTGACAGGGCTGGGCTCTTCAGAACAGA
AGC**ATG**GATCTCGGAATCCCTGACCTGCTGGACGCGTGGCTGGAGCCCCCAGAGGATATCTTCTCGACAGGATCC
GTCCTGGAGCTGGGACTCCACTGCCCCCCTCCAGAGGTTCCGGTAACTAGGCTACAGGAACAGGGACTGCAAGGC
TGGAAGTCCGGTGGGGACCGTGGCTGTGGCCTTCAAGAGAGTGAGCCTGAAGATTTCTTGAAGCTTTTCATTGAT
CCCAATGAGGTGTACTGCTCAGAAGCATCTCCTGGCAGTGACAGTGGCATCTCTGAGGACCCCTGCCATCCAGAC
AGTCCCCCTGCCCCCAGGGCAACCAGTTCTCCTATGCTCTATGAGGTTGTCTATGAGGCAGGGGCCCTGGAGAGG
ATGCAGGGGGAAACTGGGCCAAATGTAGGCCTTATCTCCATCCAGCTAGATCAGTGGAGCCCAGCATTTATGGTG
CCTGATTCCTGCATGGTCAGTGAGCTGCCCTTTGATGCTCATGCCCACATCCTGCCCAGAGCAGGCACCGTAGCC
CCAGTGCCCTGTACAACCCTGCTGCCCTGTCAAACCCTGTTCCTGACCGATGAGGAGAAGCGTCTGCTGGGGCAG
GAAGGGGTTTCCCTGCCCTCTCACCTGCCCCTCACCAAGGCAGAGGAGAGGGTCCTCAAGAAGGTCAGGAGGAAA
ATCCGTAACAAGCAGTCAGCTCAGGACAGTCGGCGGCGGAAGAAGGAGTACATTGATGGGCTGGAGAGCAGGGTG
GCAGCCTGTTCTGCACAGAACCAAGAATTACAGAAAAAAGTCCAGGAGCTGGAGAGGCACAACATCTCCTTGGTA
GCTCAGCTCCGCCAGCTGCAGACGCTAATTGCTCAAACTTCCAACAAAGCTGCCCAGACCAGCACTTGTGTTTTG
ATTCTTCTTTTTTCCCTGGCTCTCATCATCCTGCCCAGCTTCAGTCCATTCCAGAGTCGACCAGAAGCTGGGTCT
GAGGATTACCAGCCTCACGGAGTGACTTCCAGAAATATCCTGACCCACAAGGACGTAACAGAAAATCTGGAGACC
CAAGTGGTAGAGTCCAGACTGAGGGAGCCACCTGGAGCCAAGGATGCAAATGGCTCAACAAGGACACTGCTTGAG
AAGATGGGAGGGAAGCCAAGACCCAGTGGGCGCATCCGGTCCGTGCTGCATGCAGATGAGATG**TGA**GCTGGAACA
GACCTTCCTGGCCCACTTCCTGATCACAAGGAATCCTGGGCTTCCTTATGGCTTTGCTTCCCACTGGGATTCCTA
CTTAGGTGTCTGCCCTCAGGGGTCCAAATCACTTCAGGACACCCCAAGAGATGTCCTTTAGTCTCTGCCTGAGGC
CTAGTCTGCATTTGTTTGCATATATGAGAGGGTACCTCAAATACTTCTGTTATGTATCTGTGATTTTATTTCTTC
TTTGGGTATAGGGTTGAGGGGAAATAAGTTTTGAGTGAGAAATAAACGTTTTAGCTGAAATTGT

FIGURE 435

MDLGIPDLLDAWLEPPEDIFSTGSVLELGLHCPPPEVPVTRLQEQGLQGWKSGGDRGCGLQESEPEDFLKLFIDP
NEVYCSEASPGSDSGISEDPCHPDSPPAPRATSSPMLYEVVYEAGALERMQGETGPNVGLISIQLDQWSPAFMVP
DSCMVSELPFDAHAHILPRAGTVAPVPCTTLLPCQTLFLTDEEKRLLGQEGVSLPSHLPLTKAEERVLKKVRRKI
RNKQSAQDSRRRKKEYIDGLESRVAACSAQNQELQKKVQELERHNISLVAQLRQLQTLIAQTSNKAAQTSTCVLI
LLFSLALIILPSFSPFQSRPEAGSEDYQPHGVTSRNILTHKDVTENLETQVVESRLREPPGAKDANGSTRTLLEK
MGGKPRPSGRIRSVLHADEM

FIGURE 436

GCGAGGCGCCACCGACGCGGAAGACTATAAGCCCCAGCGGGCGACGACCGAACGCCCCCGGGAACACCGGGCCCC
GAGCTCGGTCCCGCGCCCGAGGATCCTCCACGGGGCTAGATGGCTGCGTCGGGGGCGGGAGCGGAGGTGAGCGGG
CGCTAGGGCCGCGAGCCCCCGCCGGCCCTTCCTCCAGCGCCCTGCGGACCCCGCAGAAGGCGCTCGCCTCCCTAG
CCCGCAAAAACATATCGATTTTTCTCGCTGTGGCAACGGGGACGTCCTGATAGATCCTCTGCTCCAATAGGCAAC
TCCGGCCTTCCCTGCCCTGACCTGGAACCTCTGGGAGGGCTGCAGAGTAAGTGCCGCCTCTGCGCTCCGACGGAG
GCACGAGGCCTGTGGAGTAGGTCCCTCTGTTCCGACAGGTGCGACACTTGGCGCTCC**ATG**CTTGCGGGTGCCGGG
AGGCCTGGCCTCCCCCAGGGCCGCCACCTCTGCTGGTTGCTCTGTGCTTTCACCTTAAAGCTCTGCCAAGCAGAG
GCTCCCGTGCAGGAAGAGAAGCTGTCAGCAAGCACCTCAAATTTGCCATGCTGGCTGGTGGAAGAGTTTGTGGTA
GCAGAAGAGTGCTCTCCATGCTCTAATTTCCGGGCTAAAACTACCCCTGAGTGTGGTCCCACAGGATATGTAGAG
AAAATCACATGCAGCTCATCTAAGAGAAATGAGTTCAAAAGCTGCCGCTCAGCTTTGATGGAACAACGCTTATTT
TGGAAGTTCGAAGGGGCTGTCGTGTGTGTGGCCCTGATCTTCGCTTGTCTTGTCATCATTCGTCAGCGACAATTG
GACAGAAAGGCTCTGGAAAAGGTCCGGAAGCAAATCGAGTCCATA**TAG**CTACATTCCACCCTTGTATCCTGGGTC
TTAGAGACCCTATCTCAGACAGTGAAAGTGAAATGGACTGATTTGCACTCTTGGTTCTTTGGAGCCTTGTGGTGG
AATCCCCTTTTCCCCATCTTCTTCTTTCAGATCATTAATGAGCAGAATAAAAAGAGTAAAATGGT

FIGURE 437

MLAGAGRPGLPQGRHLCWLLCAFTLKLCQAEAPVQEEKLSASTSNLPCWLVEEFVVAEECSPCSNFRAKTTPECG
PTGYVEKITCSSSKRNEFKSCRSALMEQRLFWKFEGAVVCVALIFACLVIIRQRQLDRKALEKVRKQIESI

FIGURE 438

GAATTCGAGGATCCGGGTACCATGGAGGAAAACTTCTTCCTGGCCTGGGCTCCGTGCCGCTCTGTTTGCCAACC
GTCCAGTCCCGCCTACCAGTGCCGGGCGCTCCCCACCCCTCCCCCGGCTCCCCCGGTGTCCGCC**ATG**GCCAAAGC
CTACGACCACCTCTTCAAGTTGCTGCTGATCGGGGACTCGGGGGTGGGCAAGACTTGTCTGATCATTCGCTTTGC
AGAGGACAACTTCAACAACACTTACATCTCCACCATCGGAATTGATTTCAAGATCCGCACTGTGGATATAGAGGG
GAAGAAGATCAAACTACAAGTCTGGGACACGGCTGGCCAAGAGCGGTTCAAGACAATAACTACTGCCTACTACCG
TGGAGCCATGGGCATTATCCTAGTATACGACATCACGGATGAGAAATCTTTCGAGAATATTCAGAACTGGATGAA
AAGCATCAAGGAGAATGCCTCGGCTGGGGTGGAGCGCCTCTTGCTGGGGAACAAATGTGACATGGAGGCCAAGAG
GAAGGTGCAGAAGGAGCAGGCCGATAAGTTGGCTCGAGAGCATGGAATCCGATTTTTCGAAACTAGTGCTAAATC
CAGTATGAATGTGGATGAGGCTTTTAGTTCCCTGGCCCGGGACATCTTGCTCAAGTCAGGAGGCCGGAGATCAGG
AAACGGCAACAAGCCTCCCAGTACTGACCTGAAAACTTGTGACAAGAAGAACACCAACAAGTGCTCCCTGGGC**TG**
AGGACCCTTTCTTGCCTCCCCACCCCGGAAGCTGAACCTGAGGGAGACAACGGCAGAGGGAGTGAGCAGGGGAGA
AATAGCAGAGGGGCTTGGAGGGTCACATAGGTAGATGGTAAAGAGAATGAGGAGAAAAAGGAGAAAAGGGAAAAG
CAGAAAGGAAAAAAAGGAAGAGAGAGGAAGGGAGAAGGGAGAGGAATGAATTGAGGAAGTGAAAGAAGGCAAGGA
GGTAGGAAGAGAGGGAGGAGGAAAGGAAGGAGAGAGATGCCTCAGGCTTCAGACCTTACCTGGGTTTTCAGGGCA
AACATAAATGTAAATACACTGATTTATTCTGTTACTAGATCAGGTTTTAGGGTCCTGCAAAAGGCTAGCTCGGCA
CTACACTAGGGAATTTGCTCCTGTTCTGTCACTTGTCATGGTCTTTCTTGGTATTAAAGGCCACCATTTGCACAA
AAAAAAAAAAAAACCATGGTACCCGGATCCTCGAATTC

FIGURE 439

MAKAYDHLFKLLLIGDSGVGKTCLIIRFAEDNFNNTYISTIGIDFKIRTVDIEGKKIKLQVWDTAGQERFKTITT
AYYRGAMGIILVYDITDEKSFENIQNWMKSIKENASAGVERLLLGNKCDMEAKRKVQKEQADKLAREHGIRFFET
SAKSSMNVDEAFSSLARDILLKSGGRRSGNGNKPPSTDLKTCDKKNTNKCSLG

FIGURE 440

CCTTTCCGGCGGTGACGACCTACGCACACGAGAAC**ATG**CCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAG
AGGAGAAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCCAG
GATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCT
GCCAGCCTACAGGAGGAAAAGCAAGGCTTACAGAAGGATGTTCCTTCAGGAGGAAGCAGCAC**TAA**AAGCACTCTG
AGTCAAGATGAGTGGGAAACCATCTCAATAAACACATTTTGGAT

FIGURE 441

MPLAKDLLHPSPEEEKRKHKKKRLVQSPNSYFMDVKCPGCYKITTVFSHAQTVVLCVGCSTVLCQPTGGKARLTE
GCSFRRKQH

FIGURE 442

ACTCAGGCAGCAGCCCCTTCTTTCTTGCCCCAGTCTCCAGTTCTCCAGTGTTCACAGGTGAGCCTACCAACAGCC
ACTGCTC**ATG**ATGGAGGCCATCAAGAAAAAGATGCAGATGCTGAAGTTAGACAAGGAGAATGCTCTGGATCGGGC
AGAGCAAGCTGAAGCTGAGCAGAAGCAGGCAGAAGAAAGAAGTAAACAGCTGGAGGATGAGCTGGCAGCCATGCA
GAAGAAGCTGAAAGGGACAGAGGATGAGCTGGACAAGTATTCTGAAGCTTTGAAGGATGCCCAGGAGAAGCTGGA
ACTGGCAGAGAAGAAGGCTGCTGATGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGA
AGAGCTGGACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGA
GAGTGAGAGAGGTATGAAGGTTATTGAAAACCGGGCCTTAAAAGATGAAGAAAAGATGGAACTCCAGGAAATCCA
ACTCAAAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCAT
TGAAGGAGACTTGGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCTAAGTGTTCTGAGCTGGAGGAGGAGCT
GAAGAATGTCACCAACAACCTCAAGTCTCTTGAGGCTCAGGCGGAGAAGTACTCTCAAAAAGAAGATAAATATGA
GGAAGAAATCAAGATTCTTACTGATAAACTCAAGGAGGCAGAGACCCGTGCTGAGTTTGCTGAGAGATCGGTAGC
CAAGCTGGAAAAGACAATTGATGACCTGGAAGATGAGCTCTATGCCCAGAAACTGAAGTACAAGGCCATTAGCGA
GGAGCTGGACCACGCCCTCAATGACATGACCTCTATA**TAA**TTATCACCGTTTCTGCTCTGTTCTGGATCTGCCCC
CTTTACTCCTCGGGGAACCCAAGGCCCCACTCTCGCTCTGGATTCCATTTGGGTCAGCCTGGCTGGTCCCCAAGG
CATTAGGATGGGGGAGCAAAAAGCAACTTATGTATTTTCTTCCACCCCCACCCCAAATTAAAATGTTAAGCTGCT
GGA

FIGURE 443

MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTEDELDKYSEALKDAQEKLELA
EKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEEKMELQEIQLK
EAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESKCSELEEELKNVTNNLKSLEAQAEKYSQKEDKYEEE
IKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALNDMTSI

FIGURE 444

GTCAGCGGGGAAGCTGGAAGGCGTCGTTCTCCTTTCCCAGCTCTCCTGCCTGTCCGCCATGTTTTCAGGCCGGGT
CTGGCTTGGTCTTCCCCCGTAAGGAAATGGCCGGGGAGCTCCAGGGGACCCAGGCGCCGTCGCTTCGGCGGAGCT
GGGCTGACCAGCCAGGACAGCGGGGTAAACCCGAACAATTCTGCGCGAGGTAGGGAGGCC**ATG**GCGTCCGGCAGT
AACTGGCTCTCCGGGGTGAATGTCGTGCTGGTGATGGCCTACGGGAGCCTGGACTTGAAAGAGGAGATTGATATT
CGACTCTCCAGGGTTCAGGATATCAAGTATGAGCCCCAGCTCCTTGCAGATGATGATGCTAGACTACTACAACTG
GAAACCCAGGGAAATCAAAGTTGCTACAACTATCTGTATAGGATGAAAGCTCTGGATGCCATTCGTACCTCTGAG
ATCCCATTTCATTCTGAAGGCCGGCATCCCCGTTCCTTAATGGGCAAGAATTTCCGCTCCTACCTGCTGGATCTG
CGAAACACTAGTACGCCTTTCAAGGGTGTACGCAAAGCACTCATTGATACCCTTTTGGATGGCTATGAAACAGCC
CGCTATGGGACAGGGGTCTTTGGCCAGAATGAGTACCTACGCTATCAGGAGGCCCTGAGTGAGCTGGCCACTGCG
GTTAAAGCACGAATTGGGAGCTCTCAGCGACATCACCAGTCAGCAGCCAAAGACCTAACTCAGTCCCCTGAGGTC
TCCCCAACAACCATCCAGGTGACATACCTCCCCTCCAGTCAGAAGAGTAAACGTGCCAAGCACTTCCTTGAATTG
AAGAGCTTTAAGGATAACTATAACACATTGGAGAGTACTCTG**TGA**CGGAGCTGAAGGACTCTTGCCGTAGATTAA
GCCAGTCAGTTGCAATGTGCAAGACAGGCTGCTTGCCGGGCCGCCCTCGGAACATCTGGCCCAGCAGGCCCAGAC
TGTATCCATCCAAGTTCCCGTTGTATCCAGAGTTCTTAGAGCTTGTGTCTAAAGGGTAATTCCCCAACCCTTCCT
TATGAGCATTTTTAGAACATTGGCTAAGACTATTTTCCCCCAGTAGCGCTTTTTTCTGGATTTGCATTCGGGTGT
TATTCTTAATGTTTCTGTCAAAGCTTCTTAAAAATCTTCACTTGGTTTCAGCCATAGTTCACCTTCCCTGTTCCA
GGTTTATTTAATTCCAAAGGTGAGAGTTGGAGTGAGATGTCTTCCATATCTATACCTTTGTGCACAGTTGAATGG
GAACTGTTTGGGTTTAGGGCATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAACTGGTGGGAGGTCAAGTGG
GGAAGTTGGTGAATGTGGAATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTTGCAGCTTTCCTGACATGC
AAGGATCTACTTTAATTCCACACTCTCATTAATAAATTGAATAAAAGGGAATGTTTTGGCACCTGATATAATCTG
CCAGGCTATGTGACAGTAGGAAGGAATGGTTTCCCCTAACAAGCCCAATGCACTGGTCTGACTTTATAAATTATT
TAATAAAATGAACTATTATCAAATAAAACGTATGAATCAGTAAAAAAAAAAAAAAAAAAA

FIGURE 445

MASGSNWLSGVNVVLVMAYGSLDLKEEIDIRLSRVQDIKYEPQLLADDDARLLQLETQGNQSCYNYLYRMKALDA
IRTSEIPFHSEGRHPRSLMGKNFRSYLLDLRNTSTPFKGVRKALIDTLLDGYETARYGTGVFGQNEYLRYQEALS
ELATAVKARIGSSQRHHQSAAKDLTQSPEVSPTTIQVTYLPSSQKSKRAKHFLELKSFKDNYNTLESTL

FIGURE 446

CCCGACTAAGTGACTTAAACTCCCACCTACTCCTGGAATAAGGAGTCAAAGCCCGGATAGGCGCAGTATTCTACC
TTGTAAATACTGTTATTTGTATATACTGTAAATGATGACATCGGTGGGCACTAACCGAGCCCGGGGAAACTGGGA
ACAACCTCAAAACCAAAACCAGACACAGCACAAGCAGCGGCCACAGGCCACTGCAGAACAAATTAGACTTGCACA
GATGATTTCGGACCATAATGATGCTGACTTTGAGGAGAAGGTGAAACAATTGATTGATATTACAGGCAAGAACCA
GGATGAATGTGTGATTGCTTTGCATGACTGCAATGGAGATGTCAACAGAGCTATCAATGTTCTTCTGGAAGGAAA
CCCAGACACGCATTCCTGGGAGATGGTCGGGAAGAAGAAGGGAGTCTCAGGCCAGAAGGATGGTGGCCAGACGGA
ATCCAATGAGGAAGGCAAAGAAAATCGAGACCGGGACAGAGACTATAGTCGGCGACGTGGTGGGCCACCAAGACG
GGGGAGAGGTGCCAGCCGTGGACGAGAGTTTCGAGGTCAGGAAAATGGATTGGATGGCACCAAGAGTGGAGGGCC
TTCTGGAAGAGGAACAGAAAGAGGCAGAAGGGGCCGTGGCCGAGGCAGAGGTGGCTCTGGTAGGCGAGGAGGAAG
GTTTTCTGCTCAAGGAATGGGAACCTTTAACCCAGCTGATTATGCAGAGCCAGCCAATACTGATGATAACTATGG
CAATAGCAGCGGCAATACGTGGAACAACACTGGCCACTTTGAACCAGATGATGGGACGAGTGCATGGAGGACTGC
AACAGAGGAGTGGGGGACTGAAGATTGGAATGAAGATCTTTCTGAGACCAAGATCTTCACTGCCTCTAATGTGTC
TTCAGTGCCTCTGCCTGCGGAGAATGTGACAATCACTGCTGGTCAGAGAATTGACCTTGCTGTTCTGCTGGGGAA
GACACCATCTACAATGGAGAATGATTCATCTAATCTGGATCCGTCTCAGGCTCCTTCTCTGGCCCAGCCTCTGGT
GTTCAGTAATTCGAAGCAGACTGCCATATCACAGCCTGCTTCAGGGAACACATTTTCTCATCACAGTATGGTGAG
CATGTTAGGGAAAGGATTTGGTGATGTCGGTGAAGCTAAAGGCGGCAGTACTACAGGCTCCCAGTTCTTGGAGCA
ATTCAAGACTGCCCAAGCCCTGGCTCAGTTGGCAGCTCAGCATTCTCAGTCTGGAAGCACCACCACCTCCTCTTG
GGACATGGGCTCGACGACACAATCCCCATCACTGGTGCAGTATGATTTGAAGAACCCAAGTGATTCAGCAGTGCA
CAGCCCCTTTACAAAGCGCCAGGCTTTTACCCCATCTTCAACCATGATGGAGGTGTTCCTTCAGGAGAAGTCACC
TGCAGTGGCTACCTCCACAGCTGCACCTCCACCTCCGTCTTCTCCTCTGCCAAGCAAATCCACATCGGCTCCACA
GATGTCGCCTGGATCTTCAGACAACCAGTCCTCTAGCCCTCAGCCGGCTCAGCAGAAACTGAAACAGCAGAAGAA
AAAAGCCTCCTTGACTTCTAAGATTCCTGCTCTGGCTGTGGAGATGCCTGGCTCAGCAGATATCTCAGGGCTAAA
CCTGCAGTTTGGGGCATTGCAGTTTGGGTCAGAGCCTGTCCTTTCTGATTATGAGTCCACCCCCACCACGAGCGC
CTCTTCAAGCCAGGCTCCAAGTAGCCTGTATACCAGCACGGCCAGTGAATCATCCTCTACAATTTCATCTAACCA
GAGTCAGGAGTCTGGTTATCAGAGCGGCCCAATTCAGTCGACAACCTATACCTCCCAAAATAATGCTCAGGGCCC
TCTTTATGAACAGAGATCCACACAGACTCGGCGGTACCCCAGCTCCATCTCTTCATCACCCCAAAAGGACCTGAC
TCAGGCAAAGAATGGCTTCAGTTCTGTGCAGGCCACGCAGTTACAGACCACACAATCTGTTGAAGGTGCTACAGG
CTCTGCAGTGAAATCTGATTCACCTTCCACTTCTAGCATCCCCCCTCTCAATGAAACGGTATCTGCAGCTTCCTT
ACTGACGACAACCAATCAGCATTCATCCTCCTTGGGTGGCTTGAGCCACAGTGAGGAGATTCCAAATACTACCAC
CACACAACACAGCAGCACGTTATCTACGCAGCAGAATACCCTTTCATCATCAACATCTTCTGGGCGCACTTCGAC
ATCCACTCTTTTGCACACAAGTGTGGAGAGTGAGGCGAATCTCCATTCTTCCTCCAGCACTTTTTCCACCACATC
CAGCACAGTCTCTGCACCTCCCCCAGTGGTCAGTGTCTCCTCCAGTCTCAATAGTGGCAGTAGCCTGGGCCTCAG
CCTAGGCAGCAACTCCACTGTCACAGCCTCGACTCGAAGCTCAGTTGCTACGACTTCAGGAAAAGCTCCTCCCAA
CCTCCCTCCTGGGGTCCCGCCGTTGTTGCCTAATCCGTATATTATGGCTCCAGGGCTGTTACATGCCTACCCGCC
ACAAGTATATGGTTATGATGACTTGCAGATGCTTCAGACAAGATTTCCATTGGATTACTACAGCATCCCATTTCC
CACACCCACTACTCCGCTGACTGGGAGGGATGGTAGCCTGGCCAGCAACCCTTATTCTGGTGACCTCACAAAGTT
CGGCCGTGGGGATGCCTCCTCCCCAGCCCCGGCCACAACCTTGGCCCAACCCCAACAGAACCAGACGCAGACTCA
CCATACCACGCAGCAGACATTCCTGAACCCGGCGCTGCCTCCTGGCTACAGTTACACCAGCCTGCCATACTATAC
AGGGGTCCCGGGCCTCCCCAGCACCTTCCAGTATGGGCCTGCTGTGTTCCCTGTGGCTCCTACCTCTTCCAAGCA
GCATGGTGTGAATGTCAGTGTGAATGCATCGGCCACCCCTTTCCAACAGCCGAGTGGATATGGGTCTCATGGATA
CAACACTGGAAGAAAATATCCACCCCCTTACAAGCATTTCTGGACGGCTGAGAGCTAATTTGGCCCAAGGCTGGG
GGCTGTGTTTTGTGTGTGTGTATAAATTTGCACTGAAGTCTTGTTTCAGAAACCAGACCACTGAGGAGAGCCTGC
TGAGCTGAGGCCATGGCCTGCGTGGCTTGGGGAAATGAGTTGGTGGATACCTTCTGGGCTTTTGAACTTGCCCCT
CCCCCATTTCCCTCTCCCCCATGTGTCTGACCCTGTCTTACCCATTTCAAGTTCAAGCGGTGCAGCACCTTCGAA
GCATCAATGCACACACCTGCTGTTGCTTTTGATTTCTGGAAGGCATGTAGTTTCAACTTGTAACAAAAATATTTG
TAGTCTTCAATAAACTGTGGTATTTCTTTAGCTAAC

FIGURE 447

MMTSVGTNRARGNWEQPQNQNQTQHKQRPQATAEQIRLAQMISDHNDADFEEKVKQLIDITGKNQDECVIALHDC
NGDVNRAINVLLEGNPDTHSWEMVGKKKGVSGQKDGGQTESNEEGKENRDRDRDYSRRRGGPPRRGRGASRGREF
RGQENGLDGTKSGGPSGRGTERGRRGRGRGRGGSGRRGGRFSAQGMGTFNPADYAEPANTDDNYGNSSGNTWNNT
GHFEPDDGTSAWRTATEEWGTEDWNEDLSETKIFTASNVSSVPLPAENVTITAGQRIDLAVLLGKTPSTMENDSS
NLDPSQAPSLAQPLVFSNSKQTAISQPASGNTFSHHSMVSMLGKGFGDVGEAKGGSTTGSQFLEQFKTAQALAQL
AAQHSQSGSTTTSSWDMGSTTQSPSLVQYDLKNPSDSAVHSPFTKRQAFTPSSTMMEVFLQEKSPAVATSTAAPP
PPSSPLPSKSTSAPQMSPGSSDNQSSSPQPAQQKLKQQKKKASLTSKIPALAVEMPGSADISGLNLQFGALQFGS
EPVLSDYESTPTTSASSSQAPSSLYTSTASESSSTISSNQSQESGYQSGPIQSTTYTSQNNAQGPLYEQRSTQTR
RYPSSISSSPQKDLTQAKNGFSSVQATQLQTTQSVEGATGSAVKSDSPSTSSIPPLNETVSAASLLTTTNQHSSS
LGGLSHSEEIPNTTTTQHSSTLSTQQNTLSSSTSSGRTSTSTLLHTSVESEANLHSSSSTFSTTSSTVSAPPPVV
SVSSSLNSGSSLGLSLGSNSTVTASTRSSVATTSGKAPPNLPPGVPPLLPNPYIMAPGLLHAYPPQVYGYDDLQM
LQTRFPLDYYSIPFPTPTTPLTGRDGSLASNPYSGDLTKFGRGDASSPAPATTLAQPQQNQTQTHHTTQQTFLNP
ALPPGYSYTSLPYYTGVPGLPSTFQYGPAVFPVAPTSSKQHGVNVSVNASATPFQQPSGYGSHGYNTGRKYPPPY
KHFWTAES

FIGURE 448

CCTACAGAGGGGTCCATACCGTGTTGTTCTGGATTCCCGTTGTAACTTAAAGGGAAATTTTCACA**ATG**TCCAGAG
CCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTAGGTGGCACTA
ATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTACATCATAAATCTGAAGAGGA
CCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCCATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCT
CCAGGAATACTGGCCAGAGGGCCATGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCACTTCA
CTCCTGGAACCTTCACTAACCGGATCCAGGCAGCCTTCCGGGAGCCACAGCTTCCTGTGGTTACTGACCCCAGGG
CTGACCACCAGCCTCTCACGGAGGTATCTTATGTTAACTTACCTACCATTGCGCTGTGTAACACAGATTCTCCTC
TGCGCTATGTGGACATTGCCATCCCATGCAACAATAAGGGAGCTCACTCAGTGGGTTGGATGTGGTGGATGCTGG
CTCAGGAAGTTCTGCGCATGCGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCTGATCTCTGCTTCT
ACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAAGAGGCAGTGACCAAGGAGGAATTTCAGG
GTGAATGGACTGCTCCAGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAGACTGGTCTGAAGGTCTGCAGG
TGCCCTCTGTGTCTATTCAGTAGTTCCCTACTGAAGACTGGAGCGCTCAGCCTGCCACGGAAGACTGGTCTGCAG
CTCCCACTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGAATGGTCT**TAA**GCTGTTCTTGCATGGGCTCTTA
AGCAACATGGAAAAATGGTTGATGGAAAATAAATAAACATCAGTTTCT

FIGURE 449

MSRALDVLQMKEEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAARAIVAIENPADVS
VISSRNTGQRAMLKFAAATGATPIAGHFTPGTFTNRIQAAFREPQLPVVTDPRADHQPLTEVSYVNLPTIALCNT
DSPLRYVDIAIPCNNKGAHSVGWMWWMLAQEVLRMRGTISREHPWEVMPDLCFYRDPEEIEKEEQAAAEEAVTKE
EFQGEWTAPAPEFTATQPEVADWSEGLQVPSVSIQSSLLKTGALSLPRKTGLQLPLLRPLNGVGATTEWS

FIGURE 450A

CGAAATTGAACCGGAGCCATCTTGGGCCCGGCGCGCAGACCCGCGGAGTTTCCCGTGCCGACGCCCCGGGGCCAC
TTCCAGTGCGGAGTAGCGGAGGCGTGGGGGCCTCGAGGGGCTGGCGCGGCCCAGCGGTCGGGCCAGGGTCGTGCC
GCCGGCGGGTCGGGCCGGGCAATGCCTCGCGGGCGCAATGAATCCGCGGCAGGGGTATTCCCTCAGCGGATACTA
CACCCATCCATTTCAAGGCTATGAGCACAGACAGCTCAGGTACCAGCAGCCTGGGCCAGGATCTTCCCCCAGTAG
TTTCCTGCTTAAGCAAATAGAATTTCTCAAGGGGCAGCTCCCAGAAGCACCGGTGATTGGAAAGCAGACACCGTC
ACTGCCACCTTCCCTCCCAGGACTCCGGCCAAGGTTTCCAGTACTACTTGCCTCCAGTACCAGAGGCAGGCAAGT
GGACATCAGGGGTGTCCCCAGGGGCGTGCATCTCAGAAGTCAGGGGCTCCAGAGAGGGTTCCAGCATCCTTCACC
ACGTGGCAGGAGTCTGCCACAGAGAGGTGTTGATTGCCTTTCCTCACATTTCCAGGAACTGAGTATCTACCAAGA
TCAGGAACAAAGGATCTTAAAGTTCCTGGAAGAGCTTGGGGAAGGGAAGGCCACCACAGCACATGATCTGTCTGG
GAAACTTGGGACTCCGAAGAAAGAAATCAATCGAGTTTTATACTCCCTGGCAAAGAAGGGCAAGCTACAGAAAGA
GGCAGGAACACCCCCTTTGTGGAAAATCGCGGTCTCCACTCAGGCTTGGAACCAGCACAGCGGAGTGGTAAGACC
AGACGGTCATAGCCAAGGAGCCCCAAACTCAGACCCGAGTTTGGAACCGGAAGACAGAAACTCCACATCTGTCTC
AGAAGATCTTCTTGAGCCTTTTATTGCAGTCTCAGCTCAGGCTTGGAACCAGCACAGCGGAGTGGTAAGACCAGA
CAGTCATAGCCAAGGATCCCCAAACTCAGACCCAGGTTTGGAACCTGAAGACAGCAACTCCACATCTGCCTTGGA
AGATCCTCTTGAGTTTTTAGACATGGCCGAGATCAAGGAGAAAATCTGCGACTATCTCTTCAATGTGTCTGACTC
CTCTGCCCTGAATTTGGCTAAAAATATTGGCCTTACCAAGGCCCGAGATATAAATGCTGTGCTAATTGACATGGA
AAGGCAGGGGGATGTCTATAGACAAGGGACAACCCCTCCCATATGGCATTTGACAGACAAGAAGCGAGAGAGGAT
GCAAATCAAGAGAAATACGAACAGTGTTCCTGAAACCGCTCCAGCTGCAATCCCTGAGACCAAAAGAAACGCAGA
GTTCCTCACCTGTAATATACCCACATCAAATGCCTCAAATAACATGGTAACCACAGAAAAAGTGGAGAATGGGCA
GGAACCTGTCATAAAGTTAGAAAACAGGCAAGAGGCCAGACCAGAACCAGCAAGACTGAAACCACCTGTTCATTA
CAATGGCCCCTCAAAAGCAGGGTATGTTGACTTTGAAAATGGCCAGTGGGCCACAGATGACATCCCAGATGACTT
GAATAGTATCCGCGCAGCACCAGGTGAGTTTCGAGCCATCATGGAGATGCCCTCCTTCTACAGTCATGGCTTGCC
ACGGTGTTCACCCTACAAGAAACTGACAGAGTGCCAGCTGAAGAACCCCATCAGCGGGCTGTTAGAATATGCCCA
GTTCGCTAGTCAAACCTGTGAGTTCAACATGATAGAGCAGAGTGGACCACCCCATGAACCTCGATTTAAATTCCA
GGTTGTCATCAATGGCCGAGAGTTTCCCCCAGCTGAAGCTGGAAGCAAGAAAGTGGCCAAGCAGGATGCAGCTAT
GAAAGCCATGACAATTCTGCTAGAGGAAGCCAAAGCCAAGGACAGTGGAAAATCAGAAGAATCATCCCACTATTC
CACAGAGAAAGAATCAGAGAAGACTGCAGAGTCCCAGACCCCCACCCCTTCAGCCACATCCTTCTTTTCTGGGAA
GAGCCCCGTCACCACACTGCTTGAGTGTATGCACAAATTGGGGAACTCCTGCGAATTCCGTCTCCTGTCCAAAGA
AGGCCCTGCCCATGAACCCAAGTTCCAATACTGTGTTGCAGTGGGAGCCCAAACTTTCCCCAGTGTGAGTGCTCC
CAGCAAGAAAGTGGCAAAGCAGATGGCCGCAGAGGAAGCCATGAAGGCCCTGCATGGGGAGGCGACCAACTCCAT
GGCTTCTGATAACCAGCCTGAAGGTATGATCTCAGAGTCACTTGATAACTTGGAATCCATGATGCCCAACAAGGT
CAGGAAGATTGGCGAGCTCGTGAGATACCTGAACACCAACCCTGTGGGTGGCCTTTTGGAGTACGCCCGCTCCCA
TGGCTTTGCTGCTGAATTCAAGTTGGTCGACCAGTCCGGACCTCCTCACGAGCCCAAGTTCGTTTACCAAGCAAA
AGTTGGGGGTCGCTGGTTCCCAGCCGTCTGCGCACACAGCAAGAAGCAAGGCAAGCAGGAAGCAGCAGATGCGGC
TCTCCGTGTCTTGATTGGGGAGAACGAGAAGGCAGAACGCATGGGTTTCACAGAGGTAACCCCAGTGACAGGGGC
CAGTCTCAGAAGAACTATGCTCCTCCTCTCAAGGTCCCCAGAAGCACAGCCAAAGACACTCCCTCTCACTGGCAG
CACCTTCCATGACCAGATAGCCATGCTGAGCCACCGGTGCTTCAACACTCTGACTAACAGCTTCCAGCCCTCCTT
GCTCGGCCGCAAGATTCTGGCCGCCATCATTATGAAAAAAGACTCTGAGGACATGGGTGTCGTCGTCAGCTTGGG
AACAGGGAATCGCTGTGTGAAAGGAGATTCTCTCAGCCTAAAAGGAGAAACTGTCAATGACTGCCATGCAGAAAT
AATCTCCCGGAGAGGCTTCATCAGGTTTCTCTACAGTGAGTTAATGAAATACAACTCCCAGACTGCGAAGGATAG
TATATTTGAACCTGCTAAGGGAGGAGAAAAGCTCCAAATAAAAAAGACTGTGTCATTCCATCTGTATATCAGCAC
TGCTCCGTGTGGAGATGGCGCCCTCTTTGACAAGTCCTGCAGCGACCGTGCTATGGAAAGCACAGAATCCCGCCA
CTACCCTGTCTTCGAGAATCCCAAACAAGGAAAGCTCCGCACCAAGGTGGAGAACGGAGAAGGCACAATCCCTGT
GGAATCCAGTGACATTGTGCCTACGTGGGATGGCATTCGGCTCGGGGAGAGACTCCGTACCATGTCCTGTAGTGA
CAAAATCCTACGCTGGAACGTGCTGGGCCTGCAAGGGGCACTGTTGACCCACTTCCTGCAGCCCATTTATCTCAA
ATCTGTCACATTGGGTTACCTTTTCAGCCAAGGGCATCTGACCCGTGCTATTTGCTGTCGTGTGACAAGAGATGG
GAGTGCATTTGAGGATGGACTACGACATCCCTTTATTGTCAACCACCCCAAGGTTGGCAGAGTCAGCATATATGA
TTCCAAAAGGCAATCCGGGAAGACTAAGGAGACAAGCGTCAACTGGTGTCTGGCTGATGGCTATGACCTGGAGAT

FIGURE 450B

CCTGGACGGTACCAGAGGCACTGTGGATGGGCCACGGAATGAATTGTCCCGGGTCTCCAAAAAGAACATTTTTCT
TCTATTTAAGAAGCTCTGCTCCTTCCGTTACCGCAGGGATCTACTGAGACTCTCCTATGGTGAGGCCAAGAAAGC
TGCCCGTGACTACGAGACGGCCAAGAACTACTTCAAAAAAGGCCTGAAGGATATGGGCTATGGGAACTGGATTAG
CAAACCCCAGGAGGAAAAGAACTTTTATCTCTGCCCAGTATAGTATGCTCCAGTGACAGATGGATTAGGGTGTGT
CATACTAGGGTGTGAGAGAGGTAGGTCGTAGCATTCCTCATCACATGGTCAGGGGATTTTTTTTCTCCTTTTTT
TTTCTTTTTAAGCCATAATTGGTGATACTGAAAACTTTGGGTTCCCATTTATCCTGCTTTCTTTGGGATTGCTAG
GCAAGGTCTGGCCAGGCCCCCCTTTTTTCCCCCAAGTGAAGAGGCAGAAACCTAAGAAGTTATCTTTTCTTTCTA
CCCAAAGCATACATAGTCACTGAGCACCTGCGGTCCATTTCCTCTTAAAAGTTTTGTTTTGATTTGTTTCCATTT
CCTTTCCCTTTGTGTTTGCTACACTGACCTCTTGCGGTCTTGATTAGGTTTCAGTCAACTCTGGATCATGTCAGG
GACTGATAATTTCATTTGTGGATTACGCAGACCCCTCTACTTCCCCTCTTTCCCTTCTGAGATTCTTTCCTTGTG
ATCTGAATGTCTCCTTTTCCCCCTCAGAGGGCAAAGAGGTGAACATAAAGGATTTGGTGAAACATTTGTAAGGGT
AGGAGTTGAAAACTGCAGTTCCCAGTGCCACGGAAGTGTGATTGGAGCCTGCAGATAATGCCCAGCCATCCTCCC
ATCCTGCACTTTAGCCAGCTGCAGGGCGGGCAAGGCAAGGAAAGCTGCTTCCCTGGAAGTGTATCACTTTCTCCG
GCAGCTGGGAAGTCTAGAACCAGCCAGACTGGGTTAAGGGAGCTGCTCAAGCAATAGCAGAGGTTTCACCCGGCA
GGATGACACAGACCACTTCCCAGGGAGCACGGGCATGCCTTGGAATATTGCCAAGCTTCCAGCTGCCTCTTCTCC
TAAAGCATTCCTAGGAATATTTTCCCCGCCAATGCTGGGCGTACACCCTAGCCAACGGGACAAATCCTAGAGGGT
ATAAAATCATCTCTGCTCAGATAATCATGACTTAGCAAGAATAAGGGCAAAAAATCCTGTTGGCTTAACGTCACT
GTTCCACCCGGTGTAATATCTCTCATGACAGTGACACCAAGGGAAGTTGACTAAGTCACATGTAAATTAGGAGTG
TTTTAAAGAATGCCATAGATGTTGATTCTTAACTGCTACAGATAACCTGTAATTGAGCAGATTTAAAATTCAGGC
ATACTTTTCCATTTATCCAAGTGCTTTCATTTTTCCAGATGGCTTCAGAAGTAGGCTCGTGGGCAGGGCGCAGAC
CTGATCTTTATAGGGTTGACATAGAAAGCAGTAGTTGTGGGTGAAAGGGCAGGTTGTCTTCAAACTCTGTGAGGT
AGAATCCTTTGTCTATACCTCCATGAACATTGACTCGTGTGTTCAGAGCCTTTGGCCTCTCTGTGGAGTCTGGCT
CTCTGGCTCCTGTGCATTCTTTGAATAGTCACTCGTAAAAACTGTCAGTGCTTGAAACTGTTTCCTTTACTCATG
TTGAAGGGACTTTGTTGGCTTTTAGAGTGTTGGTCATGACTCCAAGAGCAGAGCAGGGAAGAGCCCAAGCATAGA
CTTGGTGCCGTGGTGATGGCTGCAGTCCAGTTTTGTGATGCTGCTTTTACGTGTCCCTCGATAACAGTCAGCTAG
ACACACTCAGGAGGACTACTGAGGCTCTGCGACCTTCAGGAGCTGAGCCTGCCTCTCTCCTTTAGATGACAGACC
TTCATCTGGGAACGTGCTGAGCCAGCACCCTCAGATGATTTCCCTCCAAACTGCTGACTAGGTCATCCTCTGTCT
GGTAGAGACATTCACATCTTTGCTTTTATTCTATGCTCTCTGTACTTTTGACCAAAAATTGACCAAAGTAAGAAA
ATGCAAGTTCTAAAAATAGACTAAGGATGCCTTTGCAGAACACCAAAGCATCCCAAGGAACTGGTAGGGAAGTGG
CGCCTGTCTCCTGGAGTGGAAGAGGCCTGCTCCCTGGCTCTGGGTCTGCTGGGGGCACAGTAAATCAGTCTTGGC
ACCCACATCCAGGGCAGAGAGGTCTGTGGTTCTCAGCATCAGAAGGCAGCGCAGCCCCTCTCCTCTTCAGGCTAC
AGGGTTGTCACCTGCTGAGTCCTCAGGTTGTTTGGCCTCTCTGGTCCATCTTGGGCATTAGGTTCTCCAGCAGAG
CTCTGGCCAGCTGCCTCTTCTTTAACTGGGAACACAGGCTCTCACAAGATCAGAACCCCCACTCACCCCCAAGAT
CTTATCTAGCAAGCCTGTAGTATTCAGTTTCTGTTGTAGGAAGAGAGCGAGGCATCCCTGAATTCCACGCATCTG
CTGGAAACGAGCCGTGTCAGATCGCACATCCCTGCGCCCCCATGCCCCTCTGAGTCACACAGGACAGAGGAGGCA
GAGCTTCTGCCCACTGTTATCTTCACTTTCTTTGTCCAGTCTTTTGTTTTTAATAAGCAGTGACCCTCCCTACTC
TTCTTTTTAATGATTTTTGTAGTTGATTTGTCTGAACTGTGGCTACTGTGCATTCCTTGAATAATCACTTGTAAA
AATTGTCAGTGCTTGAAGCTGTTTCCTTTACTCACATTGAAGGGACTTCGTTGGTTTTTTGGAGTCTTGGTTGTG
ACTCCAAGAGCAGAGTGAGGAAGACCCCCAAGCATAGACTCGGGTACTGTGATGATGGCTGCAGTCCAGTTTTAT
GATTCTGCTTTTATGTGTCCCTTGATAACAGTGACTTAACAATATACATTCCTCATAAATAAAAAAAAAACAAGA
ATCTGAATTCTT

FIGURE 451

GAGCCAGCGAGGAGTGAAGCTGAGCCTGGCCTCACACGCTCCTAGAGGACCACCTCCTGAGAGAGTTCTTTCACC
CCCTCTTCTTTCTCCAAGCTCCCCTCCTGCTCTCCCTCCCTGCCCAATACAATGCATTCTTGAGTGGCAGCGTCT
GGACTCCAGGCAGCCCCAGAGAACCGAAGCAAGCCAAAGAGAGGACTGGAGCCAAGATACTGGTGGGGGAGATTG
GATGCCTGGCTTTCTTTGAGGACATCTTTGGAGCGAGGGTGGCTTTGGGGTGGGGGCTTGTGCTGCAGGGAATAC
AGCCAGGCCCCAAGATGGACACTTCTGGGCACTTCCATGACTCGGGGGTGGGGGACTTGGATGAAGACCCCAAGT
GCCCCTGTCCATCCTCTGGGGATGAGCAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCCACCACCGCCAG
CGCCACCAGCAGCCCCCCAGCAGCCCCTGGGACCCTCGCTGCAGCCTCAGCCTCCGCAGCTTCAGCAGCAGCAGC
AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCACCGCATCCCCTGTCTCAGCTCGCCCAACTCCAGAGCCAGCCCG
TCCACCCTGGCCTGCTGCACTCCTCTCCCACCGCTTTCAGGGCCCCCCCTTCGTCCAACTCCACCGCCATCCTCC
ACCCTTCCTCCAGGCAAGGCAGCCAGCTCAATCTCAATGACCACTTGCTTGGCCACTCTCCAAGTTCCACAGCTA
CAAGTGGGCCTGGCGGAGGCAGCCGGCACCGACAGGCCAGCCCCCTGGTGCACCGGCGGGACAGCAACCCCTTCA
CGGAGATCGCCATGAGCTCCTGCAAGTATAGCGGTGGGGTCATGAAGCCCCTCAGCCGCCTCAGCGCCTCCCGGA
GGAACCTCATCGAGGCCGAGACTGAGGGCCAACCCCTCCAGCTTTTCAGCCCTAGCAACCCCCCGGAGATCGTCA
TCTCCTCCCGGGAGGACAACCATGCCCACCAGACCCTGCTCCATCACCCTAATGCCACCCACAACCACCAGCATG
CCGGCACCACCGCCAGCAGCACCACCTTCCCCAAAGCCAACAAGCGGAAAAACCAAAACATTGGCTATAAGCTGG
GACACAGGAGGGCCCTGTTTGAAAAGAGAAAGCGACTGAGTGACTATGCTCTGATTTTTGGGATGTTTGGAATTG
TTGTTATGGTGATAGAGACCGAGCTCTCTTGGGGTTTGTACTCAAAGGACTCCATGTTTTCGTTGGCCCTGAAAT
GCCTTATCAGTCTGTCCACCATCATCCTTTTGGGCTTGATCATCGCCTACCACACACGTGAAGTCCAGCTCTTCG
TGATCGACAATGGCGCGGATGACTGGCGGATAGCCATGACCTACGAGCGCATCCTGTACATCAGCCTGGAGATGC
TGGTGTGCGCCATCCACCCCATTCCTGGCGAGTACAAGTTCTTCTGGACGGCACGCCTGGCCTTCTCCTACACAC
CCTCCCGGGCGGAGGCCGATGTGGACATCATCCTGTCTATCCCCATGTTCCTGCGCCTGTACCTGATCGCCCGAG
TCATGCTGCTGCACAGCAAGCTCTTCACCGATGCCTCGTCCCGCAGCATCGGGGCCCTCAACAAGATCAACTTCA
ACACCCGCTTTGTCATGAAGACGCTCATGACCATCTGCCCTGGCACTGTGCTGCTCGTGTTCAGCATCTCTCTGT
GGATCATTGCTGCCTGGACCGTCCGTGTCTGTGAAAGGTACCATGACCAGCAGGACGTAACTAGTAACTTTCTGG
GTGCCATGTGGCTCATCTCCATCACATTCCTTTCCATTGGTTATGGGGACATGGTGCCCCACACATACTGTGGGA
AAGGTGTCTGTCTCCTCACTGGCATCATGGGTGCAGGCTGCACTGCCCTTGTGGTGGCCGTGGTGGCCCGAAAGC
TGGAACTCACCAAAGCGGAGAAGCACGTTCATAACTTCATGATGGACACTCAGCTCACCAAGCGGATCAAGAATG
CTGCAGCCAATGTCCTTCGGGAAACATGGTTAATCTATAAACACACAAAGCTGCTAAAGAAGATTGACCATGCCA
AAGTGAGGAAACACCAGAGGAAGTTCCTCCAAGCTATCCACCAGTTGAGGAGCGTCAAGATGGAACAGAGGAAGC
TGAGTGACCAAGCCAACACTCTGGTGGACCTTTCCAAGATGCAGAATGTCATGTATGACTTAATCACAGAACTCA
ATGACCGGAGCGAAGACCTGGAGAAGCAGATTGGCAGCCTGGAGTCGAAGCTGGAGCATCTCACCGCCAGCTTCA
ACTCCCTGCCGCTGCTCATCGCCGACACCCTGCGCCAGCAGCAGCAGCAGCTCCTGTCTGCCATCATCGAGGCCC
GGGGTGTCAGCGTGGCAGTGGGCACCACCCACACCCCAATCTCCGATAGCCCCATTGGGGTCAGCTCCACCTCCT
TCCCGACCCCGTACACAAGTTCAAGCAGTTGCTAAATAAATCTCCCCACTCCAGAAGCATTACCCATAGGTCTTA
AGATGCAAATCAACTCTCTCCTGGTCGCTTTGCCATCAAGAAACATTCAGACCAGGGAACGGAAAGAAGAGAGAC
CGAGCTAATTAACTAACTCATGTTCATTCAGCGTGCTTGGTCCGACATGCCTTGAAACCAGAAATCTAATCTCTG
TTTAGGTGCCTCTACTTGGGAGCGGGAAGAGGAGATGACAGGAAGCGACGCCTCTGGCAGGGCCCTTGCTGCAGA
GTTGGTGGAGAACAGAAATCCACGCTCAATCTCAGGTCTTCACGCGGGGGGTGGGGGTCAGATGCACTGAAGTAG
CCAACAGCGAAGCCAGTCCAGAAGAGGGGTCCGCTGGGAGGGAGGGTTGTGTCAGGCTTGGGGGATGGGCTCTTC
GCCATGGGGGTCTTTGAACACACCTCTCTCCTTTCCTTTTGTCTACGGAAGCCTCTGGGTGACAAAAGTAAAAGA
GAGCTGCCCACAACTTGCCAAAACAGATATACTCGAATCAGACTGAAAAAAAAA

FIGURE 452

GAAGGTTCTGGGCGGGGCTGGACTGTTCTAAGTGAGTTCGGGTGGGGGAGCTTCACGAGGGGAGGCTGCTCTGTG
AAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCTCCCCATATCTGTTTGGACATGAGCTGAGGGCACGGT
CGCGGGCGGTCAGCCCTGTTCGCAGCTACGGCGAGGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGG
CCGCGTCCATTCCGCGCGGTGTCCCGATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGC
GGCCCC**ATG**GCCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAGGAC
TTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAG
GAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGG
AAGGACATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGC
ATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTATGGG
GCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGG
GTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTT
GAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTT**TAG**TCACTAGGTTCTAGG
AGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCGAGG
TGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGAC
CTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTG
TGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGA
TGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACAC
TCTCAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCTCGGG

FIGURE 453

MAPLGGAPRLVLLFSGKRKSGKDFVTEALQSRLGADVCAVLRLSGPLKEQYAQEHGLNFQRLLDTSTYKEAFRKD
MIRWGEEKRQADPGFFCRKIVEGISQPIWLVSDTRRVSDIQWFREAYGAVTQTVRVVALEQSRQQRGWVFTPGVD
DAESECGLDNFGDFDWVIENHGVEQRLEEQLENLIEFIRSRL

FIGURE 454

ATGGGGCCTGAAACTGTCTGGGTCTGAGCTGGGGAGCGGAAGCCACTTGTCCCTCTCCCTCCCCAGGACTTCTGT
GACTCCTGGGCCACAGAGGTCCAACCAGGCTAAGGGCCTGGGGATACCCCCTGCCTGGCCCCCTTGCCCAAACTG
GCAGGGGGGCCAGGCTGGGCAGCAGCCCCTCTTTCACCTCAACTATGGATCTCCTGCCCCCCAAGCCCAAGTACA
ATCCACTCCGGAATGAGTCTCTGTCATCGCTGGAGGAAGGGGCTTCTGGGTCCACCCCCCCGGAGGAGCTGCCTT
CCCCATCAGCTTCATCCCTGGGGCCCATCCTGCCTCCTCTGCCTGGGGACGATAGTCCCACTACCCTGTGCTCCT
TCTTCCCCCGGATGAGCAACCTGAGGCTGGCCAACCCGGCTGGGGGGCGCCCAGGGTCTAAGGGGGAGCCAGGAA
GGGCAGCTGATGATGGGGAGGGGATCGTAGGGGCAGCCATGCCAGACTCAGGCCCCCTACCCCTCCTCCAGGACA
TGAACAAGCTGAGTGGAGGCGGCGGGCGCAGGACTCGGGTGGAAGGGGGCCAGCTTGGGGGCGAGGAGTGGACCC
GCCACGGGAGCTTTGTCAATAAGCCCACGCGGGGCTGGCTGCATCCCAACGACAAAGTCATGGGACCCGGGGTTT
CCTACTTGGTTCGGTACATGGGTTGTGTGGAGGTCCTCCAGTCAATGCGTGCCCTGGACTTCAACACCCGGACTC
AGGTCACCAGGGAGGCCATCAGTCTGGTGTGTGAGGCTGTGCCGGGTGCTAAGGGGGCGACAAGGAGGAGAAAGC
CCTGTAGCCGCCCGCTCAGCTCTATCCTGGGGAGGAGTAACCTGAAATTTGCTGGAATGCCAATCACTCTCACCG
TCTCCACCAGCAGCCTCAACCTCATGGCCGCAGACTGCAAACAGATCATCGCCAACCACCACATGCAATCTATCT
CATTTGCATCCGGCGGGGATCCGGACACAGCCGAGTATGTCGCCTATGTTGCCAAAGACCCTGTGAATCAGAGAG
CCTGCCACATTCTGGAGTGTCCCGAAGGGCTTGCCCAGGATGTCATCAGCACCATTGGCCAGGCCTTCGAGTTGC
GCTTCAAACAATACCTCAGGAACCCACCCAAACTGGTCACCCCTCATGACAGGATGGCTGGCTTTGATGGCTCAG
CATGGGATGAGGAGGAGGAAGAGCCACCTGACCATCAGTACTATAATGACTTCCCGGGGAAGGAACCCCCCTTGG
GGGGGGTGGTAGACATGAGGCTTCGGGAAGGAGCCGCTCCAGGGGCTGCTCGACCCACTGCACCCAATGCCCAGA
CCCCCAGCCACTTGGGAGCTACATTGCCTGTAGGACAGCCTGTTGGGGGAGATCCAGAAGTCCGCAAACAGATGC
CACCTCCACCACCCTGTCCAGGCAGAGAGCTTTTTGATGATCCCTCCTATGTCAACGTCCAGAACCTAGACAAGG
CCCGGCAAGCAGTGGGTGGTGCTGGGCCCCCCAATCCTGCTATCAATGGCAGTGCACCCCGGGACCTGTTTGACA
TGAAGCCCTTCGAAGATGCTCTTCGCGTGCCTCCACCTCCCCAGTCGGTGTCCATGGCTGAGCAGCTCCGAGGGG
AGCCCTGGTTCCATGGGAAGCTGAGCCGGCGGGAGGCTGAGGCACTGCTGCAGCTCAATGGGGACTTCCTGGTAC
GGGAGAGCACGACCACACCTGGCCAGTATGTGCTCACTGGCTTGCAGAGTGGGCAGCCTAAGCATTTGCTACTGG
TGGACCCTGAGGGTGTGGTTCGGACTAAGGATCACCGCTTTGAAAGTGTCAGTCACCTTATCAGCTACCACATGG
ACAATCACTTGCCCATCATCTCTGCGGGCAGCGAACTGTGTCTACAGCAACCTGTGGAGCGGAAACTGTGATCTG
CCCTAGCGCTCTCTTCCAGAAGATGCCCTCCAATCCTTTCCACCCTATTCCCTAACTCTCGGGACCTCGTTTGGG
AGTGTTCTGTGGGCTTGGCCTTGTGTCAGAGCTGGGAGTAGCATGGACTCTGGGTTTCATATCCAGCTGAGTGAG
AGGGTTTGAGTCAAAAGCCTGGGTGAGAATCCTGCCTCTCCCCAAACATTAATCACCAAAGTATTAATGTACAGA
GTGGCCCCTCACCTGGGCCTTTCCTGTGCCAACCTGATGCCCCTTCCCCAAGAAGGTGAGTGCTTGTCATGGAAA
ATGTCCTGTGGTGACAGGCCCAGTGGAACAGTCACCCTTCTGGGCAAGGGGGAACAAATCACACCTCTGGGCTTC
AGGGTATCCCAGACCCCTCTCAACACCCGCCCCCCCCATGTTTAAACTTTGTGCCTTTGACCATCTCTTAGGTCT
AATGATATTTTATGCAAACAGTTCTTGGACCCCTGAATTCAATGACAGGGATGCCAACACCTTCTTGGCTTCTGG
GACCTGTGTTCTTGCTGAGCACCCCTCTCCGGTTTGGGTTGGGATAACAGAGGCAGGAGTGGCAGCTGTCCCCTCT
CCCTGGGGATATGCAACCCTTAGAGATTGCCCCAGAGCCCCACTCCCGGCCAGGCGGGAGATGGACCCCTCCCTT
GCTCAGTGCCTCCTGGCCGGGGCCCCTCACCCCAAGGGGTCTGTATATACATTTCATAAGGCCTGCCCTCCCATG
TTGCATGCCTATGTACTCTACGCCAAAGTGCAGCCCTTCCTCCTGAAGCCTCTGCCCTGCCTCCCTTTCTGGGAG
GGCGGGGTGGGGGTGACTGAATTTGGGCCTCTTGTACAGTTAACTCTCCCAGGTGGATTTTGTGGAGGTGAGAAA
AGGGGCATTGAGACTATAAAGCAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAACTGCATTCTTTTAAAG
TTTTATATGCATATATTTTAGGGCTGTAGACTTACTTTCCTATTTTCTTTTCCATTGCTTATTCTTGAGCACAAA
ATGATAATCAATTATTACATTTATACATCACCTTTTTGACTTTTCCAAGCCCTTTTACAGCTCTTGGCATTTTCC
TCGCCTAGGCCTGTGAGGTAACTGGGATCGCACCTTTTATACCAGAGACCTGAGGCAGATGAAATTTATTTCCAT
CTAGGACTAGAAAAACTTGGGTCTCTTACCGCGAGACTGAGAGGCAGAAGTCAGCCCGAATGCCTGTCAGTTTCA
TGGAGGGGAAACGCAAAACCTGCAGTTCCTGAGTACCTTCTACAGGCCCGGCCCAGCCTAGGCCCGGGGTGGCCA
CACCACAGCAAGCCGGCCCCCCCTCTTTTGGCCTTGTGGATAAGGGAGAGTTGACCGTTTTCATCCTGGCCTCCT
TTTGCTGTTTGGATGTTTCCACGGGTCTCACTTATACCAAAGGGAAAACTCTTCATTAAAGTCCGTATTTCTTCT

FIGURE 455

GAAAGAGCCGGTGAAGGGGCAGAACAGGCAGGTTCCCTCGACCCAGGACCCCCTGTTCCCAGGCTATGGCCCCCA
GTGCCCTGTAGACCTGGCAGGCCCCCCGTGCTTGCGACCCCTATTTGGGGGTCTGGGTGGCTACTGGAGGGCCTT
GCAGAGGGGCAGAGAAGGCAGGACCATGACATCTAGGGCCTCTGAACTTTCTCCGGGGCGCAGCGTGACGGCTGG
CATCATCATTGTTGGAGATGAGATCCTTAAGTTGGAAACAACAAATGGCTTTTGAGTCCAAGAGTGATGCAATCA
CAGTGACGCATTAAAACGGTTACTCCGGAGACATCAGAGCACTGTGGCTGGAGGCTGGGAGCCTGGCCAGGAAGC
TGTCGCCATTGTCCAGGTGAAAGGTGCTAAGGACCTGCTTGGTGGCAGTGGGGACAGAAAGAAGAAAGCAGGCCA
GGCGTGGTGGCTCACACCTATAATTCCAGCACTTTGGGAGGCTGAGGCAGGAGGATCACTTGAGACCAGGAATTC
AACACCAGCCTGGGCAACATGGCAAGACCCCATTTCTACAAAAAAAATTTAAAATGAGCTGAATGTGGTGGCACG
CGCCTGTAGTCCCAGCTACTCGGAAGGCTGGGGTGGCCCTTGAAGCCAGGAGGTTGAGGCTGCAGTGAACTGTGA
CTGAGCCACTATACTCCAGCCTGGGTGACAGAGACCCAGCTTTAAAACCAAACAAATGGATTTTCCCACTCTTGT
GTCCAGTCCAGGCCCCTCAGCAGCCTGAGGTGGTGTCCTTCAAAGAGCAGAGCACTGCATCATCAGGTGG**ATG**CA
GCCATCATCTTCAACCCCTCCCCTTCATCCCTACAGTACTGATGGCCTCATCTTCCCCTTCAACCCCCAGGGACA
CACTCAGGACACCAACACCTTCTTTCTGTGCCGGACACTGCGCTCCCTAGGGGTCCAGGTTTGCCGAGTCTCAGT
TGTACCTGATGAGGTAGCCACCATTGCAGCTGAGGTCACTTCTTTCTCCAACCGCTTCACCCATGTCCTCACAGC
AGGGGGCATCGGCCCCACTCATGATGATGTGACCTTTGAGGCAGTGGCACAGGCCTTTGGAGATGAGCTGAAGCC
ACACCCCAAGTTGGAAGCAGCCACCAAAGCCCTAGGAGGGGAAGGCTGGGAGAAGCTATCATTGGTGCCCTCCTC
TGCCCGCCTGCATTATGGCACAGATCCTTGCACTGGTCAACCTTTCAGATTCCCTCTGGTCTCCGTCCGAAACGT
CTACCTCTTCCCAGGCATTCCAGAGCTGCTGCGGCGGGTGCTGGAGGGGATGAAGGGACTATTCCAAAACCCAGC
TGTTCAGTTCCACTCAAAGGAGCTATATGTGGCTGCTGATGAAGCCTCCATCGCCCCCATTCTGGCTGAGGCCCA
GGCCCACTTTGGACGTAGGCTTGGCCTGGGTTCCTACCCTGACTGGGGCAGCAACTACTATCAGGTGAAGCTGAC
TCTAGACTCAGAGGAAGAAGGACCCCTGGAGGAATGCTTGGCCTACCTGACTGCCCGTTTGCCCCAGGGATCGCT
GGTCCCCTACATGCCCAACGCTGTGGAGCAGGCCAGTGAGGCTGTATACAAACTCGCTGAATCAGGTAGGGACCT
TATGGAGGAGGGGCATTATGCCCAAAGCCATTGGTGGCACCCCAGATCTCAG**TAA**TGCAGGGGCTGTTGGGTGCT
TCCTGCAAATCCCTGAGAGGGCAGAAGATAGCTTCTGTTAATTCATTATTCTTCCAATAAATGTTGATTGAGTAC
CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 456

MQPSSSTPPLHPYSTDGLIFPFNPQGHTQDTNTFFLCRTLRSLGVQVCRVSVVPDEVATIAAEVTSFSNRFTHVL
TAGGIGPTHDDVTFEAVAQAFGDELKPHPKLEAATKALGGEGWEKLSLVPSSARLHYGTDPCTGQPFRFPLVSVR
NVYLFPGIPELLRRVLEGMKGLFQNPAVQFHSKELYVAADEASIAPILAEAQAHFGRRLGLGSYPDWGSNYYQVK
LTLDSEEEGPLEECLAYLTARLPQGSLVPYMPNAVEQASEAVYKLAESGRDLMEEGHYAQSHWWHPRSQ

FIGURE 457

CGCTGCC**ATG**CGGCTGGCGCTGCTCTGGGCCCTGGGGCTCCTGGGCGCGGGCAGCCCTCTGCCTTCCTGGCCGCT
CCCAAATATAGGTGGCACTGAGGAGCAGCAGGCAGAGTCAGAGAAGGCCCCGAGGGAGCCCTTGGAGCCCCAGGT
CCTTCAGGACGATCTCCCAATTAGCCTCAAAAAGGTGCTTCAGACCAGTCTGCCTGAGCCCCTGAGGATCAAGTT
GGAGCTGGACGGTGACAGTCATATCCTGGAGCTGCTACAGAATAGGGAGTTGGTCCCAGGCCGCCCAACCCTGGT
GTGGTACCAGCCCGATGGCACTCGGGTGGTCAGTGAGGGACACACTTTGGAGAACTGCTGCTACCAGGGAAGAGT
GCGGGGATATGCAGGCTCCTGGGTGTCCATCTGCACCTGCTCTGGGCTCAGAGGCTTGGTGGTCCTGACCCCAGA
GAGAAGCTATACCCTGGAGCAGGGGCCTGGGGACCTTCAGGGTCCTCCCATTATTTCGCGAATCCAAGATCTCCA
CCTGCCAGGCCACACCTGTGCCCTGAGCTGGCGGGAATCTGTACACACTCAGACGCCACCAGAGCACCCCCTGGG
ACAGCGCCACATTCGCCGGAGGCGGGATGTGGTAACAGAGACCAAGACTGTGGAGTTGGTGATTGTGGCTGATCA
CTCGGAGGCCCAGAAATACCGGGACTTCCAGCACCTGCTAAACCGCACACTGGAAGTGGCCCTCTTGCTGGACAC
ATTCTTCCGGCCCCTGAATGTACGAGTGGCACTAGTGGGCCTGGAGGCCTGGACCCAGCGTGACCTGGTGGAGAT
CAGCCCAAACCCAGCTGTCACCCTCGAAAACTTCCTCCACTGGCGCAGGGCACATTTGCTGCCTCGATTGCCCCA
TGACAGTGCCCAGCTGGTGACTGGTACTTCATTCTCTGGGCCTACGGTGGGCATGGCCATTCAGAACTCCATCTG
TTCTCCTGACTTCTCAGGAGGTGTGAACATGGACCACTCCACCAGCATCCTGGGAGTCGCCTCCTCCATAGCCCA
TGAGTTGGGCCACAGCCTGGGCCTGGACCATGATTTGCCTGGGAATAGCTGCCCCTGTCCAGGTCCAGCCCCAGC
CAAGACCTGCATCATGGAGGCCTCCACAGACTTCCTACCAGGCCTGAACTTCAGCAACTGCAGCCGACGGGCCCT
GGAGAAAGCCCTCCTGGATGGAATGGGCAGCTGCCTCTTCGAACGGCTGCCTAGCCTACCCCCTATGGCTGCTTT
CTGCGGAAATATGTTTGTGGAGCCGGGCGAGCAGTGTGACTGTGGCTTCCTGGATGACTGCGTCGATCCCTGCTG
TGATTCTTTGACCTGCCAGCTGAGGCCAGGTGCACAGTGTGCATCTGACGGACCCTGTTGTCAAAATTGCCAGCT
GCGCCCGTCTGGCTGGCAGTGTCGTCCTACCAGAGGGGATTGTGACTTGCCTGAATTCTGCCCAGGAGACAGCTC
CCAGTGTCCCCCTGATGTCAGCCTAGGGGATGGCGAGCCCTGCGCTGGCGGGCAAGCTGTGTGCATGCACGGGCG
TTGTGCCTCCTATGCCCAGCAGTGCCAGTCACTTTGGGGACCTGGAGCCCAGCCCGCTGCGCCACTTTGCCTCCA
GACAGCTAATACTCGGGGAAATGCTTTTGGGAGCTGTGGGCGCAACCCCAGTGGCAGTTATGTGTCCTGCACCCC
TAGAGATGCCATTTGTGGGCAGCTCCAGTGCCAGACAGGTAGGACCCAGCCTCTGCTGGGCTCCATCCGGGATCT
ACTCTGGGAGACAATAGATGTGAATGGGACTGAGCTGAACTGCAGCTGGGTGCACCTGGACCTGGGCAGTGATGT
GGCCCAGCCCCTCCTGACTCTGCCTGGCACAGCCTGTGGCCCTGGCCTGGTGTGTATAGACCATCGATGCCAGCG
TGTGGATCTCCTGGGGGCACAGGAATGTCGAAGCAAATGCCATGGACATGGGGTCTGTGACAGCAACAGGCACTG
CTACTGTGAGGAGGGCTGGGCACCCCCTGACTGCACCACTCAGCTCAAAGCAACCAGCTCCCTGACCACAGGGCT
GCTCCTCAGCCTCCTGGTCTTATTGGTCCTGGTGATGCTTGGTGCCGGCTACTGGTACCGTGCCCGCCTGCACCA
GCGACTCTGCCAGCTCAAGGGACCCACCTGCCAGTACAGGGCAGCCCAATCTGGTCCCTCTGAACGGCCAGGACC
TCCGCAGAGGGCCCTGCTGGCACGAGGCACTAAGTCTCAGGGGCCAGCCAAGCCCCCACCCCCAAGGAAGCCACT
GCCTGCCGACCCCCAGGGCCGGTGCCCATCGGGTGACCTGCCCGGCCCAGGGGCTGGAATCCCGCCCCTAGTGGT
ACCCTCCAGACCAGCGCCACCGCCTCCGACAGTGTCCTCGCTCTACCTC**TGA**CCTCTCCGGAGGTTCCGCTGCCT
CCAAGCCGGACTTAGGGCTTCAAGAGGCGGGCGTGCCCTCTGGAGTCCCCTACCATGACTGAAGGCGCCAGAGAC
TGGCGGTGTCTTAAGACTCCGGGCACCGCCACGCGCTGTCAAGCAACACTCTGCGGACCTGCCGGCGTAGTTGCA
GCGGGGGCTTGGGGAGGGGCTGGGGGTTGGACGGGATTGAGGAAGGTCCGCACAGCCTGTCTCTGCTCAGTTGCA
ATAAACGTGACATCTTGGGAGCGTTAAAAAAAAAAAAAAA

FIGURE 458

MRLALLWALGLLGAGSPLPSWPLPNIGGTEEQQAESEKAPREPLEPQVLQDDLPISLKKVLQTSLPEPLRIKLEL
DGDSHILELLQNRELVPGRPTLVWYQPDGTRVVSEGHTLENCCYQGRVRGYAGSWVSICTCSGLRGLVVLTPERS
YTLEQGPGDLQGPPIISRIQDLHLPGHTCALSWRESVHTQTPPEHPLGQRHIRRRRDVVTETKTVELVIVADHSE
AQKYRDFQHLLNRTLEVALLLDTFFRPLNVRVALVGLEAWTQRDLVEISPNPAVTLENFLHWRRAHLLPRLPHDS
AQLVTGTSFSGPTVGMAIQNSICSPDFSGGVNMDHSTSILGVASSIAHELGHSLGLDHDLPGNSCPCPGPAPAKT
CIMEASTDFLPGLNFSNCSRRALEKALLDGMGSCLFERLPSLPPMAAFCGNMFVEPGEQCDCGFLDDCVDPCCDS
LTCQLRPGAQCASDGPCCQNCQLRPSGWQCRPTRGDCDLPEFCPGDSSQCPPDVSLGDGEPCAGGQAVCMHGRCA
SYAQQCQSLWGPGAQPAAPLCLQTANTRGNAFGSCGRNPSGSYVSCTPRDAICGQLQCQTGRTQPLLGSIRDLLW
ETIDVNGTELNCSWVHLDLGSDVAQPLLTLPGTACGPGLVCIDHRCQRVDLLGAQECRSKCHGHGVCDSNRHCYC
EEGWAPPDCTTQLKATSSLTTGLLLSLLVLLVLVMLGAGYWYRARLHQRLCQLKGPTCQYRAAQSGPSERPGPPQ
RALLARGTKSQGPAKPPPPRKPLPADPQGRCPSGDLPGPGAGIPPLVVPSRPAPPPPTVSSLYL

FIGURE 459

CGACTTTCCCGATCGCCAGGCAGGAGTTTCTCTCGGTGACTACTATCGCTGTC**ATG**TCTGGTCGTGGCAAGCAAG
GAGGCAAGGCCCGCGCCAAGGCCAAGTCGCGCTCGTCCCGCGCTGGCCTTCAGTTCCCGGTAGGGCGAGTGCATC
GCTTGCTGCGCAAAGGCAACTACGCGGAGCGAGTGGGGGCCGGCGCGCCCGTCTACATGGCTGCGGTCCTCGAGT
ATCTGACCGCCGAGATCCTGGAGCTGGCGGGCAACGCGGCTCGGGACAACAAGAAGACGCGCATCATCCCTCGTC
ACCTCCAGCTGGCCATCCGCAACGACGAGGAACTGAACAAGCTGCTGGGCAAAGTCACCATCGCCCAGGGCGGCG
TCTTGCCTAACATCCAGGCCGTACTGCTCCCTAAGAAGACGGAGAGTCACCACAAGGCAAAGGGCAAG**TGA**GGCT
GACGTCCGGCCCAAGTGGGCCCAGCCCGGCCCGCGTCTCGAAGGGGCACCTGTGAACTCAAAAGGCTCTTTTCAG
AGCCACCCA

FIGURE 460

MSGRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNK
KTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPKKTESHHKAKGK

FIGURE 461

CTTTCGCC**ATG**GCTGCCGGGCCGATCTCCGAGCGGAATCAGGATGCCACTGTGTACGTGGGGGGCCTGGATGAGA
AGGTTAGTGAACCGCTGCTGTGGGAACTGTTTCTCCAGGCTGGACCAGTAGTCAACACCCACATGCCAAAGGATA
GAGTCACTGGCCAGCACCAAGGCTATGGCTTTGTGGAATTCTTGAGTGAGGAAGATGCTGACTATGCCATTAAGA
TCATGAACATGATCAAACTCTATGGGAAGCCAATACGGGTGAACAAAGCATCAGCTCACAACAAAAACCTGGATG
TAGGGGCCAACATTTTCATTGGGAACCTGGACCCTGAGATTGATGAGAAGTTGCTTTATGATACTTTCAGCGCCT
TTGGGGTCATCTTACAAACCCCCAAAATTATGCGGGACCCTGACACAGGCAACTCCAAAGGTTATGCCTTTATTA
ATTTTGCTTCATTTGATGCTTCGGATGCAGCAATTGAAGCCATGAATGGGCAGTACCTCTGTAACCGTCCTATCA
CCGTATCTTATGCCTTCAAGAAGGACTCCAAGGGTGAGCGCCATGGCTCAGCAGCCGAACGACTTCTGGCAGCTC
AGAACCCGCTCTCCCAGGCTGATCGCCCTCATCAGCTGTTTGCAGATGCACCTCCTCCACCCTCTGCTCCCAATC
CTGTGGTATCATCATTGGGGTCTGGGCTTCCTCCACCAGGCATGCCTCCTCCTGGCTCCTTCCCACCCCCAGTGC
CACCTCCTGGAGCCCTCCCACCTGGGATACCCCCAGCCATGCCCCCACCACCTATGCCTCCTGGGGCTGCAGGAC
ATGGCCCCCCATCGGCAGGAACCCCAGGGGCAGGACATCCTGGTCATGGACACTCACATCCTCACCCATTCCCAC
CGGGTGGGATGCCCCATCCAGGGATGTCTCAGATGCAGCTTGCACACCATGGCCCTCATGGCTTAGGACATCCCC
ACGCTGGACCCCCAGGCTCTGGGGGCCAGCCACCGCCCCGACCACCACCTGGAATGCCTCATCCTGGACCTCCTC
CAATGGGCATGCCCCCCCGAGGGCCTCCATTCGGATCTCCCATGGGTCACCCAGGTCCTATGCCTCCGCATGGTA
TGCGTGGACCTCCTCCACTGATGCCCCCCCATGGATACACTGGCCCTCCACGACCCCCACCCTATGGCTACCAGC
GGGGGCCTCTCCCTCCACCCAGACCCACTCCCCGGCCACCAGTTCCCCCTCGAGGCCCACTTCGAGGCCCTCTCC
CTCAG**TAA**ATTCACATTTTCCTTCCTCCTGTTACATTTTCCCAATATCTTTTCTATTCCTTGGACCAATCAGAGA
TGCTGTAGCTCCTTGGGGCAAAGGTACTAATCCCTTTCAGCACCCCCACTCCATTCCCCTTTTTAATGTAACTTT
TTCCACAGGAGGTATTTCTTTTTTATGTTGGTCCTGAGTATTTTGCAAATGCACAGAGAAAATAAAACTAAACTC
CTTGTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 462

MAAGPISERNQDATVYVGGLDEKVSEPLLWELFLQAGPVVNTHMPKDRVTGQHQGYGFVEFLSEEDADYAIKIMN
MIKLYGKPIRVNKASAHNKNLDVGANIFIGNLDPEIDEKLLYDTFSAFGVILQTPKIMRDPDTGNSKGYAFINFA
SFDASDAAIEAMNGQYLCNRPITVSYAFKKDSKGERHGSAAERLLAAQNPLSQADRPHQLFADAPPPPSAPNPVV
SSLGSGLPPPGMPPPGSFPPPVPPPGALPPGIPPAMPPPPMPPGAAGHGPPSAGTPGAGHPGHGHSHPHPFPPGG
MPHPGMSQMQLAHHGPHGLGHPHAGPPGSGGQPPPRPPPGMPHPGPPPMGMPPRGPPFGSPMGHPGPMPPHGMRG
PPPLMPPHGYTGPPRPPPYGYQRGPLPPPRPTPRPPVPPRGPLRGPLPQ

FIGURE 463A

GCCGGGAGCAGTCGCCGCTGCCGCCTCCGCCCGCGGCCGGGACCCCCGTCCTCGCCCGGGACTCCTTACCCGGGG
AACCTAGACCAGGTCTCCAGAGGCTTGTGGAAGAGAAGCAGGCGACCCTTCCTGAGTTATCCTGGCTTAGCCTCC
CAATCTGGCTCCCCTTCCCCTTCCCATTCCCCTGCTCCCCCTGTCCCTTCCCCATCCACCCAACTGAACTGGGTA
TAGGTCAAAGCTCCTCTCCTTCCTTTTCCTTCCTAGGCACTCATTGGCTAGGACCTGTTTGCTCTTTTTTTTGTG
CCCAGAGATACTGGAACACGCTTCATCTAAGTAACTGTGGGGAGGGGTCTTTTTGACTCTACAAGTCCTTGAGCA
AAAAGCTGAAAAAGAAGCAGGAGGTGGAGAAGACCCAGTGAAGTGCCCCAAGCCCCATCATGGAAGAGGGCTTCC
GAGACCGGGCAGCTTTCATCCGTGGGGCCAAAGACATTGCTAAGGAAGTCAAAAAGCATGCGGCCAAGAAGGTGG
TGAAGGGCCTGGACAGAGTCCAGGACGAATATTCCCGAAGATCGTACTCCCGCTTTGAGGAGGAGGATGATGATG
ATGACTTCCCTGCTCCCAGTGATGGTTATTACCGAGGAGAAGGGACCCAGGATGAGGAGGAAGGTGGTGCATCCA
GTGATGCTACTGAGGGCCATGACGAGGATGATGAGATCTATGAAGGGGAATATCAGGGCATTCCCCGGGCAGAGT
CTGGGGGCAAAGGCGAGCGGATGGCAGATGGGGCGCCCCTGGCTGGAGTAAGGGGGGGCTTGAGTGATGGGGAGG
GTCCCCCTGGGGGCCGGGGGGAGGCACAACGACGGAAAGAACGAGAAGAACTGGCCCAACAGTATGAAGCCATCC
TACGGGAGTGTGGCCACGGCCGCTTCCAGTGGACACTGTATTTTGTGCTTGGTCTGGCGCTGATGGCTGACGGTG
TGGAGGTCTTTGTGGTGGGCTTCGTGCTGCCCAGCGCTGAGAAAGACATGTGCCTGTCCGACTCCAACAAAGGCA
TGCTAGGCCTCATCGTCTACCTGGGCATGATGGTGGGAGCCTTCCTCTGGGGAGGTCTGGCTGACCGGCTGGGTC
GGAGGCAGTGTCTGCTCATCTCGCTCTCAGTCAACAGCGTCTTCGCCTTCTTCTCATCTTTTGTCCAGGGTTACG
GCACTTTCCTCTTCTGCCGCCTACTTTCTGGGGTTGGGATTGGAGGGTCCATCCCCATTGTCTTCTCCTATTTCT
CCGAGTTTCTGGCCCAGGAGAAACGAGGGGAGCATTTGAGCTGGCTCTGCATGTTTTGGATGATTGGTGGCGTGT
ACGCAGCTGCTATGGCCTGGGCCATCATCCCCCACTATGGGTGGAGTTTTCAGATGGGTTCTGCCTACCAGTTCC
ACAGCTGGAGGGTCTTCGTCCTCGTCTGCGCCTTTCCTTCTGTGTTTGCCATTGGGGCTCTGACCACGCAGCCTG
AGAGCCCCCGTTTCTTCCTAGAGAATGGAAAGCATGATGAGGCCTGGATGGTGCTGAAGCAGGTCCATGATACCA
ACATGCGAGCCAAAGGACATCCTGAGCGAGTGTTCTCAGTAACCCACATTAAGACGATTCATCAGGAGGATGAAT
TGATTGAGATCCAGTCGGACACAGGGACCTGGTACCAGCGCTGGGGGGTCCGGGCCTTGAGCCTAGGGGGGCAGG
TTTGGGGGAATTTTCTCTCCTGTTTTGGTCCCGAATATCGGCGCATCACTCTGATGATGATGGGTGTGTGGTTCA
CCATGTCATTCAGCTACTATGGCCTGACCGTCTGGTTTCCTGACATGATCCGCCATCTCCAGGCAGTGGACTACG
CATCCCGCACCAAAGTGTTCCCCGGGGAGCGCGTAGAGCATGTAACTTTTAACTTCACGTTGGAGAATCAGATCC
ACCGAGGCGGGCAGTACTTCAATGACAAGTTCATTGGGCTGCGGCTCAAGTCAGTGTCCTTTGAGGATTCCCTGT
TTGAAGAGTGTTATTTTGAGGATGTCACATCCAGCAACACGTTTTTCCGCAACTGCACATTCATCAACACTGTGT
TCTATAACACTGACCTGTTCGAGTACAAGTTTGTGAACAGCCGTCTGATAAACAGTACATTCCTGCACAACAAGG
AGGGCTGCCCGCTAGACGTGACAGGGACGGGCGAAGGTGCCTACATGGTATACTTTGTGAGCTTCCTGGGGACAC
TGGCAGTGCTTCCTGGGAATATCGTGTCTGCCCTGCTCATGGACAAGATCGGCAGGCTCAGAATGCTTGCTGGCT
CCAGCGTGATGTCCTGTGTCTCCTGCTTCTTCCTGTCTTTTGGGAACAGTGAGTCGGCCATGATCGCTCTGCTCT
GCCTTTTTGGCGGGGTCAGCATTGCATCCTGGAATGCGCTGGACGTGTTGACTGTTGAACTCTACCCCTCAGACA
AGAGGACCACAGCTTTTGGCTTCCTGAATGCCCTGTGTAAGCTGGCAGCTGTGCTGGGGATCAGCATCTTCACAT
CCTTCGTGGGAATCACCAAGGCTGCACCCATCCTCTTTGCCTCAGCTGCCCTTGCCCTTGGCAGCTCTCTGGCCC
TGAAGCTGCCTGAGACCCGGGGGCAGGTGCTGCAGTGAAGGGGTCTCTAGGGCTTTGGGATTGGCAGGCACACTG
TGAGACCAACAACTCCTTCCTTCCCCTCCCTGCCCTGCCATCCTGACCTCCAGAGCCCTCACTCCCCACTCCCCG
TGTTTGGTGTCTTAGCTGTGTGTGCGTGTGCGTGTGCATGTGTGTAAACCCCGTGGGCAGGGACTACAGGGAAGG
CTCCTTCATCCCAGTTTTGAGATGAAGCTGTACTCCCCATTTCCCACTGCCCTTGACTTTGCACAAGAGAAGGCT
GAGCCCCATCCTTCTCCCCCTGTTAGAGAGGGGCCCTTGCTTCCCTGTTCCAGGGGTTCCAGAATAGGCTTCCTG
CCTTCCCCATCATTCCCTCTGCCTAGGCCCTGGTGAAACCACAGGTATGCAATTATGCTAGGGGCTGGGGCTCTG
GTGTAGACCATGGACCAAAAGAACTTCTTAGAGTCTGAAGAGTGGGCCTCGGGTGCCCTCTCACATCTCCTGTTG
GATGCTGGGGGAGAAGCAATAAACCTCAGCCCTCTGGCCTCCACTTTCCTCTCAATTTGGGCTGCAAATATGAAG
CCTGAATTTTATGAAATTAGCTTTCTGATTCTTATTTATTAATAGATTAAGTTCTGAGGCAGCTCCGCAGGACTG
TGTGTGAATGTGTATGTATACTTACATATGTGTGTGCATGTGCCATGGGGCGGGGGGTATCACTATACTGTCCTC
AAATATAAGCCAAGGGTAATTTCAGCGGATGCACACACAACCCTGCCTCCCACAGTTCCTCCCCTAATCTGGTTT
CTGTGTTGAGCCTGGGATGGAGGAGCCCTAGGCCAGCCTGGGATAAGAGTCCCACAGTCTAGGGAGATCTGAGGG
CATCCGACAAGGCCCATCTCCTTCCCTCCTCAAGAAGCAGAGGCCTCCTCTGGAGTGAGAGGCTCCACCCACTAC

FIGURE 463B

AGCACAGGCGGGAATAGCACAGCTGCCCTCCCATGCTCCCTACCTGTCCCCTCACAGGGAGGGGAGCAGGGGAGG
GAAAGAAACCAGGCATCTGGTCAAACCAGCAGATCAAAAAGCACAAAGAGCTGGGGCAGAGGCAGGAAGCAGGGG
CCCTCCTGGCAGCTCCTCTGAGTGGGGAGAGGTTGGGCAGTGAGTGAGGGACCCCTAATGCAGGGACTAGAAGCC
TCAGTTTCCCCATTTTACCCTTCCACACAATAGCCTCTGTAGGTTAGGCTGCCCCATCCCACCCTACTCTGTGTG
GCTGCTTTCTTTGGTGCCCTCCCCTCACCCCACTGTAGCTGTGACGTGTTGTAGTTTTTAGATGTTTGTAAAATG
TTTAAAAAAATGTTAAAAGGAAAAAAGTGAAAATAACAAAAAAGAAAATCAAAATTCACCTTCGTCATGCTGCGT
CCAGTGCCCCAACCCTGTGGTCACTCTCCCCATTTTGTAACACTGTACCAGGTGGTGACTGTTTAACTCTTTGGT
GTCTGTGCTCAAAAGACTGCCTTCTCCAGTGCCCAGTGTATGAGTGTGTGCCCTGTGCCCTTGTCCCTCACTCCC
CACATGCTGGACGTAGCCCTCTTCCTCGCACCCCTGGGAGGGACCCATCCATCTCCCTTGCTCTCCTGGGAACC
CTAAACCCAACTCTGTTGATGTGAAAAATGCAGTGAAAAATATTGACGAAAAATAAAACGGAAACAAATCCTCAA
AAT

FIGURE 464

MEEGFRDRAAFIRGAKDIAKEVKKHAAKKVVKGLDRVQDEYSRRSYSRFEEEDDDDDFPAPSDGYYRGEGTQDEE
EGGASSDATEGHDEDDEIYEGEYQGIPRAESGGKGERMADGAPLAGVRGGLSDGEGPPGGRGEAQRRKEREELAQ
QYEAILRECGHGRFQWTLYFVLGLALMADGVEVFVVGFVLPSAEKDMCLSDSNKGMLGLIVYLGMMVGAFLWGGL
ADRLGRRQCLLISLSVNSVFAFFSSFVQGYGTFLFCRLLSGVGIGGSIPIVFSYFSEFLAQEKRGEHLSWLCMFW
MIGGVYAAAMAWAIIPHYGWSFQMGSAYQFHSWRVFVLVCAFPSVFAIGALTTQPESPRFFLENGKHDEAWMVLK
QVHDTNMRAKGHPERVFSVTHIKTIHQEDELIEIQSDTGTWYQRWGVRALSLGGQVWGNFLSCFGPEYRRITLMM
MGVWFTMSFSYYGLTVWFPDMIRHLQAVDYASRTKVFPGERVEHVTFNFTLENQIHRGGQYFNDKFIGLRLKSVS
FEDSLFEECYFEDVTSSNTFFRNCTFINTVFYNTDLFEYKFVNSRLINSTFLHNKEGCPLDVTGTGEGAYMVYFV
SFLGTLAVLPGNIVSALLMDKIGRLRMLAGSSVMSCVSCFFLSFGNSESAMIALLCLFGGVSIASWNALDVLTVE
LYPSDKRTTAFGFLNALCKLAAVLGISIFTSFVGITKAAPILFASAALALGSSLALKLPETRGQVLQ

FIGURE 465

GGCAGGAAAAGCGGAAGAGGGAGCGAAAACCAACGTGTTCGGTGACAGACCCCAGCGCCGACTGAGCCTCTAAAG
CGACTTCAGCTCTGCCCCACCAACACCACCGCGCGCCCGGGAACAGCCGCTCCGGGAAGAAACCTGAGGGGACTG
CGGGGGGCACGAGGGACAGCTGAGGGAAGGGAGGACGCGAGAGAAACAGCGCGAGCACGCTGAGGGCCGGGGGTT
GCCAGGAGAGGGGCCCGCGGACCCGCAGAGCGGAGGAAGGTCCGGGAGAAAAGGGGCGGGACGGAGGAGAATCCG
GGATCGCCTGGCAGAAAAAGAGAAGGGAGTTTCTGAATCCTGGGAAGAGGAGGCGTGGGTAGGGACGCTTAGCCC
GAGATCCGACAGCAGGGAACCGGAGCGCTCCGGGGGAGGGGCTTAATGCTGGGGAAGGGATGTCTTAAAAGAGGA
GAAGCTTTAAATTAGACGATCGGAGAAGGCTGAGGGAATTGCTATGAAGGGGCGGGAGCTGAAGTGTAGAGGACT
CCTTTAGACAGCAGAAAGGGAAAGCCGTTGAGAAGTTCCCTTCAAACTCCACCTGCCTCCTCTCCAATTCAAACT
CCACTCCCTTCTCCAAAAGTTAAAAGGAAAGCCAAGTTTACCACGCTCCCCTGTTCCTACTCAATAAATACTTCT
TCTACTCCGCCACCGGGAAAACAGAAAAAAAAACTAATTTCCTTCCCAATATTAGGACTTAGAAAAGCTCTAGGT
CCCGCAATTTGAATTTTAGCCTAGGGGAATCAAAATAGTAGGAGCATTACTCTTGTTTCCTTTTTCAAAATCCCA
CACCTCATCCTTCCTGCGACGCCATGTCCACCAACATTTGTAGTTTCAAGGACAGGTGCGTGTCCATCCTGTGTT
GCAAATTCTGTAAACAAGTGCTCAGCTCTAGGGGAATGAAGGCTGTTTTGCTGGCTGATACTGAAATAGACCTTT
TCTCTACAGACATCCCTCCTACCAACGCAGTGGACTTCACTGGAAGATGCTATTTCACCAAAATCTGCAAATGTA
AACTGAAGGACATCGCATGTTTAAAATGTGGGAACATTGTAGGTTATCATGTGATTGTTCCATGTAGTTCCTGTC
TTCTTTCCTGCAACAACAGACACTTCTGGATGTTTCACAGCCAGGCAGTTTATGATATTAACAGACTAGACTCCA
CAGGTGTAAACGTCCTACTTCGGGGCAACTTGCCAGAGATAGAAGAGAGTACAGATGAAGATGTGTTAAATATCT
CAGCAGAGGAGTGTATTAGATAAATGGAATTATGATATATATGATATACAAACTTTTTTCTATTTAAAAATATAT
TAATGGATCAACTTTAAAATTGTTAGTTGCCAGTGATCTTTTTTGGAAAACAAAAATGGGGCATTTGTTGATTTA
TTTATTTTCTGTCTCTAATTAGTTACCTCAGTTTGATTGAAGCCAGTGGAGTTGTGCTTTTCCTCTACTTCTACT
TCCTCTCCCCCACCTTTTTCTGCCCAGTGTAGGTGTATTCTTAAATTCAGACGGGAAGATTCTTTCACATATCAC
TCAGTTACCTCCCAATCTGGGGGAGTTTTTCTTACAACTTGATACCAGATACCATTAATTTTACATTCCTGAATA
AAGGCCTAGTACCCACGCATATTTCAACCATGCATATATCAAGTTCAACCGAGTTTTAATAGGGGATTAAAAAAA
CAAGCTGTTAGGTTTCCATGGGCACTGGTTCTCATAGGTTCTATTGGTGATAACTGCTTTAACATGGAGCAAGAG
TTTGTGAATCAGGAAATAGAATAAATTAAAATTTAAAATATATAGAGGAATCCTCTTGATTGCTCAGCATGATGT
TAGATAAATGAGTTTGTCAGAAAATATCAGTATACGCTGTTTACCAATGTTATTTATTTACATTCTTCTAAAGCC
ATTATGGATATTGTATTATGAGAGCTAAACCTAAATAAGTTATCCTGTTCCCTAGGACCTTCTCTGTAAATAGTG
AATTTTAGACGAGTGGTCTGTCCTAAATCTTAAATAGAAAAAAAAACTAAAGCGATTTGCTTAAGCCATTGTACA
TTATAAAGAGCTGTTTTGTTTTGCTTTGCTTTGCTTTGTTTTGTTTTTTAAAGCTGCATTCAGAGCTACAAAGG
AATAGGAAAGTAGGGTAGTGTTGGATTCTGGTTTTATGTAACTCTAAAATAAATGTATCTCTTTAATATCTCAGT
TGTAGGGATTTTGTCAATACCAAAGCAGACTGAGTTGTGGTTTTGTAAATAAAGTTTTTTCTAAAAATGACCATT
CTTCCTTTAATTTTTTGTTATGCCCACATATTGTATGTAAAAATATAAATAAATAGTACTTAAAGTAT

FIGURE 466

CAGCAGTGCTGTTTACTCATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAAAAGGACCA
AGAAGAGGAAGAAGACCAAGGCCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGT
CTTGCAGGACTCACTGGATAGATGTTATTCAACTCCTTCCAGTTGTCTTGAACAGCCTGACTCCTGCCAGCCCTA
TGGAAGTTCCTTTTATGCATTGGAGGAAAAGCATGTTGGCTTTTCTCTTGACGTGGGAGAAATTGAAAAGAAGGG
GAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAGAAGGAAAGAAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCA
AAACCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGATGAGAAAGGGCCTGAAGTCTTGCAGGACTCACTGGA
TAGATGTTATTCAACTCCTTCAGGTTGTCTTGAACTGACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTACAT
ATTGGAGCAACAGCGTGTTGGCTTGGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGACCA
AGACCCATCATGCCCCAGGCTCAGCGGGGAGCTGTTGGATGAGAAAGAGCCTGAAGTCTTGCAGGAGTCACTGGA
TAGATGCTATTCAACTCCTTCAGGTTGTCTTGAACTGACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTACAT
ATTGGAGCAACAGCGTGTTGGCTTGGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGACCA
AGACCCATCATGCCCCAGGCTCAGCAGGGAGCTGCTGGATGAGAAAGAGCCTGAAGTCTTGCAGGACTCACTGGG
TAGATGTTATTCGACTCCTTCAGGTTATCTTGAACTGCCTGACTTAGGCCAGCCCTACAGCAGTGCTGTTTACTC
ATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAAAAGGACCAAGAAGAGGAAGAAGACCA
AGGCCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGTCTTGCAGGACTCACTGGA
TAGATGTTATTCAACTCCTTCCAGTTGTCTTGAACAGCCTGACTCCTGCCAGCCCTATGGAAGTTCCTTTTATGC
ATTGGAGGAAAAACATGTTGGCTTTTCTCTTGACGTGGGAGAAATTGAAAAGAAGGGGAAGGGGAAGAAAAGAAG
GGGAAGAAGATCAAAGAAGGAAAGAAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAACCCACCATGCCCCAG
GCTCAACAGCATGCTGATGGAAGTGGAAGAGCCTGAAGTCTTGCAGGACTCACTGGATATATGTTATTCGACTCC
GTCAATGTACTTTGAACTACCTGACTCATTCCAGCACTACAGAAGTGTGTTTTACTCATTTGAGGAAGAGCATAT
CAGCTTCGCCCTTTACGTGGACAATAGGTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTGTTCCAGATGGG
AGTCATATTCCCACAATAAGCAGCCCTTACTAAGCCGAGAGGTGTCATTCCTGCAGGCAGGACCTATAGGCACGT
GAAGATTTGAATGAAAGTACAGTTCCATTTGGAAGCCCAGACATAGGATGGGTCAGTGGGCATGGCTCTATTCCT
ATTCTCAAACCATGCCAGTGGCAACCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACACGTTCAC
ATAACTGTGCAGCACATGCCGGGAGTGATCAGTCAGACATTTTAATTTGAACCACGTATCTCTGGGTAGCTACAA
AATTCCTCAGGGATGTCATTTTGCAGGCATGTCTCTGAGCTTCTATACCTGCTCAAGGTCATTGTCATCTTTGTG
TTTAGCTCATCCAAAGGTGTTACCCTGGTTTCAATGAACCTAACCTCATTCTTTGTGTCTTCAGTGTTGGCTTGT
TTTAGCTGATCCATCTGTAACACAGGAGGGATCCTTGGCTGAGGATTGTATTTCAGAACCACCAACTGCTCTTGA
CAATTGTTAACCCGCTAGGCTCCTTTGGTTAGAGAAGCCACAGTCCTTCAGCCTCCAATTGGTGTCAGTACTTAG
GAAGACCACAGCTAGATGGACAAACAGCATTGGGAGGCCTTAGCCCTGCTCCTCTCAATTCCATCCTGTAGAGAA
CAGGAGTCAGGAGCCGCTGGCAGGAGACAGCATGTCACCCAGGACTCTGCCGGTGCAGAATATGAGCAATGCCAT
GTTCTTGCAGAAAACGCTTAACCTGAGTTTCATAGGAGGTAATCACCAGACAACTGCAGAATGTAGAACACTGAG
CAGGACAACTGACCTGTCTCCTTCACATAGTCCATATCACCACAAATCACACAACAAAAAGGAGAAGAGATATTT
TCGGTTGAAAAAAAGTAAAAAGATA

FIGURE 467

MDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEEQYLGLALD
VDRIKKDQEEEEDQGPPCPRLSRELLEVAEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLD
VGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLNGVLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQ
HYRSVFYSFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFTQ

FIGURE 468

ATGACGCGAGACCCCGCCCCCGCAGCGCCCGCTTCCAAGATGGCGGCAGCGATGCCTGCCCGGCTGTTGGGGTGG
CGGTGACGACAGGCAGCAAAAGACCAGCTGGTCCCAGATTCGCTGCTGGAGTGCTGGATGGAGCCTTTCTCTGCC
CTCTGTGACATTTCCAATTTTAGATAATGCCTCACATCTCTGTCCCCCCGGACCCCCTGGAGCCCCCATGATCC
CTAAGAAGACAGCTTGAACCTAGATCTCACCCCCAGGATGTTGCGGAGGCTGCTGGAGCGGCCTTGCACGCTGGC
CCTGCTTGTGGGCTCCCAGCTGGCTGTCATGATGTACCTGTCACTGGGGGGCTTCCGAAGTCTCAGTGCCCTATT
TGGCCGAGATCAGGGACCGACATTTGACTATTCTCACCCTCGTGATGTCTACAGTAACCTCAGTCACCTGCCTGG
GGCCCCAGGGGGTCCTCCAGCTCCTCAAGGTCTGCCCTACTGTCCAGAACGATCTCCTCTCTTAGTGGGTCCTGT
GTCGGTGTCCTTTAGCCCAGTGCCATCACTGGCAGAGATTGTGGAGCGGAATCCCCGGGTAGAACCAGGGGGCCG
GTACCGCCCTGCAGGTTGTGAGCCCCGCTCCCGAACAGCCATCATTGTGCCTCATCGTGCCCGGGAGCACCACCT
GCGCCTGCTGCTCTACCACCTGCACCCCTTCTTGCAGCGCCAGCAGCTTGCTTATGGCATCTATGTCATCCACCA
GGCTGGAAATGGAACATTTAACAGGGCAAAACTGTTGAACGTTGGGGTGCGAGAGGCCCTGCGTGATGAAGAGTG
GGACTGCCTGTTCTTGCACGATGTGGACCTCTTGCCAGAAAATGACCACAATCTGTATGTGTGTGACCCCCGGGG
ACCCCGCCATGTTGCCGTTGCTATGAACAAGTTTGGATACAGCCTCCCGTACCCCCAGTACTTCGGAGGAGTCTC
AGCACTTACTCCTGACCAGTACCTGAAGATGAATGGCTTCCCCAATGAATACTGGGGCTGGGGTGGTGAGGATGA
CGACATTGCTACCAGGGTGCGCCTGGCTGGGATGAAGATCTCTCGGCCCCCCACATCTGTAGGACACTATAAGAT
GGTGAAGCACCGAGGAGATAAGGGCAATGAGGAAAATCCCCACAGATTTGACCTCCTGGTCCGTACCCAGAATTC
CTGGACGCAAGATGGGATGAACTCACTGACATACCAGTTGCTGGCTCGAGAGCTGGGGCCTCTTTATACCAACAT
CACAGCAGACATTGGGACTGACCCTCGGGGTCCTCGGGCTCCTTCTGGGCCACGTTACCCACCTGGTTCCTCCCA
AGCCTTCCGTCAAGAGATGCTGCAACGCCGGCCCCCAGCCAGGCCTGGGCCTCTATCTACTGCCAACCACACAGC
CCTCCGAGGTTCACACTGACTCCTCCTTCCTGTCTACCTTAATCATGAAACCGAATTCATGGGGTTGTATTCTCC
CCACCCTCAGCTCCTCACTGTTCTCAGAGGGATGTGAGGGAACTGAACTCTGGTGCCGTGCTAGGGGGTAGGGGC
CTCTCCCTCACTGCTGGACTGGAGCTGGGCTCCTGTAGACCTGAGGGGTCCCTCTCTCTAGGGTCTCCTGTAGGG
CTTATGACTGTGAATCCTTGATGTCATGATTTTATGTGACGATTCCTAGGAGTCCCTGCCCCTAGAGTAGGAGCA
GGGCTGGACCCCAAGCCCCTCCCTCTTCCATGGAGAGAAGAGTGATCTGGCTTCTCCTCGGACCTCTGTGAATAT
TTATTCTATTTATGGTTCCCGGGAAGTTGTTTGGTGAAGGAAGCCCCTCCCTGGGCATTTTCTGCCTATGCTGGA
ATAGCTCCCTCTTCTGGTCCTGGCTCAGGGGGCTGGGATTTTGATATATTTTCTAATAAAGGACTTTGTCTCGC

FIGURE 469

MLRRLLERPCTLALLVGSQLAVMMYLSLGGFRSLSALFGRDQGPTFDYSHPRDVYSNLSHLPGAPGGPPAPQGLP
YCPERSPLLVGPVSVSFSPVPSLAEIVERNPRVEPGGRYRPAGCEPRSRTAIIVPHRAREHHLRLLLYHLHPFLQ
RQQLAYGIYVIHQAGNGTFNRAKLLNVGVREALRDEEWDCLFLHDVDLLPENDHNLYVCDPRGPRHVAVAMNKFG
YSLPYPQYFGGVSALTPDQYLKMNGFPNEYWGWGGEDDDIATRVRLAGMKISRPPTSVGHYKMVKHRGDKGNEEN
PHRFDLLVRTQNSWTQDGMNSLTYQLLARELGPLYTNITADIGTDPRGPRAPSGPRYPPGSSQAFRQEMLQRRPP
ARPGPLSTANHTALRGSH

FIGURE 470

GGCACGAGGGCCCCAGGAGAGGCAGAGAGTGAGGGAAAGGGCCTGGCCGGCATGCACAGATAGGATCACGGTCCT
GGGAGAATTCCTGCTCTTATAGTCTAACCTACCATGGCTTCTCTTTTCTCAAGGCTCCCTCATGCTGCCCTTTGG
CCCTAGTGGCTGGTTTCCAGGGCTGAGGGGACTGAGTGAGCTGCCTGAGAAAAGAGGGTAGGGAACAGAAAAGCC
AGCCAGGAGCTGTGGGAGGAAACGCCCTCAGTAAAGATGACCGCGGTCACTGTTATCTAAACGCAAGTGAAGCCG
AGTCACAGGACCCGGATGTTGTCAGTTCGACGGTAAACGACCCTGCCAGCTTCCAAGAGGGCGGCTTCACTGTGC
GAATAGGTGAGAAGCCAAGAAGGAGGCGCGCTGGAGTTACTTCCGCCCGGTTCTCCTTCCCGCAGTCTGCAGCCG
GAGTAAG**ATG**GCGGCGCTGAGGGCTTTGTGCGGCTTCCGGGGCGTCGCGGCCCAGGTGCTGCGGCCTGGGGCTGG
AGTCCGATTGCCGATTCAGCCCAGCAGAGGTGTTCGGCAGTGGCAGCCAGATGTGGAATGGGCACAGCAGTTTGG
GGGAGCTGTTATGTACCCAAGCAAAGAAACAGCCCACTGGAAGCCTCCACCTTGGAATGATGTGGACCCTCCAAA
GGACACAATTGTGAAGAACATTACCCTGAACTTTGGGCCCCAACACCCAGCAGCGCATGGTGTCCTGCGACTAGT
GATGGAATTGAGTGGGGAGATGGTGCGGAAGTGTGATCCTCACATCGGGCTCCTGCACCGAGGCACTGAGAAGCT
CATTGAATACAAGACCTATCTTCAGGCCCTTCCATACTTTGACCGGCTAGACTATGTGTCCATGATGTGTAACGA
ACAGGCCTATTCTCTAGCTGTGGAGAAGTTGCTAAACATCCGGCCTCCTCCTCGGGCACAGTGGATCCGAGTGCT
GTTTGGAGAAATCACACGTTTGTTGAACCACATCATGGCTGTGACCACACATGCCCTGGACCTTGGGGCCATGAC
CCCTTTCTTCTGGCTGTTTGAAGAAAGGGAGAAGATGTTTGAGTTCTACGAGCGAGTGTCTGGAGCCCGAATGCA
TGCTGCTTATATCCGGCCAGGAGGAGTGCACCAGGACCTACCCCTTGGGCTTATGGATGACATTTATCAGTTTTC
TAAGAACTTCTCTCTTCGGCTTGATGAGTTGGAGGAGTTGCTGACCAACAATAGGATCTGGCGAAATCGGACAAT
TGACATTGGGGTTGTAACAGCAGAAGAAGCACTTAACTATGGTTTTAGTGGAGTGATGCTTCGGGGCTCAGGCAT
CCAGTGGGACCTGCGGAAGACCCAGCCCTATGATGTTTACGACCAGGTTGAGTTTGATGTTCCTGTTGGTTCTCG
AGGGGACTGCTATGATAGGTACCTGTGCCGGGTGGAGGAGATGCGCCAGTCCCTGAGAATTATCGCACAGTGTCT
AAACAAGATGCCTCCTGGGGAGATCAAGGTTGATGATGCCAAAGTGTCTCCACCTAAGCGAGCAGAGATGAAGAC
TTCCATGGAGTCACTGATTCATCACTTTAAGTTGTATACTGAGGGCTACCAAGTTCCTCCAGGAGCCACATATAC
TGCCATTGAGGCTCCCAAGGGAGAGTTTGGGGTGTACCTGGTGTCTGATGGCAGCAGCCGCCCTTATCGATGCAA
GATCAAGGCTCCTGGTTTTGCCCATCTGGCTGGTTTGGACAAGATGTCTAAGGGACACATGTTGGCAGATGTCGT
TGCCATCATAGGTACCCAAGATATTGTATTTGGAGAAGTAGATCGG**TGA**GCAGGGGAGCAGCGTTTGATCCCCCC
TGCCTATCAGCTTCTTCTGTGGAGCCTGTTCCTCACTGGAAATTGGCCTCTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTATGTTCGTGTACACTTGGCTGTCAGGCTTTCTGTGCATGTACTAAAAAAGGAGAAATTATAATAAAT
TAGCCGTCTTGCGGCCCCTAGGCCTAAAAAAAAAAAAAAAAAAA

FIGURE 471

MAALRALCGFRGVAAQVLRPGAGVRLPIQPSRGVRQWQPDVEWAQQFGGAVMYPSKETAHWKPPPWNDVDPPKDT
IVKNITLNFGPQHPAAHGVLRLVMELSGEMVRKCDPHIGLLHRGTEKLIEYKTYLQALPYFDRLDYVSMMCNEQA
YSLAVEKLLNIRPPPRAQWIRVLFGEITRLLNHIMAVTTHALDLGAMTPFFWLFEEREKMFEFYERVSGARMHAA
YIRPGGVHQDLPLGLMDDIYQFSKNFSLRLDELEELLTNNRIWRNRTIDIGVVTAEEALNYGFSGVMLRGSGIQW
DLRKTQPYDVYDQVEFDVPVGSRGDCYDRYLCRVEEMRQSLRIIAQCLNKMPPGEIKVDDAKVSPPKRAEMKTSM
ESLIHHFKLYTEGYQVPPGATYTAIEAPKGEFGVYLVSDGSSRPYRCKIKAPGFAHLAGLDKMSKGHMLADVVAI
IGTQDIVFGEVDR

FIGURE 472

CCGGAACCCAAGATGGCTGCGCTGTTGCTGAGACACGTTGGTCGTCATTGCCTCCGAGCCCACTTTAGCCCTCAG
CTCTGTATCAGAAATTGGTCTCTTCCCATGGCGATGTCCATCTGCCACCGTGGCACTGGTATTGCTTTGAGTGCA
GGGGTCTCTCTTTTTGGCATGTCGGCCCTGTTACTCCCTGGGAACTTTGAGTCTTATTTGGAACTTGTGAAGTCC
CTGTGTCTGGGGCCAGCACTGATCCACACAGCTAAGTTTGCACTTGTCTTCCCTCTCATGTATCATACCTGGAAT
GGGATCCGACACTTGATGTGGGACCTAGGAAAAGGCCTGAAGATTCCCCAGCTATACCAGTCTGGAGTGGTTGTC
CTGGTTCTTACTGTGTTGTCCTCTATGGGGCTGGCAGCCATGTGAAGAAAGGAGGCTCCCAGCATCATCTTCCTA
CACATTATTACATTCACCCATCTTTCTGTTTGTCATTCTTATCTCCAGCCTGGGAAAAGTTCTCCTTATTTGTTT
AGATCCTTTTGTATTTTCAGATCTCCTTGGAGCAGTAGAGTACCTGGTAGACCATAATAGTGGAAAAGGGTCTAG
TTTTCCCCTTGTTTCTAAAGATGAGGTGGCTGCATCTCTCTCCATATTGGGCTTT

FIGURE 473

AATCATAGTGAAAGATTCGTTTTCATTGCAGAGTGGTATGATCCAAATGCTTCACTTCTTCGACGTTATGAGCTT
TTATTTTACCCAGGGGATGGATCTGTTGAAATGCATGATGTAAAGAATCATCGCACCTTTTTAAAGCGGACCAAA
TATGATAACCTGCACTTGGAAGATTTATTTATAGGCAACAAAGTGAATGTCTTTTCTCGACAACTGGTATTAATT
GACTATGGGGATCAATATACAGCTCGCCAGCTGGGCAGTAGGAAAGAAAAAACGCTAGCCCTAATTAAACCAGAT
GCAATATCAAAGGCTGGAGAAATAATTGAAATAATAAACAAAGCTGGATTTACTATAACCAAACTCAAAATGATG
ATGCTTTCAAGGAAAGAAGCATTGGATTTTCATGTAGATCACCAGTCAAGACCCTTTTTCAATGAGCTGATCCAG
TTTATTACAACTGGTCCTATTATTGCCATGGAGATTTTAAGAGATGATGCTATATGTGAATGGAAAAGACTGCTG
GGACCTGCAAACTCTGGAGTGGCACGCACAGATGCTTCTGAAAGCATTAGAGCCCTCTTTGGAACAGATGGCATA
AGAAATGCAGCGCATGGCCCTGATTCTTTTGCTTCTGCGGCCAGAGAAATGGAGTTGTTTTTTCCTTCAAGTGGA
GGTTGTGGGCCGGCAAACACTGCTAAATTTACTAATTGTACCTGTTGCATTGTTAAACCCCATGCTGTCAGTGAA
GGACTGTTGGGAAAGATCCTGATGGCTATCCGAGATGCAGGTTTTGAAATCTCAGCTATGCAGATGTTCAATATG
GATCGGGTTAATGTTGAGGAATTCTATGAAGTTTATAAAGGAGTAGTGACCGAATATCATAGGACATGGTGACAG
AAATGTATTCTGGCCCTTGTGTAGCAATGGAGATTCAACAGAATAATGCTACAAAGACATTTCGAGAATTTTGTG
GACCTGCTGATCCTG

FIGURE 474

GCCCTTGCCTTGAGTCAGTGCGCTGCTCTCCAGCCCGCTTGAACGCTCCCCGCAGCCACCGCCACCCATTGGA**AT**
GGCCAACAGGGGACCTGCATATGGCCTGAGCCGGGAGGTGCAGCAGAAGATTGAGAAACAATATGATGCAGATCT
GGAGCAGATCCTGATCCAGTGGATCACCACCCAGTGCCGAAAGGATGTGGGCCGGCCCCAGCCTGGACGCGAGAA
CTTCCAGAACTGGCTCAAGGATGGCACGGTGCTATGTGAGCTCATTAATGCACTGTACCCCGAGGGGCAGGCCCC
AGTAAAGAAGATCCAGGCCTCCACCATGGCCTTCAAGCAGATGGAGCAGATCTCTCAGTTCCTGCAAGCAGCTGA
GCGCTATGGCATTAACACCACTGACATCTTCCAAACTGTGGACCTCTGGGAAGGAAAGAACATGGCCTGTGTGCA
GCGGACGCTGATGAATCTGGGTGGGCTGGCAGTAGCCCGAGATGATGGGCTCTTCTCTGGGGATCCCAACTGGTT
CCCTAAGAAATCCAAGGAGAATCCTCGGAACTTCTCAGATAACCAGCTGCAAGAGGGCAAGAACGTGATCGGGTT
ACAGATGGGCACCAACCGCGGGGCGTCTCAGGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTC**TGA**TC
CCACCCCAGGCCTTGCCCCTGCCCTCCCACGAATGGTTAATATATATGTAGATATATATTTTAGCAGTGACATTC
CCAGAGAGCCCCAGAGCTCTCAAGCTCCTTTCTGTCAGGGTGGGGGGTTCAGCCTGTCCTGTCACCTCTGAGGTG
CCTGCTGGCATCCTCTCCCCCATGCTTACTAATACATTCCCTTCCCCATAGCCATCAAAACTGGACCAACTGGCC
TCTTCCTTTCCCCTGGGACCAAAATTTAGGGGCCTCAGTCCCTCACCGCCATGCCCTGGCCTATTCTGTCTCTCC
TTCTTCCCCCTGGCCTGTTCTGTCTCTGAGCTCTGTGTCCTCCGTTCATTCCATGGCTGGGAGTCACTGATGCTG
CCTCTGCCTTCTGATGCTGGACTGGCCTTGCTTCTACAAGTATGCTTCTCCCACAGCTGTGGCTGCAGGAACTTA
ATTTATAGGGAGGAGCCTGTGGCAGCTGCTGCCCCAGCCACAGCTGCACTGACTGTGCTCACCACACATCTGGGG
CAGCCTTCCCTGGCAGGGGCCCTCGTGGCTTCTCATTTTCCATTCCCTTCACTGTGGCTAAGGGGTGGGGTGAGG
GGATGGAGAGGGAGGGCTGCCTACCATGGTCTGGGGCTTGAGGAAGATGAGTTTGTTGATTTAAATAAAGAATTT
GTCATTTTTG

FIGURE 475

MANRGPAYGLSREVQQKIEKQYDADLEQILIQWITTQCRKDVGRPQPGRENFQNWLKDGTVLCELINALYPEGQA
PVKKIQASTMAFKQMEQISQFLQAAERYGINTTDIFQTVDLWEGKNMACVQRTLMNLGGLAVARDDGLFSGDPNW
FPKKSKENPRNFSDNQLQEGKNVIGLQMGTNRGASQAGMTGYGMPRQIL

FIGURE 476A

GTGGAGCCGAGCGGTGCGGAGCAGATCTGGTGGTTCTCCGGAGAGCAGCTTCCTCGGGTGTTACATGAGCCAAGC
CCTCACTGTACAGAAGAGTGAGAGCTGAAACCTGTTCCCTGAGCTGATCAGAAGGACATCCCTTGGCCCCTCCAT
CTGGGCTCCTGTGGATAGGAGGGGCTGGGTGAGCAGGCCAGCTGGGCTATGGTGTGGTGCCTCGGCCTGGCCGTC
CTCAGCCTGGTCATCAGCCAGGGGGCTGACGGTCGAGGGAAGCCTGAGGTGGTATCGGTGGTGGGCCGGGCTGGG
GAGAGTGTGGTGCTGGGCTGTGACCTGCTGCCCCCGGCCGGCCGGCCCCCCCTGCATGTCATCGAGTGGCTGCGC
TTTGGATTCCTGCTTCCCATCTTCATCCAGTTCGGCCTCTACTCTCCCCGAATTGACCCTGATTACGTGGGACGA
GTCCGGCTGCAGAAGGGGGCCTCTCTCCAGATTGAGGGTCTCCGGGTGGAAGACCAGGGCTGGTACGAGTGCCGC
GTGTTCTTCCTGGACCAGCACATCCCTGAAGACGATTTTGCTAACGGCTCCTGGGTGCATCTGACAGTCAATTCA
CCCCCTCAATTCCAGGAGACACCTCCTGCTGTGTTGGAAGTGCAGGAACTGGAGCCTGTGACCCTGCGTTGTGTG
GCCCGTGGCAGCCCCCTGCCTCATGTGACGTGGAAGCTCCGAGGAAAGGACCTTGGCCAGGGCCAGGGCCAGGTG
CAAGTGCAGAACGGGACGCTGCGGATCCGCCGGGTAGAGCGAGGCAGCTCTGGGGTCTACACCTGCCAAGCCTCC
AGCACTGAGGGCAGCGCCACCCACGCCACCCAGCTGCTAGTGCTAGGACCCCCAGTCATCGTGGTGCCCCCCAAG
AACAGCACAGTCAATGCCTCCCAGGATGTTTCATTGGCCTGCCATGCTGAGGCATACCCTGCTAACCTCACCTAC
AGCTGGTTCCAGGACAACATCAATGTCTTCCACATTAGCCGCCTGCAGCCCCGGGTGCGGATCCTGGTGGACGGG
AGCCTGCGGCTGCTGGCCACCCAGCCTGATGATGCCGGCTGCTACACCTGTGTGCCCAGCAATGGCCTCCTGCAT
CCACCCTCAGCCTCTGCCTACCTCACTGTGCTCTACCCAGCCCAGGTGACAGCTATGCCTCCTGAGACACCCCTG
CCCATAGGCATGCCGGGGGTGATCCGCTGCCCGGTTCGTGCCAACCCCCCACTGCTCTTTGTCAGCTGGACCAAG
GATGGAAAGGCCCTGCAGCTGGACAAGTTCCCTGGCTGGTCCCAGGGCACAGAAGGCTCACTGATCATCGCCCTG
GGGAACGAGGATGCCCTGGGAGAATACTCCTGCACCCCCTACAACAGTCTTGGTACCGCCGGGCCCTCTCCTGTG
ACCCGCGTGCTGCTCAAGGCTCCCCCAGCTTTTATAGAGCGGCCCAAGGAAGAATATTTCCAAGAAGTAGGGCGG
GAGCTGCTCATCCCCTGCTCCGCCCAAGGGGACCCTCCTCCTGTTGTCTCTTGGACCAAGGTGGGCCGGGGGCTG
CAAGGCCAGGCCCAGGTGGACAGCAACAGCAGCCTCATCCTGCGACCATTGACCAAGGAGGCCCACGGGCACTGG
GAATGCAGTGCCAGCAATGCTGTGGCCCGAGTGGCCACCTCCACGAACGTCTACGTGCTGGGCACTAGCCCTCAT
GTTGTCACCAATGTGTCCGTGGTGGCTTTGCCCAAGGGTGCCAATGTCTCCTGGGAGCCTGGCTTTGATGGTGGT
TATCTGCAGAGATTCAGTGTCTGGTACACCCCACTGGCCAAGCGTCCTGACCGAATGCACCATGACTGGGTGTCC
TTGGCAGTGCCTGTGGGGGCTGCTCACCTCCTAGTGCCAGGGCTGCAGCCCCACACCCAGTACCAGTTCAGCGTG
CTAGCTCAGAACAAGCTGGGGAGTGGTCCCTTCAGCGAAATCGTCTTGTCTGCTCCGGAAGGGCTTCCTACCACG
CCAGCTGCACCCGGGCTTCCCCCAACAGAGATACCGCCTCCCCTGTCCCCTCCGCGGGGTCTGGTGGCAGTGAGG
ACACCCCGGGGGGTACTCCTGCATTGGGATCCCCCAGAGCTGGTCCCTAAGAGACTGGATGGCTACGTCTTGGAA
GGCCGGCAAGGCTCCCAGGGCTGGGAGGTGCTGGACCCGGCTGTGGCAGGCACAGAAACAGAGCTGCTGGTGCCA
GGCCTCATCAAGGTATGTTCTCTACGAGTTCCGCCTCGTGGCCTTCGCGGGCAGCTTCGTCAGCGACCCCAGCAA
CACGGCCAACGTCTCCACTTCCGGTCTGGAGGTCTACCCTTCGCGCACGCAGCTGCCGGGCCTCCTGCCTCAGCC
CGTGCTGGCCGGCGTGGTGGGCGGAGTCTGCTTTCTGGGAGTGGCCGTCCTTGTGAGCATCCTGGCCGGCTGCCT
CCTGAACCGGCGCAGGGCTGCCCGCCGCCGCCGCAAGCGCCTCCGCCAAGATCCACCTCTTATCTTCTCTCCGAC
CGGGAAGTCAGCTGCACCCTCTGCTCTGGGCTCAGGCAGTCCTGACAGCGTGGCGAAGCTGAAGCTCCAGGGATC
CCCAGTCCCCAGCCTGCGCCAGAGTCTGCTCTGGGGGGATCCTGCCGGAACTCCCAGCCCCCACCCGGATCCTCC
ATCTAGCCGGGGACCCTTACCTCTGGAGCCCATTTGCCGGGGCCCAGACGGGCGCTTTGTGATGGGGCCCACTGT
GGCGGCCCCCCAGGAAAGGTCAGGCCGGGAGCAGGCAGAACCTCGGACTCCAGCCCAGCGTCTGGCCCGGTCCTT
TGACTGTAGCAGCAGCAGCCCCAGTGGGGCACCCCAGCCCCTCTGCATTGAAGACATCAGCCCTGTGGCACCCCC
TCCAGCAGCCCCACCCAGTCCCTTGCCAGGTCCTGGACCCCTGCTCCAGTACCTGAGCCTGCCCTTCTTCCGAGA
GATGAATGTGGATGGGGACTGGCCCCCGCTTGAGGAGCCCAGCCCTGCTGCACCCCCAGATTACATGGATACCCG
GCGCTGTCCCACCTCATCTTTCCTTCGTTCTCCAGAAACCCCTCCTGTATCCCCCAGGGAATCACTTCCTGGGGC
TGTGGTAGGGGCTGGGGCCACTGCAGAGCCCCCTTACACAGCCCTGGCTGACTGGACACTGAGGGAGCGGCTGCT
GCCAGGCCTTCTCCCTGCTGCCCCTCGAGGCAGCCTCACCAGCCAGAGCAGTGGGCGAGGCAGCGCTTCGTTCCT
GCGGCCCCCCTCCACAGCCCCCTCTGCAGGAGGCAGCTACCTCAGCCCTGCTCCAGGAGACACCAGCAGCTGGGC
CAGTGGCCCTGAGAGATGGCCCCGAAGGGAGCATGTGGTGACAGTCAGCAAGAGGAGGAACACATCTGTGGACGA
GAACTATGAGTGGGACTCAGAATTCCCTGGGGACATGGAATTGCTGGAGACTTTGCACCTGGGCTTGGCCAGCTC
CCGGCTCAGACCTGAAGCTGAGCCAGAGCTAGGTGTGAAGACTCCAGAGGAGGGCTGCCTCCTGAACACTGCCCA

FIGURE 476B

TGTTACTGGCCCTGAGGCCCGCTGTGCTGCCCTTCGGGAGGAATTCCTGGCCTTCCGCCGCCGCCGAGATGCTAC
TAGGGCTCGGCTACCAGCCTATCGACAGCCAGTCCCCCACCCCGAACAGGCCACTCTGCTGTGAACATCCCTGAT
GTGAGGCTGTGAAAAGGCATATGGACCTGCAAAGGAGGCCCCCAACCAGACAGACCTAGTTTCAAACGAGGGCAC
TGCCCCTGCCTGCCCCTTTGGTGCCCAGGCACAGACCCTGATAGTGGGTTTGGGTCACCTTGGTATGGAATGTAT
GTGCTGACCCCCTAGGTGAGTCTGGGGATTGGAACAGGGATCTTAGGTCTGCCTCTCTCTCTCTCTCTCTCTCTC
TCTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGAAGTTTTTTACAGGTGAATAAACAAAGTTTGAAAGATG

FIGURE 477

TTTCCGTGCTACCTACAGAGGGGTCCATATGGCGTTGTTCTGGATTCCCGTCGTTAACTCAAAGGGAAACTTTCA
CA**ATG**TCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACT
TAGGTGGCACCAATCTTGACTTACAGATGGAACAGTATATCTATAAAAGGAAAAGTGATGGCATCTACATCATAA
ATCTGAAGGGAACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCTATTGTTGCCATTGAAAACCCTGCTGATGTCA
GTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTG
CTGGCCACTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCTGGGAGCCATGGCTTCTTATGGTTA
CTGACCCCAGGGGC**TGA**CCATCAGCCTCTCACAGAGGCATCTTATGTTAATCTACCTACCATCGCTCTGTGTAAC
ACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCGTGCAACAACAAGGGAGCTCACTGAGTGGGTTTGATG
TGGTGGATGCTGGCTCGGGAAGTACTGTGCATGCGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCT
GATCTCTGCTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAAAAGGCAGTGACCAAG
GAGGAATTTCAGGGTGAATGGTCTGCTCCAGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAGACTGGTTT
GAAGGTATACAGGTGCCCTCTGTGCCTATTCAGCAGTTCCTACTGAACAATGGAGCACTCAGCCTGCCACGGAAT
ACTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGAATGGTCTTAAGCTGTTCTTG
CATGGGCTCTTAAGCAACATGGAAAAATGGTTGATGGAAAATAAACATCAGTTTCT

FIGURE 478

MSGALDVLQMKEEDVLKFLAAGTHLGGTNLDLQMEQYIYKRKSDGIYIINLKGTWEKLLLAARAIVAIENPADVS
VISSRNTGQRAVLKFAAATGATPIAGHFTPGTFTNQIQAAFWEPWLLMVTDPRG

FIGURE 479

AAAGGGAAACTTTCACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTG
CAGCAGGAACCCACTTAGGTGGCACCAATCTTGACTTACAGATGGAACAGTATATCTATAAAAGGAAAAGTGATG
GCATCTACATCATAAATCTGAAGGGAACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCTATTGTTGCCATTGAAA
ACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTG
GAGCCACTCCAATTGCTGGCCACTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCATCTTATGTTAATCTAC
CTACCATCGCTCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCGTGCAACAACAAGGGAG
CTCACTGAGTGGGTTTGATGTGGTGGATGCTGGCTCGGGAAGTACTGTGCATGCGTGGCACCATTTCCCGTGAAC
ACCCATGGGAGGTCATGCCTGATCTCTGCTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTG
CTGA

FIGURE 480

MSGALDVLQMKEEDVLKFLTAGTHLGGTNLDFQMEQYIYKRRSDGIYIINLKRTWEKLLLAARAIVAIENPAVVS
VISSRNTGQRAVLKFAAVTGATPIAGRFTPGNFTNQIQEASYVNLPTIALCNTDSPLHFVDIAIPCNNKGAH

FIGURE 481A

AGGTAGCAAG<u>ATG</u>GCCGCCGCTGAGGAAGGCTGTAGTGTCGGGGCCGAAGCGGACAGGGAATTGGAGGAGCTTCT
GGAAAGTGCTCTTGATGATTTCGATAAAGCCAAACCCTCCCCAGCACCCCCTTCTACCACCACGGCCCCTGATGC
TTCGGGGCCCCAGAAGAGATCGCCAGGAGACACTGCCAAAGATGCCCTCTTCGCTTCCCAAGAGAAGTTTTTCCA
GGAACTATTCGACAGTGAACTGGCTTCCCAAGCCACTGCGGAGTTCGAGAAGGCAATGAAGGAGTTGGCTGAGGA
AGAACCCCACCTGGTGGAGCAGTTCCAAAAGCTCTCAGAGGCTGCAGGGAGAGTGGGCAGTGATATGACCTCCCA
ACAAGAATTCACTTCTTGCCTAAAGGAAACACTAAGTGGATTAGCCAAAAATGCCACTGACCTTCAGAACTCCAG
CATGTCGGAAGAAGAGCTGACCAAGGCCATGGAGGGGCTAGGCATGGACGAAGGGGATGGGGAAGGGAACATCCT
CCCCATCATGCAGAGTATTATGCAGAACCTACTCTCCAAGGATGTGCTGTACCCATCACTGAAGGAGATCACAGA
AAAGTATCCAGAATGGTTGCAGAGTCATCGGGAATCTCTACCTCCAGAGCAGTTTGAAAAATATCAGGAGCAGCA
CAGCGTCATGTGCAAAATATGTGAGCAGTTTGAGGCAGAGACCCCCACAGACAGTGAAACCACTCAAAAGGCTCG
TTTTGAGATGGTGCTGGATCTTATGCAGCAGCTACAAGATTTAGGCCATCCTCCAAAAGAGCTGGCTGGAGAGAT
GCCTCCTGGCCTCAACTTTGACCTGGATGCCCTCAATCTTTCGGGCCCACCAGGTGCCAGTGGTGAACAGTGTCT
GATCATG<u>TGA</u>AACACAACACGTTTTCCTCTCTGAGTCCCAGCTATGGGGAACATCTGGAGTCAGCAGAACCATTG
GGACCTGAGGCAGGAGTGTCACCTGCGGGAGAAGTCTGCCCGCTGCCCTCTGTCATCCCATTCAAGATTGTGCCA
TACCAGCTGAGGTTTTTCCTCTGTCTCTCTAGGAATAGGGTCTGTTTCACAGGCCATTTCTGTGAACCCTACTCC
ATTGTGGTTTCTGCCACTATCAAAGTTCCAGCTACCTGCAAGGTGAAGGAAGGCATCCCTTTTGGGGCATGCACT
TTCTTTCCTTTCTCAAAATAATGTTATATGTGGCCACACTGATGTTCACCTTTACGTCCAGGGTCTTTGTGCCTT
GTCTCTACTCCCTCTCTTGGATCTGGGGAGGAGGGGCAGAGACCTGGGACTCTGTATTTCTATAGTTCTCCTGGC
AGAGCCTTTGAGAATGGGGAGAAACAGCCTGGGCTGGGGCTACAGGTCTGTCACTATGCTCTCTTGCCTTCAGAC
AGACCATTCTGAATTCTCTAAAGGGAAAGGGCTTTTGCATCTAATCACAATAGAGTTGAAAGAGAGGCCTTAGGA
TTCTCCTCTCTCTAGGTGCTGAGCCCTCACCTCCCTGTTCCAGGCTGAGAACTCAAATGGTTACCCTGCTTCTTC
CTACAATGCTGTGTGATATGGGTGAACCCAGCCCCTGACCTTCCTCTATCCCCTGCCCATCCTCCCTTTTACCTC
CTCTCTTTTTTAAACACCTGTTTATCCCAACCTTTTTGAGCTCAAGCTGTGATAAAGAAGGGCCCATCCTATTTC
CCCTCATCTAGTCCATTTACGATTCTCACTGACTCCCCGTCTTCCTGGCAGACACAAATAAACCCAGTGTCAGGT
CTAGGAAATTAATGGCTATTCTTCCCCAGATACATTCTGGCTTATTTGAGATACATGATTCTCTTAGAATCCTGT
CCCTTGGTTCAGGAAAGTAGCTTGGAAAAGGAGTAGGGGTATAGCTTGGGTCCCTTTTCCTGCAAGGCCCCATGG
GGCAGAATATAATAAATATTCTGAGTGAGGAGTGTGGTCTTTTTCTGATCTTCCTCAGCTTCCGTAAGTTGCAGA
GTGAGGTATATTAGGAGACTAGTTCTACACAATATTGTAATGCTGGGTTCCATCAACACCCACCTTCCACAACTC
AGTCTGCACCTCAGTTGGCAAAGGAGACTGGATGGCCATCTTTCCTCATGTTCCCTTGAGTATTTCAATGTAGAA
AGCCCTTCAAGTGGTATTATATTTTAACCTTTTACATTATTGTTATTAATGTTAGTAATATATTGTTATGTTTTC
TAAATTATTTTTCTTTAAGCTGACGTGGCTTTTTTTCTGTGGCTCCCAGTGGGTCTACGGACCTTGGCTGACATA
TGTTGGTAGGTACTCTGGTCAGCTCAGCTGGCTGTCCTGGTTCACTCAGAAGATAAGTCTCTCCAAAGCAAATTC
ACATGCATTATGAGTCGCTTTGAGCTTCTGACATGTCACTTGCCCCGAGGTTAAAACTTTTCACCCCTTGAAGAC
CTTACATGTTTTATGGTATTGGTGAGGAAGGAAATGTTCTCAAGGTCTCAGGCTATTTGGGAAATTCCAACTCCT
ATACCTTACCAGAGCATGGAAGAGCCCAGATCTGAATGTAAAACGTCTCTGTTCTGCCAGAGATGGAAAAAATAC
AGGTATACTTGTGATATAGTCATGGGGCTTCAGTGTCACTATTTTCTCCTTAAAGCTCCAGCCAAAAACTGGACA
AGGATAGAGAGGAGGAGGGAAGAACAAAAGAGCCCTTCTCTATGAACCTTGTGCCTTCTGTCCTACCAGTTTTCT
TTTACAGATTCTCACTTCTGCTAGCCTAGCCAGGGCTTACTCCAGGAATCTAAATAGATGCCCTAGTCCACTTTA
TCTTTGTTCCCAAGGCACTCATTTTTATTTTGATTTTGATTGAATGTGAGCAGGTTGACCTCAGGTCACACTTTG
TTCCAAAAACTTTTGGAATTATTCCAGGACTTGTGGTGGAGTTATGGTACTCTAGGGCAGTCTTTCTCAAACTAT
GTATGGTAAAGGACCAGGTTTTTTGTTTTCCAGTCCTTCACTTATCAATATGCATTCCTATTGCCGATGACAGGT
ATGGAGTTCACACTGTGTGCTGCCGACCCGGCAAGTTTGACAGCACCCAAACTGGCCAGACTGTTCTGTAGGTTA
AGTCCATTGATCATGTACTTGGATATCACAGCAACATTGAAATGCTAAAAAGTTTTTAAACACTCTCAATTTCTA
ATTCACCATGTCACAGACTGGTGAAAAAAAAAAAAAAGGTGTTCACTGACCAGCACAAGTCTGCAGATCATCTTTG
AGTAGCACTGTTTTGGGGCCCTCGGTCTCTCTGAAGACCCTAGCAGAACTGATACCTACCTGTATCTCTTGTTCT
CTCCTATTTGAGTTTCACTTCCAGAGAACTTGTTCTTCAGCAAGAATGTGTCACTAGTAAGGACATCTCTAGCAT
TTCTCTAGCCTTCCTTTTCTGCTGCTCAAAAATAATCGTTACAAAGCTTAGGTTTAAGCTGTATATGAAATATTT
ATGCGACTCTCAAACTTTAAAGGAGTTGCTCCTTTGTTCCAAAATTAAATGTGTTAGATAAATTTGTGATTGTAT

FIGURE 481B

GGGTGGCTTCATGAATTAAGAATTGAATTAATACAGACTTTTTGATAATAAAAAAAAAAAAA

FIGURE 482

MAAAEEGCSVGAEADRELEELLESALDDFDKAKPSPAPPSTTTAPDASGPQKRSPGDTAKDALFASQEKFFQELF
DSELASQATAEFEKAMKELAEEEPHLVEQFQKLSEAAGRVGSDMTSQQEFTSCLKETLSGLAKNATDLQNSSMSE
EELTKAMEGLGMDEGDGEGNILPIMQSIMQNLLSKDVLYPSLKEITEKYPEWLQSHRESLPPEQFEKYQEQHSVM
CKICEQFEAETPTDSETTQKARFEMVLDLMQQLQDLGHPPKELAGEMPPGLNFDLDALNLSGPPGASGEQCLIM

FIGURE 483A

GAGAAGGGACCTTCAGGTCCAGGCAAAGGGGGAACTTCTGTCGTGGGAACGAAAAAGAAAGAGGATTTACAGGGT
GGGGGGACAGAGGGGCAGCAGGAACCAGAAGGGAGACAGTGGCGGTCGCGGCGGGGCCGATCCGAGAGTTCCCCT
TAGAGAACGGAGCTCACGGGCGGGGAGGCCTCACCTGCTAGTAGGACGCAGAAAGACAGAAGGCGAAGGAGACCC
CGACTTCCCGGGTCAGCCCCAGAGCCACCCCCTGCCGTAGCCATCTTGCCTCTCTGCTGAGCGGAAGCCCCCGTT
CGGCTCCTGTCTGTTAGCGGCCTCTCTAGGCTACCACTGACACCGTCTCTGTGGCCCGGAGCCTAAGAGACCGGA
AGTTCGTGTTTCCAGGCGCTTCCGGAAACCGCGGGAGAGGGTCGCTGACGTGGAGGCGTCCGAAGGGCAGCAGGG
TGTGTCGGGGCTCGGATTAAGACATCGGAGTCGGAGACCTGAGAGATGTTAACCAAATTCGAGACCAAGAGCGCG
CGGGTCAAAGGGCTCAGCTTTCACCCCAAAAGACCTTGGATCCTGACTAGTTTACATAATGGGGTCATCCAGTTA
TGGGACTATCGGATGTGCACTCTCATTGACAAGTTTGATGAACATGATGGTCCAGTGCGAGGCATTGACTTCCAT
AAGCAGCAGCCACTGTTCGTCTCTGGAGGAGATGACTATAAGATTAAGGTTTGGAATTACAAGCTTCGGCGCTGT
CTTTTCACATTGCTTGGGCACTTAGATTATATTCGCACCACGTTTTTTCATCATGAATATCCCTGGATTCTGAGT
GCCTCCGATGATCAGACCATCCGAGTGTGGAACTGGCAATCTAGAACCTGTGTTTGTGTGTTAACAGGGCACAAC
CATTATGTGATGTGTGCTCAGTTCCACCCCACAGAAGACTTGGTAGTATCAGCCAGCCTGGACCAGACTGTGCGC
GTTTGGGATATTTCTGGTCTGAGGAAAAAAAACCTGTCCCCTGGTGCGGTGGAATCGGATGTGAGAGGAATAACT
GGGGTTGATCTATTTGGAACTACAGATGCAGTGGTGAAGCATGTACTAGAGGGTCACGATCGTGGAGTAAACTGG
GCTGCCTTCCACCCCACTATGCCCCTTATTGTATCTGGGGCAGATGATCGTCAAGTGAAGATCTGGCGCATGAAT
GAATCAAAGGCATGGGAGGTTGATACCTGCCGGGGCCATTACAACAATGTATCTTGTGCCGTCTTCCACCCTCGC
CAAGAGTTGATCCTCAGCAATTCTGAGGACAAGAGTATTCGAGTCTGGGATATGTCTAAGCGGACTGGGGTTCAG
ACTTTCCGCAGAGACCATGATCGTTTCTGGGTCCTAGCTGCTCACCCTAACCTTAACCTCTTTGCAGCAGGCCAT
GATGGTGGTATGATTGTGTTTAAGCTGGAACGGGAACGGCCAGCCTATGCTGTTCATGGCAATATGCTACACTAT
GTCAAGGACCGATTCTTACGACAGCTGGATTTCAACAGCTCCAAAGATGTAGCTGTGATGCAGTTGCGGAGTGGT
TCCAAGTTTCCAGTATTCAATATGTCATACAATCCAGCAGAAAATGCAGTCCTGCTTTGTACAAGAGCTAGCAAT
CTAGAGAATAGTACCTATGACCTGTACACCATCCCTAAAGATGCTGACTCCCAGAATCCTGATGCGCCTGAAGGG
AAACGATCCTCAGGCCTGACAGCCGTTTGGGTCGCTCGAAATCGGTTTGCTGTCCTAGATCGGATGCATTCGCTT
CTGATCAAGAATCTGAAGAATGAGATCACCAAAAAGGTACAGGTGCCCAACTGTGATGAGATCTTCTATGCTGGC
ACAGGCAATCTCCTGCTTCGAGATGCGGACTCTATCACACTCTTTGACGTACAGCAGAAGCGGACTCTGGCATCT
GTGAAGATTTCTAAAGTGAAATACGTTATCTGGTCAGCAGACATGTCACATGTAGCACTACTAGCCAAACACGCC
ATTGTGATCTGTAACCGCAAACTGGATGCTTTATGTAACATTCATGAGAACATTCGTGTCAAGAGTGGGGCCTGG
GATGAGAGTGGGGTATTTATCTATACCACAAGCAACCACATCAAATATGCTGTCACCACTGGGGACCACGGGATC
ATTCGAACTCTGGATTTACCCATCTATGTCACACGGGTGAAGGGCAACAATGTATACTGCCTAGACAGGGAGTGT
CGTCCCCGGGTACTCACCATTGATCCCACTGAGTTCAAATTCAAGCTGGCCCTGATCAACAGAAAATATGATGAG
GTACTGCACATGGTGAGGAATGCCAAACTAGTTGGCCAGTCTATTATTGCTTATCTCCAGAAGAAGGGCTATCCT
GAAGTGGCACTGCATTTTGTCAAGGATGAGAAAACTCGCTTTAGTCTGGCACTGGAGTGTGGAAACATTGAGATT
GCTCTGGAAGCAGCCAAAGCACTGGATGACAAGAACTGCTGGGAAAAGCTGGGAGAAGTGGCCCTGCTGCAGGGG
AACCACCAGATTGTGGAAATGTGCTATCAGCGTACCAAAAACTTTGACAAACTTTCCTTCCTGTATCTTATCACT
GGCAACTTAGAAAAACTTCGCAAGATGATGAAGATTGCTGAGATCAGAAAGGACATGAGTGGCCACTATCAGAAT
GCCCTATACCTGGGTGATGTGTCAGAGCGTGTGCGGATCCTGAAGAACTGTGGACAGAAGTCCCTGGCCTATCTC
ACAGCTGCTACCCATGGCTTAGATGAAGAAGCTGAGAGCCTAAAGGAGACATTTGACCCAGAGAAGGAGACAATC
CCAGACATTGACCCTAATGCCAAGCTGCTCCAGCCACCTGCACCTATCATGCCATTGGATACCAATTGGCCTTTA
TTGACTGTATCCAAAGGATTTTTTGAAGGCACCATTGCCAGCAAAGGGAAGGGAGGAGCACTGGCTGCTGACATT
GACATTGACACTGTTGGTACAGAGGGCTGGGGAGAGGATGCAGAGCTGCAGTTGGATGAAGATGGGTTTGTGGAG
GCTACAGAAGGTTTGGGGGATGATGCTCTTGGCAAGGGACAGGAAGAAGGAGGTGGCTGGGATGTAGAAGAAGAT
CTGGAGCTCCCTCCTGAGCTGGATATATCCCCTGGGGCAGCTGGTGGGGCTGAAGATGGTTTCTTTGTGCCCCCA
ACCAAGGGAACAAGTCCAACTCAGATCTGGTGTAATAACTCTCAGCTTCCAGTTGATCACATCCTGGCAGGCTCT
TTCGAAACAGCCATGCGGCTCCTTCATGACCAAGTAGGGGTAATCCAGTTTGGCCCCTACAAGCAACTGTTCCTA
CAGACATACGCCCGAGGCCGCACAACCTATCAGGCTCTGCCCTGCCTACCCTCCATGTATGGCTATCCTAATCGC
AACTGGAAGGATGCAGGGCTGAAGAATGGTGTACCAGCTGTGGGCCTGAAGCTTAATGACCTCATCCAACGGTTG
CAGCTGTGCTACCAGCTCACCACAGTTGGCAAATTTGAGGAGGCTGTGGAAAAATTCCGTTCCATCCTTCTCAGT

FIGURE 483B

GTGCCACTTCTTGTTGTGGACAATAAACAAGAGATTGCAGAGGCCCAGCAGCTCATCACCATTTGCCGTGAGTAC
ATTGTGGGTTTGTCCGTGGAGACAGAAAGGAAGAAGCTGCCCAAAGAGACTCTAGAACAGCAGAAGCGCATCTGT
GAGATGGCAGCCTATTTCACCCACTCAAACCTGCAGCCTGTGCACATGATCCTGGTGCTGCGTACAGCCCTCAAT
CTGTTCTTCAAGCTCAAGAACTTCAAGACAGCTGCCACCTTTGCTCGGCGCCTACTAGAACTCGGGCCCAAGCCT
GAGGTGGCCCAACAGACCCGAAAAATCCTGTCTGCCTGTGAGAAGAATCCCACAGATGCCTACCAGCTCAATTAT
GACATGCACAACCCCTTTGACATTTGTGCTGCATCATATCGGCCCATCTACCGTGGAAAGCCAGTAGAAAAGTGT
CCACTCAGTGGGGCCTGCTATTCCCCTGAGTTCAAAGGTCAAATCTGCAGGGTCACCACAGTGACAGAGATTGGC
AAAGATGTGATTGGTTTAAGGATCAGTCCTCTGCAGTTTCGCTAAGGCCCCCTTTGTGTGCATGGGTCAGTCACC
ATATGTTCCCCCCAGAGAATGTGTCTATATCCTCCTTCTAACAGCACCTTCCCCCTGCAGCTACTCTTCAGATCT
GGCTCTCTGTACCCTAAAACCTAGTATCTTTTTCTCTTCTATGGAAAATCCGAAGGTCTAAACTTGACTTTTTTG
AGGTCTTCTCAACTTGACTACAGTTGTGCTCATAATTGTCCTTGCCTTTCCAGCTTAATTATTTTAAGGAACAAA
TGAAAACTCTGGGCTGGGTGGAGTGGCTCATACCTGTAATCCCAGCACTTTGGGAGGCTACGGTGGGCAGATCAT
CTGAGGCCAGGAGTTCGAGACCTGCCTGGCCAACATGGCAACACCCCGTCTCTAATAAAAATATAAAAATTAGCC
TGGCATGGTAGCATGCGCCTATAGTCCCAGCTGCTCAGGAGGCTGAGGCATGAGAATCGCTTGAACCTAGGAGGT
GGAGGTTGCATTCAACTGAGATCATACCACTTCATTCCAGCCTGGGTGACAGAGCAAGACTCTGTCTCAAAAAAA
AAAAAAAGGAAAACTCTGTGATGGACATTTGTTTAGTAAATCCCTTCAGTATTTATCCCTCCTTTCCCCACAGCA
GCTTTCTTTCCTGTCAACTAGAAAGGAGCAGGATGTAATAAATACATTTTGGTGTGACTAGGCCACACCAACTCT
TAATCATCTCCCATTTTCCTTAGACATTTAAATTTCAAGGCAGGTACCCTCTGTGTACTCAGAAATTTGAAGAAG
TTATTTGGTTTTCCAAAATGCACACTGCGGGTTATTGATTTGTTCTTTACAACTATTGTTCTCATATTTCTCACA
CTAAATAAATCTCTATGAGAGCTTCTTG

FIGURE 484

AGCTGCGGTGTTGTGCTGTGGGGAAGGGAGAAGGATTTGTAAACCCCGGAGTGAGGTTCTGCTTACCCGAGGCCG
CTGCTGTGCGGAGACCCCCGGGTGAAGCCACTGTCATCATGTCTGACCAGGAGGCAAAACCTTCAACTGAGGACT
TGGGGGATAAGAAGGAAGGTGAATATATTAAACTCAAAGTCATTGGACAGGATAGCAGTGAGATTCACTTCAAAG
TGGTTCCAATGAATTCATTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCTGATAATCATACTCC

FIGURE 485

GAAGGATTTGTAAACCCCGGAGTGAGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGAGACCCCCGGGTGAAGCC
ACTGTCATCATGTCTGACCAGGAGGCAAAACCTTCAACTGAGGACTTGGGGGATAAGAAGGAAGGTGAATATATT
AAACTCAAAGTCATTGGACAGGATAGCAGTGAGATTCACTTCAAAGTGAAAATGACAACACATCTCAAGAAACTC
AAAGAATCATACTGTCAAAGACAGGGCGTTCCAATGAATTCATTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCT
GATAATCATACTCCAAAAGAACTGGGAATGGAGGAAGAAGATGTGATTGAAGTTTATCAGGAACAAATGGGGGGT
CATTCAACAGTTTAGATATTCTTTTTATTTTTTTTCTTTTCCCTCAATCCTTTCTCATTTTTAAAAATAGTTCTT
TTGTAATGTGGTGTTAAAAACGGAATTGAAAACTGGCACCCCATCTCTTTGAAACATCTGGTAATCTGAATTCTA
GTGCTCATTATTCATTATTGTTTATTTCATTGTGCTGATTTTTGGTGATCAAGCCTCAGTCCCCTTCATATTAC
CCTCTCCTTTTTATTGTGGTGATAAATAAGATTGACCAATGCAAGCGTTCATAATAACTTGCGAATTGGCCCTGA
TGTTCTAGCATGTGATTACTTCACT

FIGURE 486

GTTTGCCAAAATCCCAGGCAGCATGGACCTCAGTCTTCTCTGGGTACTTCTGCCCCTAGTCACCATGGCCTGGGG
CCAGTATGGCGATTATGGATACCCATACCAGCAGTATCATGACTACAGCGATGATGGGTGGGTGAATTTGAACCG
GCAAGGCTTCAGCTACCAGTGTCCCCAGGGGCAGGTGATAGTGGCCGTGAGGAGCATCTTCAGCAAGAAGGAAGG
TTCTGACAGACAATGGAACTACGCCTGCATGCCCACGCCACAGAGCCTCGGGGAACCCACGGAGTGCTGGTGGGA
GGAGATCAACAGGGCTGGCATGGAATGGTACCAGACGTGCTCCAACAATGGGCTGGTGGCAGGATTCCAGAGCCG
CTACTTCGAGTCAGTGCTGGATCGGGAGTGGCAGTTTTACTGTTGTCGCTACAGCAAGAGGTGCCCATATTCCTG
CTGGCTAACAACAGAATATCCAGGTCACTATGGTGAGGAAATGGACATGATTTCCTACAATTATGATTACTATAT
CCGAGGAGCAACAACCACTTTCTCTGCAGTGGAAAGGGATCGCCAGTGGAAGTTCATAATGTGCCGGATGACTGA
ATACGACTGTGAATTTGCAAATGTTTAGATTTGCCACATACCAAATCTGGGTGAAAGGAAAGGGGCCGGGGACAG
GAGGGTGTCCACATATGTTAACATCAGTTGGATCTCCTATAGAAGTTTCTGCTGCTCTCTTTCCTTCTCCCTGAG
CTGGTAACTGCAATGCCAACTTCCTGGGCCTTTCTGACTAGTATCACACTTCTAATAAAATCCACAATTAAACCA
TGTTTCTCACTTTTCACATGTTTCATAGCAACTGCTTTATATGACTGATGATGGCTTCCTTGCACACCACATATA
CAGTGCGCATGCTTACAGCCGGGCTTCTGGAGCACCAGCTGCAGCCTGGCTACTGCTTTTTACTGCAGAATGAAC
TGCAAGTTCAGCATAGTGGAGGGGAGAGGCAGAACTGGAGGAGAGGTGCAGTGAAGGTTCTCTACAGCTAAGCCT
GTTTGAATGATACGTAGGTTCCCCACCAAAAGCAGGCTTTCTGCCCTGAGGGACATCTTCCCACTCCCCTGCTCC
ACATGAGCCATGCATGCTTAGCAATCCAAGTGCAGAGCTCTTTGCTCCAGGAGTGAGGAGACTGGGAGGTGAAAT
GGGGAAATGGAAGGGTTTGGAGGCAGAGCTGAAAACAGGGTTGGAAGGATTTCCTGAATTAGAAGACAAACGTTA
GCATACCCAGTAAGGAAAATGAGTGCAGGGGCCAGGGGAACCCGTGAGGATCACTCTCAAATGAGATTAAAAACA
AGGAAGCAGAGAATGGTCAGAGAATGGGATTCAGATTGGGAACTTGTGGGGATGAGAGTGACCAGGTTGAACTGG
GAAGTGGAAAAAGGAGTTTGAGTCACTGGCACCTAGAAGCCTGCCCACGATTCCTAGGAAGGCTGGCAGACACCC
TGGAACCCTGGGGAGCTACTGGCAAACTCTCCTGGATTGGGCCTGATTTTTTGGTGGGAAAGGCTGCCCTGGGG
ATCAACTTTCCTTCTGTGTGTGGCTCAGGAGTTCTTCTGCAGAGATGGCGCTATCTTTCCTCCTCCTGTGATGTC
CTGCTCCCAACCATTTGTACTCTTCATTACAAAAGAAATAAAAATATTAACGTTC

FIGURE 487

MDLSLLWVLLPLVTMAWGQYGDYGYPYQQYHDYSDDGWVNLNRQGFSYQCPQGQVIVAVRSIFSKKEGSDRQWNY
ACMPTPQSLGEPTECWWEEINRAGMEWYQTCSNNGLVAGFQSRYFESVLDREWQFYCCRYSKRCPYSCWLTTEYP
GHYGEEMDMISYNYDYYIRGATTTFSAVERDRQWKFIMCRMTEYDCEFANV

FIGURE 488

AGAGGAAGCCAAGAACGGTGAAAAGGCCAGGCGGAGTTCAGAGGAGGTGGACGGCCAGCACCCGGCCCAAGAGGA
GGTCCCGGAATCGCCCCAGACCTCTGGCCCAGAGGCAGAAAATAGGTGTGGGAGCCCCAGGGAGGAAAAGCCAGC
TGGAGAGGAAGCAGAG**ATG**GAAAAGGCTACAGAGGTGAAGGGGGAGAGGGTGCAAAATGAAGAGGTGGGACCTGA
ACATGACAGCCAAGAAACAAAGAAGCTGGAGGAGGGAGCTGCAGTGAAGGAGACCCCCCACAGTCCCCCTGGAGG
AGTGAAGGGCGGAGATGTCCCCAAGCAGGAAAAAGGCAAGGAAAAACAACAGGAGGGGGCAGTGCTCGAGCCAGG
CTGCAGCCCCCAGACCGGCCCTGCCCAGCTGGAGACCAGCAGTGAGGTCCAGAGCGAGCCAGCAGTCCCCAAGCC
GGAGGATGACACTCCTGTCCAGGACACTAAAATG**TGA**AGAACAGCTCATTGTGCCCCAGTGATGAAGTTGCTGGA
CACATCTCTTTGCAGGTAGCAGCAACAGTTGTAGCAGCAGCAGACGAAGCCATTGCAGAGGCAGAATATGCTGAG
TGTCTGGAGTCAGCCTGAAGACACAGGGTGGATTATTTCCTGGCCTCCACACCAAACGTTCCCTTGCAGATGGAG
ACTGAATCTGAGGGCAGCAGACTTTTATCAGCTTGAGTTTATGTCATTTGATGGACTTGGTTCAACAACAAGAAC
TTACTTAAAACAATGTACTGTGGTGATGAGTCCCAGGGGCACTGGTCAGCCTGTGGAGCCCTGGATGCTATCCAC
ACCCACCTATCCCTGCAGCTAATTTAGCTGATCTCTAATTTAACTGAGCTCTAATTTAGCTGATCAGATTTTGCT
TGGGTAAAGTTCCTTTTTAATGTTCTAAAGTGTTTACGGTTCTCAAATATCAGTTAAAAACTAATTTTAGGTGGC
CATAAACATAAAATAGAAACCCTGTAAGTTACAGAAGACCCTAAATTGTATCAAAACCCTAGAGACAACTTTTCA
ATTTGATCCAAATTTGAACTGGCCAACCAGTCTTTAAAACACTGGACTAGAAGAGATAATGATTGAAACATTTAA
AAAAAAAAAGTGCTCCATTCGCAGGAGCTTTTCCTGTCCTGTGGTTTTCCAGTTGGTGACCACCATGGGAGGTCG
CTGGCTCGGCTCACTCCCTTCTCCCACCCTTGAGAATGTGGAGAACTCCCATGGAGAGGCAGAATGGCAGGAGGT
TTCATGTCCCGCGTTGCATCTCCTCCTGAAAGAAAAGCAGTGATACCTGAATAATGCTGGCTCTCCGATTGATCC
TGTGAGGATGAATTTGCATTTCCAGAATCCTTGAGCATGGATTAGATGTTTCCTGGGAGGTGCCTTGAGTACCAT
TATGTGCAAGCTACATAATTAAAACATTTTTCTTAGTTTCCCTGGGAAGCTTTTCTTGACTCACAGCCCAGGTTC
TTCTGCCCAACACAAAAGGAGTGAGTTGGGGTCTTTAGTCTCTTCTTATTGGGTAGCTCTTGCTTTAATATTCTG
TTTGGTGAGTGTAAGGGATTCTGCAAGGGACAGGGGGCCTGACTACCCAGTCTTTGACTTGTATCCTCTCCCCTC
TTCATACACTCCTGCTGAAAAATGTTAATCCAAATACACATTTAAACTTAGGGTCGGTCCTTATTCTGATTTGAG
TATTTTAATGTCTCAGTGTGCTGATTTGGTAGTTGGAAGAATTATTCTTCTGGAGGTCTGTTAGACTACATCCTA
CACTGACTTCAGAAAACAGTCTGTCAGACAAAAAGGCCTTATGTCACCACTGGTACCTCAGTTTCCTCATCCCAT
TTACAGTTTTTCTAACTCCAGGGTAGTGTTTAGTGTTAATATTTGGGATATATTTTTTTCAAAACTGTTTTTAA
GTAGTTTGTAATTTGTAACAAACTTGTAACCTGGTTGGGACTGATATTGTCATAGCTATGATAAACTTTGGATAT
TAGCAGAATTTGGGAAAAAAAAAAAAAAAAAAAAAA

FIGURE 489

MEKATEVKGERVQNEEVGPEHDSQETKKLEEGAAVKETPHSPPGGVKGGDVPKQEKGKEKQQEGAVLEPGCSPQT
GPAQLETSSEVQSEPAVPKPEDDTPVQDTKM

FIGURE 490

GGACGTTGAGAGAACGAGGAGGAAGGAGAGAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCG
CAGCAGGGCTACAGTGCTTACAACACCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAA
AGCTATGGAACCTATGGACAGCCCATTGATGTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACC
GCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAGGCATACAGCCAGCCT
GTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCT
CAATCTGCATATGGCACTCAGCCTGCTTATCCAGCTTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTG
CAGAATGGAAACAAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGA
TATGGACAGAGTAACTGCAGTTATCCCCAGGTACCTGGGAGCTACTCCATGCAGCCAGTCACCGCACCTCCATCC
TACCCTCCTACCAGCTATTCCTCTACACAGCCAACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTAT
GGGAAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTCAACAAAGCAGCTATGGGCAGCTGCCTCCCACTAGT
TACCCACCCCAAACTTGATCCTACAGCCAAGCTCCAAGTCAGTATAGCTAACAGAGCAGCAGCTACGGGCAGCAG
AGTTCATTCTGACAGGACCACCCCAGTAGC**ATG**GGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACTAGGA
GAGAACCGGAGCATGAGTGGCCCTGATAACTGGGGCAGGGGAAGAGGGGGATTTGATCGTGGAGGCATGAGCAGA
GGTGGGCGGGGAGGAGGATGCGGTGGAATGGGCAGCGCTGGAGAGCAAGTTGGCTTCAATAAGCCTGGTGGACCC
ATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGACAACAGTGCAATTTAT
GTACAAGGATTAAATGACAATGTGACTCTAGATGATCTGGTAGACTTCTTTAAGCAGTGTGGGGTTGTTAAGATG
AACAAGAGAACTGAGCAACCCATGATCCACACCTACCTGGACAAGGAAACAAGAAAGCCCAAAGGTGATGCCACA
GTGTCCTGTGAAGACTCACCTACTGCCAAAGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAAA
CTTAAAGTCTCTCTTGCTCGGAAGAGGCCTCCAGTGAACAGTATGCAGGGTGGTATGCCACCCCATGAGGGCAGA
GGGATGCCACCACCACTCTGCGGAGGTCCAGGAGGCCCAGGAAGTCCTGGGGGACCCATGGGTCACATGGGAGGC
CGTGGAGGAGATAGAGGAGGCCTCCCTCCAAGAGGACCCCAGGGTTCCCGAGGGAACACCTCTGGAGGAGGAAAC
GTCCAGCACCAAGCTGGAGACAGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAG
AGCAACAAGTGTAAGGCTCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTCCCACCCCCGGGTGGTGATCATGGC
AGAGGTGGCCCTGGTGGCATGTGGGGAGGAAGAGGTGGCCTCATGGATCATGGTGGTCCCGGTGGAATGTTCAGA
GGTGGCTGTGGTAGAGACAGAAGTGGCTTCTGTGGTGGCTGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGAC
AAGGTGGCCCTGGGGGGCCCCCGGACCTTTGATGTAACCAATGGGAGGAAGAAGAGGAGGACG**TGA**AGGACCTGG
AAAAACGGATAAAGGCGAGCACTGTCAGGAGCGCAGAGATCAGCCCTACTAGATGCAGAGAACCCGCAGAGCTGC
ATTGACTACCAGATTTATTTTTTAAACCAGAAAATGTTTTAAATTTATAATTCCATATTTATAATGTTGGCCACA
ACATTATGATTATTCTTTCTCTGTACTTTAGTATTTTTCACCATTTGTGAAGAAACATTAAAACAAGTTAAATGG
TA

FIGURE 491

MGVYGQESGGFSGLGENRSMSGPDNWGRGRGGFDRGGMSRGGRGGGCGGMGSAGEQVGFNKPGGPMDEGPDLDLG
PPVDPDEDSDNSAIYVQGLNDNVTLDDLVDFFKQCGVVKMNKRTEQPMIHTYLDKETRKPKGDATVSCEDSPTAK
AAVEWFDGKDFQGSKLKVSLARKRPPVNSMQGGMPPHEGRGMPPPLCGGPGGPGSPGGPMGHMGGRGGDRGGLPP
RGPQGSRGNTSGGGNVQHQAGDRQCPNPGCGNQNFAWRTESNKCKAPKPEGFLPPPFPPPGGDHGRGGPGGMWGG
RGGLMDHGGPGGMFRGGCGRDRSGFCGGWAWTEVALVEEDKVALGGPRTFDVTNGRKKRRT

FIGURE 492

AACGAGGAGGAAGGAGAGAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTAC
AGTGCTTACAACACCCAGCCCACTCAAGGATATGCACAGCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGG
TTATACTACTCCAACTGCCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCAC
CACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAATCTGCATATGGCACTCAGCCTGCTTATCCAGC
TTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTGCAGAATGGAAACAAGCCCACTGAGACTAGTCAACC
TCAATCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAGTAACTGCAGTTATCCCCAGGTACC
TGGGAGCTACTCCATGCAGCCAGTCACCGCACCTCCATCCTACCCTCCTACCAGCTATTCCTCTACACAGCCAAC
TAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGAAACCGAGCAGCTATGGACAGCAGAGTAGCTA
TGGTCAACAAAGCAGCTATGGGCAGCTGCCTCCCACTAGTTACCCACCCCAAACTTGATCCTACAGCCAAGCTCC
AAGTCAGTATAGCTAACAGAGCAGCAGCTACGGGCAGCAGAGTTCATTCTGACAGGACCACCCCAGTAGCATGGG
TGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACTAGGAGAGAACCGGAGCATGAGTGGCCCTGATAACTGGGG
CAGGGGAAGAGGGGGATTTG

FIGURE 493

AACGAGGAGGAAGGAGAGAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTAC
AGTGCTTACAACACCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACC
TATGGACAGCCCATTGATGTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACCGCCTATGCAACT
TCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTAT
GGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAATCTGCATAT
GGCACTCAGCCTGCTTATCCAGCTTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTGCAGAATGGAAAC
AAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCACCAAGCTGGAGACAGGCAGTGT
CCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAGAGCAACAAGTGTAAGGCTCCAAAGCCTGAA
GGCTTCCTCCCGCCACCCTTCCCACCCCCGGGTGGTGATCATGGCAGAGGTGGCCCTGGTGGCATGTGGGGAGGA
AGAGGTGGC

FIGURE 494

GGAGGAAGGAGAGAAAATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGC
TTACAACACCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGG
ACAGCCCATTGATGTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACCGCCTATGCAACTTCTTA
TGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCAC
TGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAATCTGCATATGGCAC
TCAGCCTGCTTATCCAGCTTATGGGCAGCAGCCAGTAGCCACTGCACCTACAAGACTGCAGAATGGAAACAAGCC
CACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAGTAACTG
CAGTTATCCCCAGGTACCTGGGAGCTACTCCATGCAGCCAGTCACCGCACCTCCATCCTACCCTCCTACCAGCTA
TTCCTCTACACAGCCAACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGCAGCTGCCTCCCAC
TAGTTACCCACCCCAAACTTGATCCTACAGCCAAGCTCCAAGTCAGTATAGCTAACAGAGCAGCAGCTACGGGCA
GCAGAGTTCATTCTGACAGGACCACCCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACT
AGGAGAGAACCGGAGCATGAGTGGCCCTGAT

FIGURE 495

TTTCCGGTGCTATGCCCCGGAAGCGGAAGTGCGATCTTCGGGCTGTCAGAGTTGGTCTGTTACTCGGTGGTGGCG
GAGTCTACGGAAGCCGTTTTCGCTTCACTTTTCCTGGCTGTAGAGCGCTTTCCCCCTGGCGGGTGAGAGTGCAGA
GACGAAGGTGCGAGATGAGCACTATGTTCGCGGACACTCTCCTCATCGTTTTTATCTCTGTGTGCACGGCTCTGC
TCGCAGAGGGCATAACCTGGGTCCTGGTTTACAGGACAGACAAGTACAAGAGACTGAAGGCAGAAGTGGAAAAAC
AGAGTAAAAAATTGGAAAAGAAGAAGGAAACAATAACAGAGTCAGCTGGTCGTCTATCAATGGTTCGAATGAAAT
CCATGTTTGCTATTGGCTTTTGTTTTACTGCCCTAATGGGAATGTTCAATTCCATATTTGATGGTAGAGTGGTGG
CAAAGCTTCCTTTTACCCCTCTTTCTTACATCCAAGGACTGTCTCATCGAAATCTGCTGGGAGATGACACCACAG
ACTGTTCCTTCATTTTCCTGTATATTCTCTGTACTATGTCGATTCGACAGAACATTCAGAAGATTCTCGGCCTTG
CCCCTTCACGAGCCGCCACCAAGCAGGCAGGTGGATTTCTTGGCCCACCACCTCCTTCTGGGAAGTTCTCTTGAA
CTCAAGAACTCTTTATTTTCTATCATTCTTTCTAGACACACACACATCAGACTGGCAACTGTTTTGTAGCAAGAG
CCATAGGTAGCCTTACTACTTGGGCCTCTTTCTAGTTTTGAATTATTTCTAAGCCTTTTGGGTATGATTAGAGTG
AAAATGGCAGCCAGCAAACTTGATAGTGCTTTTGGTCCTAGATGATTTTTATCAAATAAGTGGATTGATTAGTTA
AGTTCAGGTAATGTTTATGTAATGAAAAACAAATAGCATCCTTCTTGTTTCATTTACATAAGTATTTTCTGTGGG
ACCGACTCTCAAGGCACTGTGTATGCCCTGCAAGTTGGCTGTCTATGAGCATTTAGAGATTTAGAAGAAAAATTT
ACAAGCCAAATACATGACATAAGATCAATAAAGAGGCCAAATTTTTAGCTGTTTTATGTACAAGGAGAGATCTGT
TTCATTTTGTTTTGCCGTATTTCTAGATATAAGTTTTAGCATGGGCCAGGAAGGACTAAAATAAAAGTTTTTAAG
GTACTG

FIGURE 496

MSTMFADTLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGRQQKKKIERQEEK
LKNNNRDLSMVRMKSMFAIGFCFTALMGMFNSIFDGRVVAKLPFTPLSYIQGLSHRNLLGDDTTDCSFIFLYILC
TMSIRQNIQKILGLAPSRAATKQAGGFLGPPPPSGKFS

FIGURE 497

AGACAGTTTTGAAGTTTTCAAAGACTGGCTCTGCTGTTAAGAAGTTGTACTTAAAGCGGAGGAGCTAAGCCACCT
GCCAAA**ATG**TGCAAAGGACTTGCAGCTTTGCCCCACTCATGCCTGGAAAGGGCCAAGGAGATTAAGATCAAGTTG
GGAATTCTCCTCCAGAAGCCAGACTCAGTTGGTGACCTTGTCATTCCGTACAATGAGAAGCCAGAGAAACCAGCC
AAGACCCAGAAAACCTCGCTGGACGAGGCCCTGCAGTGGCGTGATTCCCTGGACAAACTCCTGCAGAACAACTAT
GGACTTGCCAGTTTCAAAAGTTTCCTGAAGTCTGAATTCAGTGAGGAAAACCTTGAGTTCTGGATTGCCTGTGAG
GATTACAAGAAGATCAAGTCCCCTGCCAAGATGGCTGAGAAGGCAAAGCAAATTTATGAAGAATTCATTCAAACG
GAGGCTCCTAAAGAGGTGAATATTGACCACTTCACTAAGGACATCACAATGAAGAACCTGGTGGAACCTTCCCTG
AGCAGCTTTGACATGGCCCAGAAAAGAATCCATGCCCTGATGGAAAAGGATTCTCTGCCTCGCTTTGTGCGCTCT
GAGTTTTATCAGGAGTTAATCAAG**TAG**TAATTTAGCCAGGCTATGAAATCATCCTGTGAGTTATTTCCTCCATAA
TAACCCTGCATTTCCCATTAATCTACATATCTTCCCACAGCAGCTTTGCTCAGTGATACCCACATGGGAAAAATC
CCAGGGGATGTTGCTTACTCTTTTTGCCCACACTGCTTTGGATACTTATCTACTGTCCGAAGGCCTTCTTTCCCC
ACTCAATTCTTCCTGCCCTGTTATTAATTAAGATATCTTCAGCTTGTAGTCAGACCCAATCAGAATCACAGAAAA
ATCCTGCCTAAGGCAAAGAAATATAAGACAAGACTATGATATCAATGAATGTGGGTTAAGTAATAGATTTCCAGC
TAAATTGGTCTAAAAAAGAATATTAAGTGTGGACAGACCTATTTCAAAGGAGCTTAATTGATCTCACTTGTTTTA
GTTCTGATCCAGGGAGATCACCCCTCTAATTATTTCTGAACTTGGTTAATAAAAGTTTATAAGATTTTTATGAAG
CAGCCACTGTATGATATTTTAAGCAAATATGTTATTTAAAATATTGATCCTTCCCTTGGACCACCTTCATGTTAG
TTGGGTATTATAAATAAGAGATACAACCATGAATATATTATGTTTATACAAAATCAATCTGAACACAATTCATAA
AGATTTCTCTTTTATACCTTCCTCACTGGCCCCCTCCACCTGCCCATAGTCACCAAATTCTGTTTTAAATCAATG
ACCTAAGATCAACAATGAAGTATTTTATAAATGTATTTATGCTGCTAGACTGTGGGTCAAATGTTTCCATTTTCA
AATTATTTAGAATTCTTATGAGTTTAAAATTTGTAAATTTCTAAATCCAATCATGTAAAATGAAACTGTTGCTCC
ATTGGAGTAGTCTCCCACCTAAATATCAAGATGGCTATATGCTAAAAAGAGAAAATATGGTCAAGTCTAAAATGG
CTAATTGTCCTATGATGCTATTATCATAGACTAATGACATTTATCTTCAAAACACCAAATTGTCTTTAGAAAAAT
TAATGTGATTACAGGTAGAGGCCTTCTAGGTGAGACACTTTTAAGGTACACTGCATTTTGCAGAAAAAAAAAAAA
AAAAGTAATCTTTTAGCAACCCCAGTATTCCTTCACTATTTCGCTTCCTGCATTAGCAAATTTTACTTACAGTCA
AAAGTGCAGATTTATACTCCTGACGTGTCTCATTCACAGCTAAATAATAGGCCATAGGACTTTTGGTAGGTTTAA
ACTTTTAATTCTGTATTTCATGATTATAAGTCTTGCTAGAATTTTTTCTAATCTTTAGTAGATTTGATTAAATAA
TGATTCACAGAATTTAGTAACAGAATCAAACTAAGCCATGTATGAGGGTAATCGAGATGAGGATATTAACTCAAA
AGAAATAGGGTGATTTTTAAAGGATTAATAAAATTCTGAAATGTTAAGTAG

FIGURE 498

MCKGLAALPHSCLERAKEIKIKLGILLQKPDSVGDLVIPYNEKPEKPAKTQKTSLDEALQWRDSLDKLLQNNYGL
ASFKSFLKSEFSEENLEFWIACEDYKKIKSPAKMAEKAKQIYEEFIQTEAPKEVNIDHFTKDITMKNLVEPSLSS
FDMAQKRIHALMEKDSLPRFVRSEFYQELIK

FIGURE 499

GACACCTTTTAAAATGCAGAACTAACTGAGGCATTTCAGTAACTTTGCTTTCAAATCAATAAAGTCAA**ATG**TATG
GAAACATTTTGTGCCCTACTCTCCATACCCTGTGTACTCAAATTCTCTACTGTATGAATTATGCTTTAAGTAGAA
TTCAGTGCCAAGGAGAACTTGGTGAAATAAATTATTTAATTTTTTTTTATCCTTTACAAAGCCATGGATTTTA
TTTGGTTGATGTGTGCTCTGTACACAAGCCATTTCAATAGGATGGAGCTGTTAATTATTTCCAAAGAGTAATAG
ACATGCAAAAGTTTCAA**TAA**AAACTGGGCCATTAACAAATAAATTAATAAACTAATAAGCATTCCCTTCTAGGTT
TTTGCCAAACTGCCTATCCAATAACAAATTTGAGAATCGTTGAAAAAGCTAGTTATATTTCAGAGAAATGATTTT
CATTATTGAAACTGTTCTCCCTAGCAGGCCATTTTCCCTTTTTCCTGGGAGTTTAGCAAGTTTAGGAGAGAATAG
TCATGAAAAGAAAGGGAAGAAAGGGGAGAAGGGAAGAGGTTAAAAAGTAAGTGCTCAGACCTATGAACGTAATCC
CTTTGCTAGAAATATTTAAGAGCAGCTCAGCTTGGTTGAAACTGAGTTTTGTCATCTTCCATATTTGCAGGAAGG
TATTTTCTGACTTGCAATGCAGCTAGATGTAAAATTTTATTTTATCATCCTAGAAAGCCTTGACTAGAAAAATGA
ATAAATATTGAGGGTTTCCTGTCCATATCTGGCTTGCATGTGCCAGAAAGCAGAGAATAGAAAATGTAATCTCCA
ACATCCAAGCATCGAAACCCAAGGGGTAGGCAATTCTATGTAGGTTTTGGACATGAAGTTTGGTGCATCTTGGTT
TATGCTGGCTCAACTGCTATTAAACCTCTCTGGCTTATAGTCTCTTCATTCTATTAGACAAGCACGTATCGAACA
CTTGCTTCGCACAAGGCTCTTTAGTTAACAATTTAGCAGCTACTGTTTGTGTTAAACACACTTTTCACCAAATAG
GTTCTGAGGCAAACGAGAGCAATGACTATTTAAAGAAAGGCTTTCCCAGCATCACTTACACATCCCAAAACTAAA
AAGATCAACTCTTCCAACTGAGAAAAGACTCCTGGCTTTGAATGGAAACTTACAGCAGAGAGTCACAGGCCACGG
CAACAACAACGACAACAACAAACATTTGGAATATTATTCTCAACTCACGTTTTAATAATACATCTTAATTATTTT
TCTAGTAGAGAAACTACAAATCAGCCTCTTCAACATTTATATACAGTTTAATAAGCCTCTTGCAAGTTACTTGTT
CTCTCACCTGAGGTATTTTTTTCCTCCCCACCTTGCCCCTGTTCCTCCCTTCCTCTTCTCCCTTTGCAAGAGGAA
ATATTTAACATATTTGGGTCCAACTTCAATAATGTAATAATTAATACATTAAAAGCATTTAACTTCCTTTCTAGA
AAAATGCACAGGCTAAGGCATAGACAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGGAGACAAGCAATCTGA
ATAAATATTTGCCAAAAGTTCTTTTTATGTCATATAGTGTCAGGATTTGAAGGAGCTATTTTTTTAATGTTGCA
ACTAGCAACTCATCTTCGGAAGACACAGCCAGGAGAATGAAGTAGAAGTGAAAGGTTTATAAATCCATTTGTAAG
CATTTATCCCATATATTTTAAATTCAAGAAAAATTGTGTTTATCTTTAGAATTTTGTATTCAATACTTTATGTAC
TATGTGACTCATGCTTCTGGATAAATAAAGCACCAAATATGTATCTGTAACCACAATCACACATATTATATTAAA
TATATATCTATATAACAAAAAAAAAAAAAAAAAA

FIGURE 500

MYGNILCPTLHTLCTQILYCMNYALSRIQCQGELGEINYFNFFFILYKAMDFIWLMCALYTSHFNRMELLIIFQR
VIDMQKFQ

FIGURE 501

AGCGGCCCCTGCAGAGGCAGGTCCACCTGAGAGGCCGGCCGGCCTCCCAGCCCACTGTCATCCGGGGCATCACCT
ACTATAAAGCCAAGGTCTCTGAAGAAGAGAATGACATTGAAGAGCAGCAAGATGAGTTTTTCAGCGGTGACAATG
GAGTGGATTTGCTGATTGAAGATCAGCTCCTGAGACACAACGGCCTG**ATG**ACCAGTGTCACCCGGAGGCCTGCAG
CCACCCGTCAGGGACACAGCACTGCTGTGACAAGCGACCTGAACGCTCGGACCGCACCCTGGTCCTCAGCACTGC
CACAGCCCTCGACCTCAGATCCCAGCATCGCCAACCATGCCTCAGTGGGACCAACACTCCAAACAACCTCGGTGT
CTCCAGATCCCACAAGGGAGTCAGTCCTGCAGCCTTCTCCTCAGGTACCAGCCACCACTGTGGCCCACACAGCCA
CCCAGCAACCAGCAGCCCCAGCTCCTCCGGCAGTGTCTCCCAGGGAGGCATTGATGGAAGCTATGCACACAGTCC
CAGTGCCTCCCACCACAGTCAGAACAGACTCGCTGGGGAAAGATGCTCCTGCTGGGTGGGGAACAACCCCTGCCA
GCCCCACGCTGAGCCCCGAAGAAGAAGATGACATCCGGAATGTCATAGGAAGGTGCAAGGACACTCTCTCCACAA
TCACGGGGCCGACCACCCAGAACACATATGGGCGGAATGAAGGGGCCTGGATGAAGGACCCCCTGGCCAAGGATG
AGCGGATTTACGTAACCAACTATTACTACGGCAACACCCTGGTAGAGTTCCGGAACCTGGAGAACTTCAAACAAG
GTCGCTGGAGCAATTCCTACAAGCTCCCGTACAGCTGGATCGGCACAGGCCACGTGGTATACAATGGCGCCTTCT
ACTACAATCGCGCCTTCACCCGCAACATCATCAAGTACGACCTGAAGCAGCGCTACGTGGCTGCCTGGGCCATGC
TGCATGACGTGGCCTACGAGGAGGCCACCCCCTGGCGATGGCAGGGCCACTCAGACGTGGACTTTGCTGTGGACG
AGAATGGCCTATGGCTCATCTACCCGGCCCTGGACGATGAGGGCTTCAGCCAGGAGGTCATTGTCCTGAGCAAGC
TCAATGCCGCGGACCTGAGCACACAGAAGGAGACCACATGGCGCACGGGGCTCCGGAGGAATTTCTACGGCAACT
GCTTCGTCATCTGTGGGGTGCTGTATGCCGTGGATAGCTACAACCAGCGGAATGCCAACATCTCCTACGCTTTCG
ACACCCACACCAACACACAGATCGTCCCCAGGCTGCTGTTCGAGAATGAGTATTCCTATACGACCCAGATAGACT
ACAACCCCAAGGACCGCCTGCTCTATGCCTGGGACAATGGCCACCAGGTCACTTACCATGTCATCTTTGCCTAC**T**
GACACCCTTGTCCCCACAAGCAGAAGCACAGAGGGGTCACTAGCACCTTGTGTGTATGTGTGTGCGCGCACGTGT
GTGTAGGTGGGTATGTGTTGTTTAAAAATATATATTATTTTGTATAATATTGCAAATGTAAAATGACAATTTGGG
TCTATTTTTTTATATGGATTGTAGATCAATCCATACGTGTATGTGCTGGTCTCATCCTCCCCAGTTTATATTTTT
GTGCAAATGAACTTCTCCTTTTGACCAGTAACCACCTTCCTTCAAGCCTTCAGCCCCTCCAGCTCCAAGTCTCAG
ATCTCGACCATTGAAAAGGTTTCTTCATCTGGGTCTTGCAGGAGGCAGGCAACACCAGGAGCAGAAATGAAAGAG
GCAAGAAAGAAGTGCTATGTGGCGAGAAAAAAAGTTTTAATGTATTGGAGAAGTTTTAAAAAACCCAGAAAAACG
CTTTTTTTTTTTAATAAAGAAGAAATTTAAAATC

FIGURE 502

MTSVTRRPAATRQGHSTAVTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPDPTRESVLQPSPQV
PATTVAHTATQQPAAPAPPAVSPREALMEAMHTVPVPPTTVRTDSLGKDAPAGWGTTPASPTLSPEEEDDIRNVI
GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYYGNTLVEFRNLENFKQGRWSNSYKLPYSWIGT
GHVVYNGAFYYNRAFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFAVDENGLWLIYPALDDEGF
SQEVIVLSKLNAADLSTQKETTWRTGLRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPRLLFEN
EYSYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY

FIGURE 503

GGCACGAGGGATGCAAGGAGATGAGACAGTTAGATTTACTTCCTCTTTTCTAATCTGAGAGGTTTCATGTTGAAG
AAAATCAGTGTTGGGGTTGCAGGAGACCTAAACACAGTCACC**ATG**AAGCTGGGCTGTGTCCTCATGGCCTGGGCC
CTCTACCTTTCCCTTGGTGTGCTCTGGGTGGCCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAG
GGACCTGTCTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCTTCCAG
GTCAAGGCCTACACTTTCAGTGAACCCTTCCACCTGATTGTGTCCTATGACTGGCTGATCCTCCAAGGTCCAGCC
AAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGCCTGGCAAGACTGGCCACTGACTCAGGTGACC
TTCTACCGAGATGGCTCAGCTCTGGGTCCCCCCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCA
GACAGCGGGCACTACCACTGCAGTGGCATCTTCCAGAGCCCTGGTCCTGGGATCCCAGAAACAGCATCTGTTGTG
GCTATCACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAGCAGGAAGC
CCCATGACCCTGAGTTGTCAGACAAAGTTGCCCCTGCAGAGGTCAGCTGCCCGCCTCCTCTTCTCCTTCTACAAG
GATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATTCCAGATCCCCACAGCTTCAGAAGATCACTCCGGG
TCATACTGGTGTGAGGCAGCCACTGAGGACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAG
GGTGCTTCCAGCTCTGCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACTGCTCCT
GAGGAGGCCCCTGGGCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTTCTCCTCTGGGG
ATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATGCAGGATGTGAGAGTCCTCCTCGGT
CACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAAAGGCTACTGCTGAA**TAG**AAG
TAAACAGTTCATCCATGATCTCACTTAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCCTGTCCTGCACA
TATGCATAAGTACTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAAATAAATTTA
TATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTCTGCTGTCTAGATCA
GGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAACTAATGGAAGTGGATTGAATACAGCAG
TCTCAACTGGGGGCAATTTTGCCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGG
GGGTTGGGGGATGGTGGGATGTGTGTGCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTA
TAATGCACAGGGCAGTACCCCACAACGAAAAATAATCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAACCC
CAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTTCCAGCCT
CATTCAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATGGTCTGTTCTTTAGTTCTAGTTTGTATCCC
CTCAAAAGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAAGAAGTGGGCCTTTGGGAAGTGATTAG
ATCAGGAGTGCAGAGCCCTCATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCCTT
CCACCATATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCGACTCTG
TCGTTGCCTTGATCTTGAACTTCCAGCCTCCAGAACTATGAGAAATAAAATTCTGTTGTTTGTAAAAAAAAAAAA
AAAAAA

FIGURE 504

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVKAYTFSEPFHLIV
SYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCSGIFQSP
GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEF
QIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPS
SEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

FIGURE 505

AAGCAGTGGTATCAACGCAGAGTGCCCATTACGGCCGGGGGTGGCATC<u>ATG</u>TGGCAGCTGCTCCTCCCAACTGCT
CTGCTACTTCTAGTTTCAGCTGGCATGCGGACTGAAGATCTCCCAAAGGCTGTGGTGTTCCTGGAGCCTCAATGG
TACAGGGTGCTCGAGAAGGACAGTGTGACTCTGAAGTGCCAGGGAGCCTACTCCCCTGAGGACAATTCCACACAG
TGGTTTCACAATGAGAGCCTCATCTCAAGCCAGGCCTCGAGCTACTTCATTGACGCTGCCACAGTCGACGACAGT
GGAGAGTACAGGTGCCAGACAAACCTCTCCACCCTCAGTGACCCGGTGCAGCTAGAAGTCCATATCGGCTGGCTG
TTGCTCCAGGCCCCTCGGTGGGTGTTCAAGGAGGAAGACCCTATTCACCTGAGGTGTCACAGCTGGAAGAACACT
GCTCTGCATAAGGTCACATATTTACAGAATGGCAAAGGCAGGAAGTATTTTCATCATAATTCTGACTTCTACATT
CCAAAAGCCACACTCAAAGACAGCGGCTCCTACTTCTGCAGGGGGCTTGTTGGGAGTAAAAATGTGTCTTCAGAG
ACTGTGAACATCACCATCACTCAAGGTTTGGCAGTGTCAACCATCTCATCATTCTTTCCACCTGGGTACCAAGTC
TCTTTCTGCTTGGTGATGGTACTCCTTTTTGCAGTGGACACAGGACTATATTTCTCTGTGAAGACAAACATTCGA
AGCTCAACAAGAGACTGGAAGGACCATAAATTTAAATGGAGAAAGGACCCTCAAGACAAA<u>TGA</u>CCCCCATCCCAT
GGGGGTAATAAGAGCAGTAGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCTATCATCCTCAGGCCTC
TCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCCTTATCCAACTCTCGACTTTTCCTTGGTCTCCAGT
GGAAGGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGTAGCTGCATTCCTAGAAATTGAAGTTTCAG
AGCTACACAAACACTTTTCTGTCCCAACCGTTCCCTCACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 506

MWQLLLPTALLLLVSAGMRTEDLPKAVVFLEPQWYRVLEKDSVTLKCQGAYSPEDNSTQWFHNESLISSQASSYF
IDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLQAPRWVFKEEDPIHLRCHSWKNTALHKVTYLQNGKGRKY
FHHNSDFYIPKATLKDSGSYFCRGLVGSKNVSSETVNITITQGLAVSTISSFFPPGYQVSFCLVMVLLFAVDTGL
YFSVKTNIRSSTRDWKDHKFKWRKDPQDK

FIGURE 507

ATGGCGGACGGGACCTGTCAGGACGTGGCCATCGTGGGCTACAAGGACTCGCCCTCCATCTGGGCCGCCGTCCCC
GGGAAAACCTTCGCCAACATCGCGCCAGCTGAGGTTGGTGTCCTGGCTGGCAAAGACAGGTCAAGATGGGGAATT
TTGCATGGATCTTCGTATACCAAGAGTACCGGTGGAGCCCCCACCTTCAATGTCACTGTCACCAAGACTGACAAG
ACGCTAGTCCTGCTGATGGGCAAAGAAGGTGTCCACGGTGGTTTGATCAACAAGAAATGTTATGAAATGGCCTCC
CACCTTCGGCGTTCCCAGTAC**TGA**

FIGURE 508

MADGTCQDVAIVGYKDSPSIWAAVPGKTFANIAPAEVGVLAGKDRSRWGILHGSSYTKSTGGAPTFNVTVTKTDK
TLVLLMGKEGVHGGLINKKCYEMASHLRRSQY

FIGURE 509

ATGGTTGTAGGATTCACTGAGTTTGAATCCTTCCACCCAGGCCTTGCTGCTGCAGCCTCTGCCAGAGCCAGCTCC
TGGTGGACCCATGTGGAAATGGGACCTCCAGATCCCATCCTGGGAGTCACTGAAGCCTTTAAGAGGGACATCAAT
AGCAAAAAGATGAATCTGGGAGTTGGGATGATAATGGGAAGCCGCTTTGCCAGTGGTGATGGTGATAAGGATGCC
TGGGCTCTGCACCACTTCATCGAACAGGGCATTAATGTTTGTCTCTGCCAATCATATGCCAAGAACATGGGCTTA
TATGGTGAGCATGTAGGAGCCTTCACTGTGGTCTGCAAAGATGCAGATGAAGCCAAAAGGGTAGAGTCACAGTTG
AAGATCTTGATTAGTCCCATGTATTCCAACTCTCCCCTCAATGGGGCCCAGATTGCTTCTACCATTCCAAACACC
CCAGTTGGTTTGAAGGTCTGGGTCATGGGAGGCCTACATGATCATCCTCAGGTTATGAGTGACGAGAAAGAGACA
ACACTGAGAGCAGTGGCTGTCAAGTACTGGATCAGAGTCCGGCTGTGCCACTTCCTTGAAACATTCATGTCTCCG
GACCTTACTGGCTGGAAAAAACTGCAGCAGGAAGATGGCCTTACCTCACTTCTAGCTTCCAAGTCTCACAAGAGA
GCACAGGCAGAACCGAAGCCACATCCAGGACCTGGGCTGAGAACATCTGGCACATGGAGCCTG**TAG**

FIGURE 510

MVVGFTEFESFHPGLAAAASARASSWWTHVEMGPPDPILGVTEAFKRDINSKKMNLGVGMIMGSRFASGDGDKDA
WALHHFIEQGINVCLCQSYAKNMGLYGEHVGAFTVVCKDADEAKRVESQLKILISPMYSNSPLNGAQIASTIPNT
PVGLKVWVMGGLHDHPQVMSDEKETTLRAVAVKYWIRVRLCHFLETFMSPDLTGWKKLQQEDGLTSLLASKSHKR
AQAEPKPHPGPGLRTSGTWSL

FIGURE 511

CGGTTGCTTGCTGTCCCAGCGGCGCCCCCTCATCACCGTCGCC**ATG**CCCGGAGGTCTGCTTCTCGGGGACGTGGC
TCCCAACTTTGAGGCCAATACCACCGTCGGCCGCATCCGTTTCCACGACTTTCTGGGAGACTCATGGGGCATTCT
CTTCTCCCACCCTCGGGACTTTACCCCAGTGTGCACCACAGAGCTTGGCAGAGCTGCAAAGCTGGCACCAGAATT
TGCCAAGAGGAATGTTAAGTTGATTGCCCTTTCAATAGACAGTGTTGAGGACCATCTTGCCTGGAGCAAGGATAT
CAATGCTTACAATTGTGAAGAGCCCACAGAAAAGTTACCTTTTCCCATCATCGATGATAGGAATCGGGAGCTTGC
CATCCTGTTGGGCATGCTGGATCCAGCAGAGAAGGATGAAAAGGGCATGCCTGTGACAGCTCGTGTGGTGTTTGT
TTTTGGTCCTGATAAGAAGCTGAAGCTGTCTATCCTCTACCCAGCTACCACTGGCAGGAACTTTGATGAGATTCT
CAGGGTAGTCATCTCTCTCCAGCTGACAGCAGAAAAAAGGGTTGCCACCCCAGTTGATTGGAAGGATGGGGATAG
TGTGATGGTCCTTCCAACCATCCCTGAAGAAGAAGCCAAAAAACTTTTCCCGAAAGGAGTCTTCACCAAAGAGCT
CCCATCTGGCAAGAAATACCTCCGCTACACACCCCAGCCT**TAA**GTCTCTTGGAGAAGTTGGTGCTGTGAGCCAGA
GGATGTCAGCTGCCAATTGTGTTTTCCTGCAGCAATTCCATAAACACATCCTGGTGTCATCACAGCCAAGGTTTT
TAGGTTGCTATACCAATGGCTTATTAAATGAAAATGGCACTAAAAGTTTCTTGAGATTCTTTATACTCTCTGCCT
TCAGCAATCAATTCCATTCATACATCAGCACTCTGCTGGTTCTGTTTGAAATATGTTCTGTATTTAAAACTCAAA
TCTTGTTGGATCTCTGCAGGGCTTGTGACCAATGAAGTCATATTTGTTGATGGTTGACAAAGCTTGCTTCACTCC
ATCAGAGAATGACTATCAATTTTTTTTTAACTGTCCTATCACGTCCTCTCCTGTCACCCATTTTGAAGAGTGGCA
GAACTTGAAGTTCAACTTCCTCTGTAAATATCCAAGTATAAAGCCCAGGAACTTCTAGAATAACCCAGATGCGCT
TTAATTTTTTTTAATATGTTTTGATCACAGAACTTCTAGAATAACCCAGATGCTCTTTCATATTCTTTTAATACA
TCTTGATCACAGCTGGGGGAAAAAAAGCTTTTTAATTCTGTACCTTCCTAGTAGATAAGTGAAGAGCAGGGAAAG
AGACCTTTAAATATTTTGCTATAAAAAAATTTGTGATAAGTTTCTATCAAAATGGGGAGATTGCAGAAAAGGCTT
CCCTTGGCTCCCAAGGAGGTGTAGCAGGTGTGAGCAATATTAGTGCCATGTGCCTTTCACACAGGGTTTGCATTT
ATCAGTCTGTTTTCCGATGATGTGTACATGAAAGAGTACACCATGTGAAGAGAAGAGAGAATGATTGAAAATGTT
TTAGTATAGAACTCTTCTTGCAGTGGGTTGCTATTTTCTAGATTTTACTTTTTAGGGAACAAAATAAAATCCTTT
GTT

FIGURE 512

MPGGLLLGDVAPNFEANTTVGRIRFHDFLGDSWGILFSHPRDFTPVCTTELGRAAKLAPEFAKRNVKLIALSIDS
VEDHLAWSKDINAYNCEEPTEKLPFPIIDDRNRELAILLGMLDPAEKDEKGMPVTARVVFVFGPDKKLKLSILYP
ATTGRNFDEILRVVISLQLTAEKRVATPVDWKDGDSVMVLPTIPEEEAKKLFPKGVFTKELPSGKKYLRYTPQP

FIGURE 513

AGAGACCGTCCGAGGTAATTGTCTGCCACGAGTGCACATTCTGAAAACAGGAGATTTTAGTTCCTAAAAATGGGA
AGAACCTACATTGTAGAAGAGACTGTTGGCCAGTATCTTTCAAACATAAATCTCCAAGGAAAGGCTTTTGTCTCT
GGCCTTTTAATAGGACAGTGTTCGTCACAAAAGGATTATGTGATTCTTGCCACTAGAACGCCACCCAAAGAGGAG
CAAAGTGAGAACCTCAAACATCCCAAAGCTAAGTTGGATAACTTGGATGAAGAATGGGCCACAGAACATGCCTGC
CAGGTATCCAGA**ATG**CTACCAGGGGGACTTTTAGTTCTTGGAGTATTTATTATTACTACTTTAGAACTGGCAAAT
GATTTTCAAAATGCCCTGCGTAGACTAATGTTTGCTGTGGAAAAGTCTATAAATAGAAAGAGATTGTGGAATTTC
ACAGAGGAGGAAGTCTCAGAACGAGTGACACTTCACATTTGTGCTTCTACAAAAAAAATATTTTGTCGAACTTAT
GATATCCATGATCCAAAGAGTTCAGCAAGACCAGCAGATTGGAAGTATCAAAGTGGATTATCATCCTCATGGCTT
TCTTTAGAGTGTACAGTTCACATTAATATTCACATCCCACTTTCTGCTACTTCTGTCAGCTATACTCTGGAGAAA
AATACAAAGAATGGACTTACACGCTGGGCCAAGGAAATAGAAAATGGTGTTTATTTGATTAATGGACAAGTTAAA
GATGAAGATTGTGACCTATTAGAAGGACAGAAAAAATCTTCTAGAGGAAATACTCAAGCAACTAGTCATTCTTTT
GATGTCAGAGTGCTAACGCAGTTGCTCCTGAATTCAGACCACAGATCCACAGCCACAGTCCAGATATGTAGCGGT
TCTGTAAACCTTAAGGGTGCTGTGAAATGCAGAGCTTATATCCACAGCAGTAAACCCAAAGTTAAAGATGCTGTG
CAGGCAGTAAAGAGGGATATATTGAACACAGTTGCTGATCGTTGTGAAATGCTATTTGAGGATCTGCTTTTGAAT
GAAATTCCAGAAAAAAAAGATTCTGAAAAAGAGTTCCACGTCCTCCCTTATCGAGTCTTTGTTCCCCTTCCTGGA
TCCACTGTAATGTTGTGTGATTATAAATTTGACGATGAGTCAGCTGAAGAAATCAGGGACCATTTTATGGAGATG
TTGGATCACACAATTCAAATAGAAGATTTGGAAATTGCAGAGGAAACAAACACAGCTTGTATGAGTTCTTCTATG
AATAGTCAAGCTTCATTGGACAACACAGATGATGAACAACCAAAACAACCAATTAAAACTACAATGTTATTGAAA
ATTCAGCAAAACATAGGTGTGATTGCAGCATTTACAGTTGCAGTCCTTGCTGCGGGTATCTCCTTTCATTACTTC
AGTGAT**TAG**GGTGAGGCACAAAGAGTTTCTTGATCATCCAGAGAACATTGACAGACAATTATGAATAATAAAGAT
GTTAACAATCCATCTGTATTTAAAACACTAGCAGCCAGATCTGCTGCCATGATGCCTATTTGGTGTGTTTCTGAT
TAAAATGAAATCACAAGCTGCCTTGTTTAGCCTGCTTTACATTGTAGGTGGCCCGCATTTCCAGAAATAACGTTA
TGCATCTAGATGGAAGCTGCATGTAACAAATCATTATTATCTATTTTTAAAAGCTTCAAAATGATGGGATATGAT
CATAGATTTTAGTCTTACTAATCTGAATCACATATTAATCAGGACATTAAAAACTTTAACAGAGGCATGATGGCT
CACACGTATAATCCTAATGCTTTGAGAGGCTGAGGTAGGAGCATCACCTGGGGCTGGGAGGGAGTTGGAGACCAG
CCTGGATGACATAATGAGATTCTGTCTCTACTGGAAAAAAAAAAAAAAA

FIGURE 514

MLPGGLLVLGVFIITTLELANDFQNALRRLMFAVEKSINRKRLWNFTEEEVSERVTLHICASTKKIFCRTYDIHD
PKSSARPADWKYQSGLSSSWLSLECTVHINIHIPLSATSVSYTLEKNTKNGLTRWAKEIENGVYLINGQVKDEDC
DLLEGQKKSSRGNTQATSHSFDVRVLTQLLLNSDHRSTATVQICSGSVNLKGAVKCRAYIHSSKPKVKDAVQAVK
RDILNTVADRCEMLFEDLLLNEIPEKKDSEKEFHVLPYRVFVPLPGSTVMLCDYKFDDESAEEIRDHFMEMLDHT
IQIEDLEIAEETNTACMSSSMNSQASLDNTDDEQPKQPIKTTMLLKIQQNIGVIAAFTVAVLAAGISFHYFSD

FIGURE 515A

CGAGACGGAAGCGGGCTGGGAGGCGTCGGCGGCGGCAGCGCACGTGGTGACGTGCGAGGGGGTGCGGCGCGAGCG
GTCGGCGGCGGCGGAGGCAGTGTCTCCCGGTCGCGCGTGGAGGTCGGTCGCTCAGAGCTGCTGGGCGCAGTTTCT
CCGCCTGCTGCTTCGGCGCGGCTGTATCGGCGAGCGAGCGAGTTCCCGCGAGTTCTCGGTGGCGCTCCCCCTTCC
TTTCAGTCTCCACGGACTGGCCCCTCGTCCTTCTACTTGACCGCTCCCGTCTTCCGCCGCCTTCTGGCGCTTTCC
GTTGGGCCGATTCCCGCCCGCTTCCTCCTGCTTCCCATCGAAGCTCTAGAAATGAATGTTTCCATCTCTTCAGAG
ATGAACCAGATTATGATGCATCATTATCACAGAAGAAATTCGTGTCTATAGCTTTTAAGGACTTGATTACATCAT
TTTCAAGCCTGATAGTTTTGGAATCACCATTAGAGCTTAAGACACACCTGCCTTCATTTCAACCACCTGTCTTCA
TACCCTGACGAAGTGCACCTTTTAACACTCCTTTGTCCTTGGATTACTTAAGAGTTCCCAGAAATACATTTGCCA
CCAACAGAGTAGCCAAATTTATAAGGAAAA**ATG**ATTCCCAATGGATATTTGATGTTTGAGGATGAAAATTTTATT
GAGTCTTCTGTTGCCAAATTAAATGCCCTGAGGAAAAGTGGCCAGTTCTGTGATGTTCGACTTCAGGTCTGTGGC
CATGAAATGTTAGCACACAGAGCAGTGCTAGCTTGCTGCAGTCCCTATTTATTTGAAATCTTTAATAGTGATAGT
GATCCTCATGGAATTTCTCACGTTAAATTTGATGATCTCAATCCAGAAGCTGTTGAAGTCTTGTTGAATTATGCC
TACACTGCTCAGTTGAAAGCAGATAAGGAATTGGTAAAAGATGTTTATTCTGCAGCAAAAAAGCTGAAGATGGAT
CGAGTAAAGCAGGTTTGTGGTGATTATTTACTGTCTAGAATGGATGTTACCAGCTGCATCTCTTACCGAAATTTT
GCAAGTTGTATGGGAGACTCCCGTTTGTTGAATAAGGTTGATGCTTATATTCAGGAGCATTTGTTACAAATTTCT
GAAGAGGAGGAGTTTCTTAAGCTTCCAAGGCTAAAGTTGGAGGTAATGCTTGAAGATAATGTTTGCTTGCCCAGC
AATGGCAAATTATATACAAAGGTAATCAACTGGGTGCAGCGTAGCATCTGGGAGAATGGAGACAGTCTGGAAGAG
CTGATGGAAGAGGTTCAAACCTTGTACTACTCAGCTGATCACAAGCTGCTTGATGGGAACCTACTAGATGGACAG
GCTGAGGTGTTTGGCAGTGATGATGACCACATTCAGTTTGTGCAGAAAAAGCCACCACGTGAGAATGGCCATAAG
CAGATAAGTAGCAGTTCAACTGGATGTCTCTCTTCTCCAAATGCTACAGTACAAAGCCCTAAGCATGAGTGGAAA
ATCGTTGCTTCAGAAAAGACTTCAAATAACACTTACTTGTGCCTGGCTGTGCTGGATGGTATATTCTGTGTCATT
TTTCTTCATGGGAGAAACAGCCCACAGAGCTCACCAACAAGTACTCCAAAACTAAGTAAGAGTTTAAGCTTTGAG
ATGCAACAAGATGAGCTAATCGAAAAGCCCATGTCTCCTATGCAGTACGCACGATCTGGTCTGGGAACAGCAGAG
ATGAATGGCAAACTCATAGCTGCAGGTGGCTATAACAGAGAGGAATGTCTTCGAACAGTCGAATGCTATAATCCA
CATACAGATCACTGGTCCTTTCTTGCTCCCATGAGAACACCAAGAGCCCGATTTCAAATGGCTGTACTCATGGGC
CAGCTCTATGTGGTAGGTGGATCAAATGGCCACTCAGATGACCTGAGTTGTGGAGAGATGTATGATTCAAACATA
GATGACTGGATTCCTGTTCCAGAATTGAGAACTAACCGTTGTAATGCAGGAGTGTGTGCTCTGAATGGAAAGTTA
TACATCGTTGGTGGCTCTGATCCATATGGTCAAAAAGGACTGAAAAATTGTGATGTATTTGATCCTGTAACAAAG
TTGTGGACAAGCTGTGCCCCTCTTAACATTCGGAGACACCAGTCTGCAGTCTGTGAGCTTGGTGGTTATTTGTAC
ATAATCGGAGGTGCAGAATCTTGGAATTGTCTGAACACAGTAGAACGATACAATCCTGAAAATAATACCTGGACT
TTAATTGCACCCATGAATGTGGCTAGGCGAGGAGCTGGAGTGGCTGTTCTTAATGGAAAACTGTTTGTATGTGGT
GGCTTTGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAACTAGAAATGAATGGAAGATGATGGGA
AATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAACACCATTTATGCAGTGGGAGGATTCGAT
GGCAATGAATTTCTGAATACGGTGGAAGTCTATAACCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTC
CAGTTT**TAA**CAAATTTAAGACCCTCTCAAACTAACAGGCTTAGTGATGTAATTATGGTTAGTAGAGGTACACTTG
TGAATAAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTGCATACTATTAAAC
ATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATGAAGGTCTGTTTTGTGTACTTTTAAGACT
TTGGTTATTTTACTTTTTGGAAAAGAATAAACCAAGAATTGATTGGGCACATCATTTCAAGAAGTCCCCTCTCCT
CCACATTTGTTTTGCCAATTTGCACATTAAATGACTCTTCCCTCAAATGTGTACTATGGGGTAAAAGGGGTAGGG
TTTAAAGATGTAGACAGTTGGGTTTTTTAAGGGCCCTTTTTCAATAACTGGAACACTCTATAACAAAGGATACTT
ATTTAAATAGATGACATTGACTATTTTTGTTTTTATTAAAAGGAAGCTTACATGCCTACCAATATTTAATCTTTT
ATGATTGCCTTTTTATAACTTTTTATATTCTCAGCAGAGTGCTTTACCAATTGAAGTAAAATGTGGCAGGCTGGA
GTTATTGAAGCAGAGTGGCAGTCTTCAGTTTGCAGAGTAGGGGTCTGTCTTTTAAACTCTGAGTGCAAACTTCAG
AGTTCTTGCCTTGGCTGCAGTTTTTTTCCTTCAAGAATGCAGTACTAACATTTATTTGAGTGGAGTTACTGAACA
GTAACATAGCTGTGATTTTTGGTATTTGAAACACTGGTTTAAATATTTTGACTTGTTGAGGGTATGTTTTATAT
AGCAAGACATTATATAGCAGTAAAAAATGGTGTTTTATCTTCTATATAATTCCTGTTTTTATTATTAACAAAACA
GTCCTAAATAGCAGCCCTCAATTGTGAAAAAATTTACTTTAAACTACATTAGGTTGTGAATGCAGGTTTTATCAG
AACTATGTTTTTGTTCAGTTTATCTGTTCATATGGATAAATATTGGTTGGGATGACTTGGTGTCTAATGTGTAGT

FIGURE 515B

GCTACACACCTAACTTATGGGGCCAAAATAGCATGTCCTAATGCTTGCTGCTGATTTAAACACATTAAAGGTACT
TTGCAGGAAATCCTTGCACCATGGGATTAATATCCAATTGCTGCTTGTACACTCATTCATTACTAAAAGTTTTGA
GAAATTTTTTTTTCCAGTAATGAGCTTAAGAAATTTGTGGAAAATAACTCACCTGGCATCTTACATCTGAAATAA
GGAATGATATAAGGTTTTTTTTTCTCACAGAAGATGAAGCACACAGGAACCTAATGGGCCAACTGGGATGAGGTG
ACTATTCTGAGATGACTATTCAGTGGCTAACTTGGGTTAGGAAGAAAATAATTAGGTATTTTCTCCAAATGTTCA
CTGGTACTCTGCCACTTTATTTCTCTCATCTGTTACACAAAGAACCACCAGGAAAGCAAATCAGTTTGGTTGGTA
ACTCTGTAATTCCTAACTATCACTGGTTTGGTTCTGGACTAAAACTACATTGACAGATTGAATTTGCCTAATATG
ATGACTGTTTTTAATATGGATCTGTATGTGTTCTATTCAGCACAAGGAAATAAAATTTTAGTTGAGGATTCAGC

FIGURE 516

MIPNGYLMFEDENFIESSVAKLNALRKSGQFCDVRLQVCGHEMLAHRAVLACCSPYLFEIFNSDSDPHGISHVKF
DDLNPEAVEVLLNYAYTAQLKADKELVKDVYSAAKKLKMDRVKQVCGDYLLSRMDVTSCISYRNFASCMGDSRLL
NKVDAYIQEHLLQISEEEEFLKLPRLKLEVMLEDNVCLPSNGKLYTKVINWVQRSIWENGDSLEELMEEVQTLYY
SADHKLLDGNLLDGQAEVFGSDDDHIQFVQKKPPRENGHKQISSSSTGCLSSPNATVQSPKHEWKIVASEKTSNN
TYLCLAVLDGIFCVIFLHGRNSPQSSPTSTPKLSKSLSFEMQQDELIEKPMSPMQYARSGLGTAEMNGKLIAAGG
YNREECLRTVECYNPHTDHWSFLAPMRTPRARFQMAVLMGQLYVVGGSNGHSDDLSCGEMYDSNIDDWIPVPELR
TNRCNAGVCALNGKLYIVGGSDPYGQKGLKNCDVFDPVTKLWTSCAPLNIRRHQSAVCELGGYLYIIGGAESWNC
LNTVERYNPENNTWTLIAPMNVARRGAGVAVLNGKLFVCGGFDGSHAISCVEMYDPTRNEWKMMGNMTSPRSNAG
IATVGNTIYAVGGFDGNEFLNTVEVYNLESNEWSPYTKIFQF

FIGURE 517

CCTTTGCCGCTGGTCGGGATTGGG**ATG**TCGAAGAACACAGTGTCGTCGGCCCGCTTCCGGAAGGTGGACGTGGAT
GAATATGACGAGAACAAGTTCGTGGACGAAGAAGATGGGGGCGACGGCCAGGCCGGGCCCGACGAGGGCGAGGTG
GACTCCTGCCTGCGGCAAGGAAACATGACAGCTGCCCTACAGGCAGCTCTGAAGAACCCCCCTATCAACACCAAG
AGTCAGGCAGTGAAGGACCGGGCAGGCAGCATTGTCTTGAAGGTGCTCATCTCTTTTAAAGCTAATGATATAGAA
AAGGCAGTTCAATCTCTGGACAAGAATGGTGTGGATCTCCTAATGAAGTATATTTATAAAGGATTTGAGAGCCCG
TCTGACAATAGCAGTGCTATGTTACTGCAATGGCATGAAAAGGCACTTGCTGCTGGAGGAGTAGGGTCCATTGTT
CGTGTCTTGACTGCAAGAAAAACTGTG**TAG**TCTGGCAGGAAGTGGATTATCTGCCTCGGGAGTGGGAATTGCTGG
TACAAAGACCAAAACAACCAAATGCCACCGCTGCCCTGTGGGTAGCATCTGTTTCTCTCAGCTTTGCCTTCTTGC
TTTTTCATATCTGTAAAGAAAAAAATTACATATCAGTTGTCCTTTAATGAAAATTGGGATAATATAGAAGAAATT
GTGTTAAAATAGAAGTGTTTCATCCTTTCAAAACCATTTCAGTGATGTTTATACCAATCTGTATATAGTATAATT
TACATTCAAGTTTAATTGTGCAACTTTTAACCCCTGTTGGCTGGTTTTTTGTTCTGTTTTGTTTTGTATTATTTT
TAACTAATACTGAGAGATTTGGTCAGAATTTGAGGCCAGTTTCCTAGCTCATTGCTAGTCAGGAAATGATATTTA
TAAAAAATATGAGAGACTGGCAGCTATTAACATTGCAAAACTGGACCATATTTCCCTTATTTAATAAGCAAAATA
TGTTTTTGGAATAAGTGGTGGGTGAATACCACTGCCAAGTTATAGCTTTGTTTTTGCTTGCCTCCTGATTATCTG
TACTGTGGGTTTAAGTATGCTACTTTCTCTCAGCATCCAATAATCATGGCCCCTCAATTTATTTGTGGTCACCCA
GGGTTCAGAGCAAGAAGTCTTGCTTTATACAAATGTATCCATAAAATATCAGAGCTTGTTGGGCATGAACATCAA
ACTTTTGTTCCACTAATATGGCTCTGTTTGGAAAAAACTGCAAATCAGAAAGAATGATTTGCAGAAAGAAAGAAA
AACTATGGTGTAATTTAAACTCTGGGCAGCCTCTGAATGAAATGCTACTTTCTTTAGAAATATAATAGCTGCCTT
AGACATTATGAGGTATACAACTAGTATTTAAGATACCATTTAATATGCCCCGTAAATGTCTTCAGTGTTCTTCAG
GGTAGTTGGGATCTCAAAAGATTTGGTTCAGATCCAAACAAATACACATTCTGTGTTTTAGCTCAGTGTTTTCTA
AAAAAAGAAACTGCCACACAGCAAAAAATTGTTTACTTTGTTGGACAAACCAAATCAGTTCTCAAAAAATGACCG
GTGCTTATAAAAAGTTATAAATATCGAGTAGCTCTAAAACAAACCACCTGACCAAGAGGGAAGTGAGCTTGTGCT
TAGTATTTACATTGGATGCCAGTTTTGTAATCACTGACTTATGTGCAAACTGGTGCAGAAATTCTATAAACTCTT
TGCTGTTTTTGATACCTGCTTTTTGTTTCATTTTGTTTTGTTTTGTAAAAATGATAAAACTTCAGAAAATAAAAT
GTCAGTGTTGAATAAAAAAAAAAAAAAAAAAAA

FIGURE 518

MSKNTVSSARFRKVDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLRQGNMTAALQAALKNPPINTKSQAVKDRA
GSIVLKVLISFKANDIEKAVQSLDKNGVDLLMKYIYKGFESPSDNSSAMLLQWHEKALAAGGVGSIVRVLTARKT
V

FIGURE 519A

GCCAGGCAGAGTCCTACTATAGGCATGCAGCTCAGCTTGTCCCCTCCAATGAAGCATTGCTGTGAAGTTCCCTTT
CCCAGCTGCCTCCACTAATCTGCAAAAAGCACTTTCTAAAGCACTGGAAAGCCGAGATGAGGTGAAAACCAAGTG
GGGTGTTTCTGACTTCATCAAGGCCTTTATTAAATTCCACGGTCATGTGTACCTGAGTAAGAGCTTGGAAAAGTT
GAGCCCTCTTCGAGAGAAATTGGAAGAACAGTTTAAGAGGCTGCTATTCCAAAAAGCTTTCAACTCTCAGCAGTT
AGTTCATGTCACTGTCATTAACCTGTTTCAACTTCATCACCTTCGTGACTTTAGCAATGAAACCGAGCAGCACAC
TTATAGCCAAGATGAGCAGCTATGTTGGACACAGTTGCTGGCCCTCTTT**ATG**TCTTTTCTTGGCATCCTGTGCAA
GTGTCCTCTACAGAATGAGTCTCAGGAGGAGTCCTACAATGCCTATCCTCTTCCAGCAGTCAAGGTCTCCATGGA
CTGGCTAAGACTCAGACCCAGGGTCTTTCAGGAGGCAGTGGTGGATGAAAGACAGTACATTTGGCCCTGGTTGAT
TTCTCTTCTGAATAGTTTCCATCCCCATGAAGAGGACCTCTCAAGTATTAGTGCGACACCACTTCCAGAGGAGTT
TGAATTACAAGGATTTTTGGCATTGAGACCTTCTTTCAGGAACTTGGATTTTTCCAAAGGTCACCAGGGTATTAC
AGGGGACAAAGAAGGCCAGCAACGACGAATACGACAGCAACGCTTGATCTCTATAGGCAAATGGATTGCTGATAA
TCAGCCAAGGCTGATTCAGTGTGAAAATGAGGTAGGGAAATTGTTGTTTATCACAGAAATCCCAGAATTAATACT
GGAAGACCCCAGTGAAGCCAAAGAGAACCTCATTCTGCAAGAAACATCTGTGATAGAGTCGCTGGCTGCAGATGG
GAGCCCAGGGCTAAAATCAGTGCTATCTACAAGCCGAAATTTAAGCAACAACTGTGACACAGGAGAGAAGCCAGT
GGTTACCTTCAAAGAAAACATTAAGACACGAGAAGTGAACAGAGACCAAGGAAGAAGTTTTCCTCCCAAAGAGGT
GAGAAGGGACTATAGCAAAGGAATAACTGTAACTAAGAATGATGGAAAGAAGGACAACAACAAGAGGAAAACTGA
AACCAAGAAATGCACCTTAGAAAAGTTACAGGAAACAGGAAAGCAGAATGTGGCAGTGCAGGTAAAATCCCAGAC
AGAACTAAGAAAGACTCCAGTGTCTGAAGCCAGAAAAACACCTGTAACTCAAACCCCAACTCAAGCAAGTAACTC
CCAGTTCATCCCCATTCATCACCCTGGAGCCTTCCCTCCTCTTCCCAGCAGGCCAGGGTTTCCGCCCCCAACATA
TGTTATCCCCCCGCCTGTGGCATTTTCTATGGGCTCAGGTTACACCTTCCCAGCTGGTGTTTCTGTCCCAGGAAC
CTTTCTTCAGCCTACAGCTCACTCTCCAGCAGGAAACCAGGTGCAAGCTGGGAAACAGTCCCACATTCCTTACAG
CCAGCAACGGCCCTCTGGACCAGGGCCAATGAACCAGGGACCTCAACAATCACAGCCACCTTCCCAGCAACCCCT
TACATCTTTACCAGCTCAGCCAACAGCACAGTCTACAAGCCAGCTGCAGGTTCAAGCTCTAACTCAGCAACAACA
ATCCCCTACAAAAGCTGTGCCGGCTTTGGGGAAAAGCCCGCCTCACCACTCTGGATTCCAGCAGTATCAACAGGC
AGATGCCTCCAAACAGCTGTGGAATCCCCCTCAGGTTCAAGGCCCATTAGGGAAAATTATGCCTGTGAAACAGCC
CTACTACCTTCAGACCCAAGACCCCATAAAACTGTTTGAGCCGTCATTGCAACCTCCTGTAATGCAGCAGCAGCC
TCTAGAAAAAAAAATGAAGCCTTTTCCCATGGAGCCATATAACCATAATCCCTCAGAAGTCAAGGTCCCAGAATT
CTACTGGGATTCTTCCTACAGCATGGCTGATAACAGATCTGTAATGGCACAGCAAGCAAACATAGACCGCAGGGG
CAAACGGTCACCAGGAATCTTCCGTCCAGAGCAGGATCCTGTACCCAGAATGCCGTTTGAGAAATCCTTATTGGA
GAAGCCCTCAGAGCTCATGTCACATTCATCCTCTTTCCTGTCCCTCACCGGATTCTCTCTCAATCAGGAAAGATA
CCCAAATAATAGTATGTTCAATGAGGTATATGGGAAAAACCTGACATCCAGCTCCAAAGCAGAACTCAGTCCCTC
AATGGCCCCCCAGGAAACATCTCTGTATTCCCTTTTTGAAGGGACTCCGTGGTCTCCATCACTTCCTGCCAGTTC
AGATCATTCAACACCAGCCAGCCAGTCTCCTCATTCCTCTAACCCAAGCAGCCTACCCAGCTCTCCTCCAACACA
CAACCATAATTCTGTTCCATTCTCCAATTTTGGACCCATTGGGACTCCAGATAACAGGGATAGAAGGACTGCAGA
TCGGTGGAAAACTGATAAGCCAGCCATGGGTGGGTTTGGCATTGATTATCTCTCAGCAACGTCATCCTCTGAGAG
CAGTTGGCATCAGGCCAGCACTCCGAGTGGCACCTGGACAGGCCATGGCCCTTCCATGGAGGATTCCTCTGCTGT
CCTCATGGAAAGCCTAAAGTCTATCTGGTCCAGTTCCATGATGCATCCTGGACCTTCTGCTCTGGAGCAGCTGTT
AATGCAGCAGAAGCAGAAACAGCAACGGGGACAAGGCACCATGAACCCTCCACAC**TGA**GGCCAAAGTGGCAACCT
GGGAATGAAGGCTCCATAAACCATGGCATGTTGGGTTTGCAGGACTGGCCCACACAGTCCCCTGCAGGTGGCAGC
CCTCTTTTCTGTTTCTCGCTGTCAAGAGGGTGTAAGTATTCCACCAGCCCGCTGAGTGTGCACGAAATGTTCGCA
GTGCAACAAAAAGAAAAATCCATCAGGAACTCTCCGTCCCCCCGGGGCCTTCCGGAGGGAGAGAGAGAGGAACTG
CTGTTTATCTCACTCAGTTACTTGGTATCACCGCCTCTCACCTTCTCCATCGTGCATGTCCCCAGCCACATGGGA
AGTGAAAGCTGAGAAGGGAAGGCAGATGGGAGAAGCCAATGGGAACTTCTCAGTCCTTTTTTCCTCTTTGGGGAA
TAAAATAGGAATCCATTAATGATTGCTTTGCTGACTGAGAATGTAGTTGAAATTAAACATCTTTTATTATTATTA
CTCTCAGTAGTAAAATATCACACTGAATTCTTCCATACACAGGTGTGCTTCTAGTCAGTGTGTAGCAAGGAAAGC
CCCGTTCACTGCTCCTGTGAGAGGTTGGTGGTGACAGGATGGGGAACCGACCTCTTCAGCCAGTGGAAATGTTCC
ATAAGGGAGAGTTCAAGGCCTGTCAGAAGGCTCTGGTAGGCCTTCCTCTGGCCAGGAGACTCCAGCAGGGAATGC
CCTTCACTCTGTAGGTGCTCGAGCCCCAATCGAGGATACAGTGTGGGTGGTGGTGCTGGGCTGGACTAGCAGGTA

FIGURE 519B

GACTGCTGTAGGATTTCAAATTACGTTTTTGATTCCTGTACATTTTACAGTCGCACAGCAAGCAGTCTCACAGAA
GGCAGGCTAGTCCATTCACAGCCTGACACGTTCTAATAGGTAGAAGCTTTCAGTGTGGTTATTTTTTCTTTGGTT
GGTTTTTGTGCCCCCATTCTACTTCCCACCCTCCTGCCCCATCTCCATCCCTTCTTTTACCCAATGCTGTATGCT
AGTAATTGTTTTTATTCCTAATGTGTGCAACATCACATCTCCCCAAGAAGCAACAGCATGGGGTCCAGCAGTTGG
GGCCCAAAAGACAGTCTGAAGAGGAAGGAAGCAGCAGTATCTGCGTAGCCCACAGAGGGCCCAGGCCCCTGCCCA
GCTGCAGTCTCCCAGCCTCCACTTTCAGAGTGAAATTCAAGGCAGCACGGACATGTGCCCATCAGGCACAGAAGA
AAACACGACGTCGTCCATTTTGGAAGAGACGAAAGAAAGGAAAATAAACTCTTTGTATGATATTTATTAGGAGGA
AAGAGGACTGAAAATGTTCTTGTGTAGAAACAGAAGGACAGCATTTCTGTTAGTCATTTCCTGGAAAAGTAATAT
TTTAAGGGGAAATTATGGAAACAATCTAATTGTTCAATTGCTGTGCTAGTGGTAGGGTTTATTTTCTGGGAGGTC
TCTCCTTTGTGTGTCTGTATGTTTGTGTACACACACGTGCCCATCTGCTGTCCCAGAGGGGAGGGGTTGTGTGTG
CGAGTGTATGGAGTTAGTGTGGAACTTAAGAGCTGGAAGACAGCTGTAGAGCAAAGCACATCCAGGAGCCCCAGT
TGTCACTGCAGTCTGGGCAACCCCAGCAATGAAAAGGGGTGAGATAACGCTCATTGCTCTTCAGAGAGAGTGGTT
GGAGCCCCCCCCGCCCCGTATGCTTACATTATTGCTCTTTTAGTTTGACATGGTGTTTGGGTTTTGTTTTTTTGA
AAGGTCTGAAAAGGTGAAGCCCCCTACCCAATGGCAATATGAAACCTTTTGTGCTTCTCTTCAGCCCCTTCCCTG
TGTCCACCTTTCTCTCCTCTTCCCAAGCCTTTTTCCTACTACCTTTACCCAGTTTGTGTGTTTGAGCTCTGCATT
CAGGCAGCTGCAACATTCCAGTGTTTGAACTGTCACTGATTCTTGCGCCCTAGACAAGCTAACCAGGTTTACCAT
CTCACTCCCAGTAATACCCAGCTCCTATCTAAAGCCCCATTCTGCATGAGAATTTGGTGTTTGGAATGTTTTCTG
ACTCTTGGGGCGGGATTCCTCGCCTTATCATCCTCACTGTGGAGTAATGAGGGGGAGGAGAATCTTTATCAGAAA
CTGGTTTTGTGTAGTAAACTTTCTTTTGTGGTTTTTTGTTTTGTTTTCTGGGTTTTGTTTTTTGTTTTTGTCTGT
GCAAGACCTGCAGCTGCTGAAAATCAGCTTTGCCTTTAATTAAACCATGTTCTCTCC

FIGURE 520

MSFLGILCKCPLQNESQEESYNAYPLPAVKVSMDWLRLRPRVFQEAVVDERQYIWPWLISLLNSFHPHEEDLSSI
SATPLPEEFELQGFLALRPSFRNLDFSKGHQGITGDKEGQQRRIRQQRLISIGKWIADNQPRLIQCENEVGKLLF
ITEIPELILEDPSEAKENLILQETSVIESLAADGSPGLKSVLSTSRNLSNNCDTGEKPVVTFKENIKTREVNRDQ
GRSFPPKEVRRDYSKGITVTKNDGKKDNNKRKTETKKCTLEKLQETGKQNVAVQVKSQTELRKTPVSEARKTPVT
QTPTQASNSQFIPIHHPGAFPPLPSRPGFPPPTYVIPPPVAFSMGSGYTFPAGVSVPGTFLQPTAHSPAGNQVQA
GKQSHIPYSQQRPSGPGPMNQGPQQSQPPSQQPLTSLPAQPTAQSTSQLQVQALTQQQQSPTKAVPALGKSPPHH
SGFQQYQQADASKQLWNPPQVQGPLGKIMPVKQPYYLQTQDPIKLFEPSLQPPVMQQQPLEKKMKPFPMEPYNHN
PSEVKVPEFYWDSSYSMADNRSVMAQQANIDRRGKRSPGIFRPEQDPVPRMPFEKSLLEKPSELMSHSSSFLSLT
GFSLNQERYPNNSMFNEVYGKNLTSSSKAELSPSMAPQETSLYSLFEGTPWSPSLPASSDHSTPASQSPHSSNPS
SLPSSPPTHNHNSVPFSNFGPIGTPDNRDRRTADRWKTDKPAMGGFGIDYLSATSSSESSWHQASTPSGTWTGHG
PSMEDSSAVLMESLKSIWSSSMMHPGPSALEQLLMQQKQKQQRGQGTMNPPH

FIGURE 521A

ACCACCTGATCAAGGAAAAGGAAGGCACAGCGGAGCGCAGAGTGAGAACCACCAACCGAGGCGCCGGGCAGCGAC
CCCTGCAGCGGAGACAGAGACTGAGCGGCCCGGCCCCGCCATGCCTGCGCTCTGGCTGGGCTGCTGCCTCTGCTT
CTCGCTCCTCCTGCCCGCAGCCCGGGCCACCTCCAGGAGGGAAGTCTGTGATTGCAATGGGAAGTCCAGGCAGTG
TATCTTTGATCGGGAACTTCACAGACAAACTGGTAATGGATTCCGCTGCCTCAACTGCAATGACAACACTGATGG
CATTCACTGCGAGAAGTGCAAGAATGGCTTTTACCGGCACAGAGAAAGGGACCGCTGTTTGCCCTGCAATTGTAA
CTCCAAAGGTTCTCTTAGTGCTCGATGTGACAACTCCGGACGGTGCAGCTGTAAACCAGGTGTGACAGGAGCCAG
ATGCGACCGATGTCTGCCAGGCTTCCACATGCTCACGGATGCGGGGTGCACCCAAGACCAGAGACTGCTAGACTC
CAAGTGTGACTGTGACCCAGCTGGCATCGCAGGGCCCTGTGACGCGGGCCGCTGTGTCTGCAAGCCAGCTGTCAC
TGGAGAACGCTGTGATAGGTGTCGATCAGGTTACTATAATCTGGATGGGGGGAACCCTGAGGGCTGTACCCAGTG
TTTCTGCTATGGGCATTCAGCCAGCTGCCGCAGCTCTGCAGAATACAGTGTCCATAAGATCACCTCTACCTTTCA
TCAAGATGTTGATGGCTGGAAGGCTGTCCAACGAAATGGGTCTCCTGCAAAGCTCCAATGGTCACAGCGCCATCA
AGATGTGTTTAGCTCAGCCCAACGACTAGACCCTGTCTATTTTGTGGCTCCTGCCAAATTTCTTGGGAATCAACA
GGTGAGCTATGGTCAAAGCCTGTCCTTTGACTACCGTGTGGACAGAGGAGGCAGACACCCATCTGCCCATGATGT
GATTCTGGAAGGTGCTGGTCTACGGATCACAGCTCCCTTGATGCCACTTGGCAAGACACTGCCTTGTGGGCTCAC
CAAGACTTACACATTCAGGTTAAATGAGCATCCAAGCAATAATTGGAGCCCCCAGCTGAGTTACTTTGAGTATCG
AAGGTTACTGCGGAATCTCACAGCCCTCCGCATCCGAGCTACATATGGAGAATACAGTACTGGGTACATTGACAA
TGTGACCCTGATTTCAGCCCGCCCTGTCTCTGGAGCCCCAGCACCCTGGGTTGAACAGTGTATATGTCCTGTTGG
GTACAAGGGGCAATTCTGCCAGGATTGTGCTTCTGGCTACAAGAGAGATTCAGCGAGACTGGGGCCTTTTGGCAC
CTGTATTCCTTGTAACTGTCAAGGGGGAGGGGCCTGTGATCCAGACACAGGAGATTGTTATTCAGGGGATGAGAA
TCCTGACATTGAGTGTGCTGACTGCCCAATTGGTTTCTACAACGATCCGCACGACCCCCGCAGCTGCAAGCCATG
TCCCTGTCATAACGGGTTCAGCTGCTCAGTGATGCCGGAGACGGAGGAGGTGGTGTGCAATAACTGCCCTCCCGG
GGTCACCGGTGCCCGCTGTGAGCTCTGTGCTGATGGCTACTTTGGGGACCCCTTTGGTGAACATGGCCCAGTGAG
GCCTTGTCAGCCCTGTCAATGCAACAACAATGTGGACCCCAGTGCCTCTGGGAATTGTGACCGGCTGACAGGCAG
GTGTTTGAAGTGTATCCACAACACAGCCGGCATCTACTGCGACCAGTGCAAAGCAGGCTACTTCGGGGACCCATT
GGCTCCCAACCCAGCAGACAAGTGTCGAGCTTGCAACTGTAACCCCATGGGCTCAGAGCCTGTAGGATGTCGAAG
TGATGGCACCTGTGTTTGCAAGCCAGGATTTGGTGGCCCCAACTGTGAGCATGGAGCATTCAGCTGTCCAGCTTG
CTATAATCAAGTGAAGATTCAGATGGATCAGTTTATGCAGCAGCTTCAGAGAATGGAGGCCCTGATTTCAAAGGC
TCAGGGTGGTGATGGAGTAGTACCTGATACAGAGCTGGAAGGCAGGATGCAGCAGGCTGAGCAGGCCCTTCAGGA
CATTCTGAGAGATGCCCAGATTTCAGAAGGTGCTAGCAGATCCCTTGGTCTCCAGTTGGCCAAGGTGAGGAGCCA
AGAGAACAGCTACCAGAGCCGCCTGGATGACCTCAAGATGACTGTGGAAAGAGTTCGGGCTCTGGGAAGTCAGTA
CCAGAACCGAGTTCGGGATACTCACAGGCTCATCACTCAGATGCAGCTGAGCCTGGCAGAAAGTGAAGCTTCCTT
GGGAAACACTAACATTCCTGCCTCAGACCACTACGTGGGGCCAAATGGCTTTAAAAGTCTGGCTCAGGAGGCCAC
AAGATTAGCAGAAAGCCACGTTGAGTCAGCCAGTAACATGGAGCAACTGACAAGGGAAACTGAGGACTATTCCAA
ACAAGCCCTCTCACTGGTGCGCAAGGCCCTGCATGAAGGAGTCGGAAGCGGAAGCGGTAGCCCGGACGGTGCTGT
GGTGCAAGGGCTTGTGGAAAAATTGGAGAAAACCAAGTCCCTGGCCCAGCAGTTGACAAGGGAGGCCACTCAAGC
GGAAATTGAAGCAGATAGGTCTTATCAGCACAGTCTCCGCCTCCTGGATTCAGTGTCTCGGCTTCAGGGAGTCAG
TGATCAGTCCTTTCAGGTGGAAGAAGCAAAGAGGATCAAACAAAAAGCGGATTCACTCTCAAGCCTGGTAACCAG
GCATATGGATGAGTTCAAGCGTACACAGAAGAATCTGGGAAACTGGAAAGAAGAAGCACAGCAGCTCTTACAGAA
TGGAAAAAGTGGGAGAGAGAAATCAGATCAGCTGCTTTCCCGTGCCAATCTTGCTAAAAGCAGAGCACAAGAAGC
ACTGAGTATGGGCAATGCCACTTTTTATGAAGTTGAGAGCATCCTTAAAAACCTCAGAGAGTTTGACCTGCAGGT
GGACAACAGAAAAGCAGAAGCTGAAGAAGCCATGAAGAGACTCTCCTACATCAGCCAGAAGGTTTCAGATGCCAG
TGACAAGACCCAGCAAGCAGAAAGAGCCCTGGGGAGCGCTGCTGCTGATGCACAGAGGGCAAAGAATGGGGCCGG
GGAGGCCCTGGAAATCTCCAGTGAGATTGAACAGGAGATTGGGAGTCTGAACTTGGAAGCCAATGTGACAGCAGA
TGGAGCCTTGGCCATGGAAAAGGGACTGGCCTCTCTGAAGAGTGAGATGAGGGAAGTGGAAGGAGAGCTGGAAAG
GAAGGAGCTGGAGTTTGACACGAATATGGATGCAGTACAGATGGTGATTACAGAAGCCCAGAAGGTTGATACCAG
AGCCAAGAACGCTGGGGTTACAATCCAAGACACACTCAACACATTAGACGGCCTCCTGCATCTGATGGACCAGCC
TCTCAGTGTAGATGAAGAGGGGCTGGTCTTACTGGAGCAGAAGCTTTCCCGAGCCAAGACCCAGATCAACAGCCA
ACTGCGGCCCATGATGTCAGAGCTGGAAGAGAGGGCACGTCAGCAGAGGGGCCACCTCCATTTGCTGGAGACAAG

FIGURE 521B

CATAGATGGGATTCTGGCTGATGTGAAGAACTTGGAGAACATTAGGGACAACCTGCCCCCAGGCTGCTACAATAC
CCAGGCTCTTGAGCAACAGTGAAGCTGCCATAAATATTTCTCAACTGAGGTTCTTGGGATACAGATCTCAGGGCT
CGGGAGCCATGTCATGTGAGTGGGTGGGATGGGGACATTTGAACATGTTTAATGGGTATGCTCAGGTCAACTGAC
CTGACCCCATTCCTGATCCCATGGCCAGGTGGTTGTCTTATTGCACCATACTCCTTGCTTCCTGATGCTGGGCAA
TGAGGCAGATAGCACTGGGTGTGAGAATGATCAAGGATCTGGACCCCAAAGAATAGACTGGATGGAAAGACAAAC
TGCACAGGCAGATGTTTGCCTCATAATAGTCGTAAGTGGAGTCCTGGAATTTGGACAAGTGCTGTTGGGATATAG
TCAACTTATTCTTTGAGTAATGTGACTAAAGGAAAAAACTTTGACTTTGCCCAGGCATGAAATTCTTCCTAATGT
CAGAACAGAGTGCAACCCAGTCACACTGTGGCCAGTAAAATACTATTGCCTCATATTGTCCTCTGCAAGCTTCTT
GCTGATCAGAGTTCCTCCTACTTACAACCCAGGGTGTGAACATGTTCTCCATTTTCAAGCTGGAAGAAGTGAGCA
GTGTTGGAGTGAGGACCTGTAAGGCAGGCCCATTCAGAGCTATGGTGCTTGCTGGTGCCTGCCACCTTCAAGTTC
TGGACCTGGGCATGACATCCTTTCTTTTAATGATGCCATGGCAACTTAGAGATTGCATTTTTATTAAAGCATTTC
CTACCAGCAAAGCAAATGTTGGGAAAGTATTTACTTTTTCGGTTTCAAAGTGATAGAAAAGTGTGGCTTGGGCAT
TGAAAGAGGTAAAATTCTCTAGATTTATTAGTCCTAATTCAATCCTACTTTTCGAACACCAAAAATGATGCGCAT
CAATGTATTTTATCTTATTTTCTCAATCTCCTCTCTCTTTCCTCCACCCATAATAAGAGAATGTTCCTACTCACA
CTTCAGCTGGGTCACATCCATCCCTCCATTCATCCTTCCATCCATCTTTCCATCCATTACCTCCATCCATCCTTC
CAACATATATTTATTGAGTACCTACTGTGTGCCAGGGGCTGGTGGGACAGTGGTGACATAGTCTCTGCCCTCATA
GAGTTGATTGTCTAGTGAGGAAGACAAGCATTTTTAAAAAATAAATTTAAACTTACAAACTTTGTTTGTCACAAG
TGGTGTTTATTGCAATAACCGCTTGGTTTGCAACCTCTTTGCTCAACAGAACATATGTTGCAAGACCCTCCCATG
GGGGCACTTGAGTTTTGGCAAGGCTGACAGAGCTCTGGGTTGTGCACATTTCTTTGCATTCCAGCTGTCACTCTG
TGCCTTTCTACAACTGATTGCAACAGACTGTTGAGTTATGATAACACCAGTGGGAATTGCTGGAGGAACCAGAGG
CACTTCCACCTTGGCTGGGAAGACTATGGTGCTGCCTTGCTTCTGTATTTCCTTGGATTTTCCTGAAAGTGTTTT
TAAATAAAGAACAATTGTTAGA

FIGURE 522

CCCAACCGCAGTTGACTAGCACCTGCTACCGCGCCTTTGCTTCCTGGCGCACGCGGAGCCTCCTGGAGCCTGCCA
CCATCCTGCCTACTACGTGCTGCCCTGCGCCCGCAGCCATGTGCCGCACCCTGGCCGCCTTCCCCACCACCTGCC
TGGAGAGAGCCAAAGAGTTCAAGACACGTCTGGGGATCTTTCTTCACAAATCAGAGCTGGGCTGCGATACTGGGA
GTACTGGCAAGTTCGAGTGGGGCAGTAAACACAGCAAAGAGAATAGAAACTTCTCAGAAGATGTGCTGGGGTGGA
GAGAGTCGTTCGACCTGCTGCTGAGCAGTAAAAATGGAGTGGCTGCCTTCCACGCTTTCCTGAAGACAGAGTTCA
GTGAGGAGAACCTGGAGTTCTGGCTGGCCTGTGAGGAGTTCAAGAAGATCCGATCAGCTACCAAGCTGGCCTCCA
GGGCACACCAGATCTTTGAGGAGTTCATTTGCAGTGAGGCCCCTAAAGAGGTCAACATTGACCATGAGACCCACG
AGCTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGAAGACACGTACCCTGA
TGGAGAAGGACTCCTACCCACGCTTCCTGAAGTCGCCTGCTTACCGGGACCTGGCTGCCCAAGCCTCAGCCGCCT
CTGCCACTCTGTCCAGCTGCAGCCTGGACGAGCCCTCACACACCTGAGTCTCCACGGCAGTGAGGAAGCCAGCCG
GGAAGAGAGGTTGAGTCACCCATCCCCGAGGTGGCTGCCCCTGTGTGGGAGGCAGGTTCTGCAAAGCAAGTGCAA
GAGGACAAAAAAAAAAAAAAAAAAAAAAAAAATGCGCTCCAGCAGCCTGTTTGGGAAGCAGCAGTCTCTCCTTCA
GATACTGTGGGACTCATGCTGGAGAGGAGCCGCCCACTTCCAGGACCTGTGAATAAGGGCTAATGATGAGGGTTG
GTGGGGCTCTCTGTGGGGCAAAAAGGTGGTATGGGGGTTAGCACTGGCTCTCGTTCTCACCGGAGAAGGAAGTGT
TCTAGTGTGGTTTAGGAAACATGTGGATAAAGGGAACCATGAAAATGAGAGGAGGAAAGACATCCAGATCAGCTG
TTTTGCCTGTTGCTCAGTTGACTCTGATTGCATCCTGTTTTCCTAATTCCCAGACTGTTCTGGGCACGGAAGGGA
CCCTGGATGTGGAGTCTTCCCCTTTGGCCCTCCTCACTGGCCTCTGGGCTAGCCCAGAGTCCCTTAGCTTGTACC
TCGTAACACTCCTGTGTGTCTGTCCAGCCTTGCAGTCATGTCAAGGCCAGCAAGCTGATGTGACTCTTGCCCCAT
GCGAGATATTTATACCTCAAACACTGGCCTGTGAGCCCTTTCCAAGTCAGTGGAGAGCCCTGAAAGGAGGCTCAC
TTGAATCCAGCTCAGTGCTCTGGGTGGCCCCCTGCAGGTGGCCCCTGACCCTGCGTTGCAGCAGGGTCCACCTGT
GAGCAGGCCCGCCCTGGGGCCTCTTCCTGGATGTGCCCTCTCTGAGTTCTGTGCTGTCTCTTGGAGGCAGGGCCC
AGGAGAACAAAGTGTGGAGGCCTCGGGGAGTGGCTTTTCCAGCTCTCATGCCCCGCAGTGTGGAACAAGGCAGAA
AAGGATCCTAGGAAATAAGTCTCTTGGCGGTCCCTGAGAGTCCTGCTGAAATCCAGCCAGTGTTTTTTGTGGTAT
GAGAACAGGCAAAAAGAGATGCCCCGAGATAGAAGGGGAGCCTTGTGTTTCTTTCCTGCAGACGTGAGATGAACA
CTGGAGTGGGCAGAGGTGGCCCAGGACCATGGCACCCTTAGAGTGCAGAAGCTGGGGGGAGAGGCTGCTTCGAAG
GGCAGGACTGGGGATAATCAGAACCTGCCTGTCACCTCAGGGCATCACTGAACAAACATTTCCTGATGGCAACTC
CTGCGGCAGAGCCCAGGCTGGGGAAGTGAACTACCCAGGGCAGCCCCTTTGTGGCCCAGGATAATCAACACTGTT
CTCTCTGTACCATGAGCTCCTCCAGGAGATTATTTAAGTGTATTGTATCATTGGTTTCTGTGATTGTCATAACA
TTGTTTTTGTTATTGTTGGTGCTGTTGTTATTTATTATTGTAATTTCAGTTTGCCTCTACTGGAGAATCTCAGCA
GGGGTTTCAGCCTGACTGTCTCCCTTTCTCTACCAGACTCTACCTCTGAATGTGCTGGGAACCTCTTGGAGCCTG
TCAGGAACTCCTCACTGTTTAAATATTTATTTATTGTGACAAATGGAGCTGGTTTCCTAGATATGAATGATGTTT
GCAATCCCCATTTTCCTGTTTCAGCATGTTATATTCTTATAAAATAAAAGCAAAAGTCAAATATG

FIGURE 523

GGGTGCGGGGCTGCTGGCGGCTCTGCAGAGTCGAGAGTGGGAGAAGAGCGGAGCGTGTGAGCAGTACTGCGGCCT
CCTCTCCTCTCCTAACCTCGCTCTCGCGGCCTAGCTTTACCCGCCCGCCTGCTCGGCGACCAGCGGGGATCCTCC
CCCAGCCGCAAGTCCACGAAGAAAGCAACGAATGAAAATTATGAAGACAACGAGAAGTCAGACTCCTCCGGGTCG
CGCTCCAGCTGCTTCGGCTTCGTCGCCTACTCTGTGAACTCCGGGGAGAGATCTCGAGTCAAGATTAAGACCTTA
ACCCACCAACCTGCCTGTTCGGACACCCCCCGGGCCGGCCGCTGTCTGTCCCCTTCTCCATCGCCCTCTCCCAGA
AAGCTCCGGTGCTTGGACCAGCTAGAGTCTGAGAAAGAGGAGAGGCGCGAACGCCACTCCAAAAAGAGAAGGGTT
AAAGAGGGCAACCCTAACGATACGCTTGACTTTCTGTGGCTGGGAACACCTTCCACCATGACCACCTCAGCAAGT
TCCCACTTAAATAAAGGCATCAAGCAGGTGTACATGTCCCTGCCTCAGGGTGAGAAAGTCCAGGCCATGTATATC
TGGATCGATGGTACTGGAGAAGGACTGCGCTGCAAGACCCGGACCCTGGACAGTGAGCCCAAGTGTGTGGAAGAG
TTGCCTGAGTGGAATTTCGATGGCTCTAGTACTTTACAGTCTGAGGGTTCCAACAGTGACATGTATCTCGTGCCT
GCTGCCATGTTTCGGGACCCCTTCCGTAAGGACCCTAACAAGCTGGTGTTATGTGAAGTTTTCAAGTACAATCGA
AGGCCTGCAGAGACCAATTTGAGGCACACCTGTAAACGGATAATGGACATGGTGAGCAACCAGCACCCCTGGTTT
GGCATGGAGCAGGAGTATACCCTCATGGGGACAGATGGGCACCCCTTTGGTTGGCCTTCCAACGGCTTCCCAGGG
CCCCAGGGTCCATATTACTGTGGTGTGGGAGCAGACAGAGCCTATGGCAGGGACATCGTGGAGGCCCATTACCGG
GCCTGCTTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGTCATGCCTGCCCAGTGGGAATTTCAGATT
GGACCTTGTGAAGGAATCAGCATGGGAGATCATCTCTGGGTGGCCCGTTTCATCTTGCATCGTGTGTGTGAAGAC
TTTGGAGTGATAGCAACCTTTGATCCTAAGCCCATTCCTGGGAACTGGAATGGTGCAGGCTGCCATACCAACTTC
AGCACCAAGGCCATGCGGGAGGAGAATGGTCTGAAGTACATCGAGGAGGCCATTGAGAAACTAAGCAAGCGGCAC
CAGTACCACATCCGTGCCTATGATCCCAAGGGAGGCCTGGACAATGCCCGACGTCTAACTGGATTCCATGAAACC
TCCAACATCAACGACTTTTCTGCTGGTGTAGCCAATCGTAGCGCCAGCATACGCATTCCCCGGACTGTTGGCCAG
GAGAAGAAGGGTTACTTTGAAGATCGTCGCCCCTCTGCCAACTGCGACCCCTTTTCGGTGACAGAAGCCCTCATC
CGCACGTGTCTTCTCAATGAAACCGGCGATGAGCCCTTCCAGTACAAAAATTAAGTGGACTAGACCTCCAGCTGT
TGAGCCCCTCCTAGTTCTTCATCCCACTCCAACTCTTCCCCCTCTCCCAGTTGTCCCGATTGTAACTCAAAGGGT
GGAATATCAAGGTCGTTTTTTTCATTCCATGTGCCCAGTTAATCTTGCTTTCTTTGTTTGGCTGGGATAGAGGGG
TCAAGTTATTAATTTCTTCACACCTACCCTCCTTTTTTTCCCTATCACTGAAGCTTTTTAGTGCATTAGTGGGGA
GGAGGGTGGGGAGACATAACCACTGCTTCCATTTAATGGGGTGCACCTGTCCAATAGGCGTAGCTATCCGGACAG
AGCACGTTTGCAGAAGGGGGTCTCTTCTTCCAGGTAGCTGAAAGGGGAAGACCTGACGTACTCTGGTTAGGTTAG
GACTTGCCCCTCGTGGTGGAAACTTTTCTTAAAAAGTTATAACCAACTTTTCTATTAAAAGTGGGAATTAGGAGAG
AAGGTAGGGGTTGGGAATCAGAGAGAATGGCTTTGGTCTCTTGCTTGTGGGACTAGCCTGGCTTGGGACTAAATG
CCCTGCTCTGAACACGAAGCTTAGTATAAACTGATGGATATCCCTACCTTGAAAGAAGAAAAGGTTCTTACTGCT
TGGTCCTTGATTTATCACACAAAGCAGAATAGTATTTTTATATTTAAATGTAAAGACAAAAAACTATATGTATGG
TTTTGTGGATTATGTGTGTTTTGCTAAAGGAAAAAACCATCCAGGTCACGGGGCACCAAATTTGAGACAAATAGT
CGGATTAGAAATAAAGCATCTCATTTTGAGTAGAGAGCAAGGGAAGTGGTTCTTAGATGGTGATCTGGGATTAGG
CCCTCAAGACCCTTTTGGGTTTCTGCCCTGCCCACCCTCTGGAGAAGGTGGGCACTGGATTAGTTAACAGACAAC
ACGTTACTAGCAGTCACTTGATCTCCGTGGCTTTGGTTTAAAGACACACTTGTCCACATAGGTTTAGAGATAAG
AGTTGGCTGGTCAACTTGAGCATGTTACTGACAGAGGGGGTATTGGGGTTATTTTCTGGTAGGAATAGCATGTCA
CTAAAGCAGGCCTTTTGATATTAAATTTTTTAAAAAGCAAAATTATAGAAGTTTAGATTTTAATCAAATTTGTAG
GGTTTCTAGGTAATTTTTACAGAATTGCTTGTTTGCTTCAACTGTCTCCTACCTCTGCTCTTGGAGGAGATGGGG
ACAGGGCTGGAGTCAAAACACTTGTAATTTTGTATCTTGATGTCTTTGTTAAGACTGCTGAAGAATTATTTTTTT
TCTTTTATAATAAGGAATAAACCCCACCTTTATTCCTTCATTTCATCTACCATTTTCTGGTTCTTGTGTTGGCTG
TGGCAGGCCAGCTGTGGTTTTCTTTTGCCATGACAACTTCTAATTGCCATGTACAGTATGTTCAAAGTCAAATAA
CTCCTCATTGTAAACAAACTGTGTAACTGCCCAAAGCAGCACTTATAAATCAGCCTAACAT

FIGURE 524A

GCGGGGAGGGGCGGGGCTATGGAGAGGAGGAGGAAGATGGCGGGCGGGCTGCTCTGAAGAGACCTCGGCGGCGGC
GGAGGAGGAGAGAAGCGCAGCGCCGCGCCGCGCCGGGGCCCATGTGGGGAGGAGTCGGAGTCGCTGTTGCCGCCG
CCGCCTGTAGCTGCTGGACCCGAGTGGGAGTGAGGGGGAAACGGCAGGATGAAGTTCGCCGAGCACCTCTCCGCG
CACATCACTCCCGAGTGGAGGAAGCAATACATCCAGTATGAGGCTTTCAAGGATATGCTGTATTCAGCTCAGGAC
CAGGCACCTTCTGTGGAAGTTACAGATGAGGACACAGTAAAGAGGTATTTTGCCAAGTTTGAAGAGAAGTTTTTC
CAAACCTGTGAAAAAGAACTTGCCAAAATCAACACATTTTATTCAGAGAAGCTCGCAGAGGCTCAGCGCAGGTTT
GCTACACTTCAGAATGAGCTTCAGTCATCACTGGATGCACAGAAAGAAAGCACTGGTGTTACTACGCTGCGACAA
CGCAGAAAGCCAGTCTTCCACTTGTCCCATGAGGAACGTGTCCAACATAGAAATATTAAAGACCTTAAACTGGCC
TTCAGTGAGTTCTACCTCAGTCTAATCCTGCTGCAGAACTATCAGAATCTGAATTTTACAGGGTTTCGAAAAATC
CTGAAAAAGCATGACAAGATCCTGGAAACATCTCGTGGAGCAGATTGGCGAGTGGCTCACGTAGAGGTGGCCCCA
TTTTATACATGCAAGAAAATCAACCAGCTTATCTCTGAAACTGAGGCTGTAGTGACCAATGAACTTGAAGATGGT
GACAGACAAAAGGCTATGAAGCGTTTACGTGTCCCCCCTTTGGGAGCTGCTCAGCCTGCACCAGCATGGACTACT
TTTAGAGTTGGCCTATTTTGTGGAATATTCATTGTACTGAATATTACCCTTGTGCTTGCCGCTGTATTTAAACTT
GAAACAGATAGAAGTATATGGCCCTTGATAAGAATCTATCGGGGTGGCTTTCTTCTGATTGAATTCCTTTTTCTA
CTGGGCATCAACACGTATGGTTGGAGACAGGCTGGAGTAAACCATGTACTCATCTTTGAACTTAATCCGAGAAGC
AATTTGTCTCATCAACATCTCTTTGAGATTGCTGGATTCCTCGGGATATTGTGGTGCCTGAGCCTTCTGGCATGC
TTCTTTGCTCCAATTAGTGTCATCCCCACATATGTGTATCCACTTGCCCTTTATGGATTTATGGTTTTCTTCCTT
ATCAACCCCACCAAAACTTTCTACTATAAATCCCGGTTTTGGCTGCTTAAACTGCTGTTTCGAGTATTTACAGCC
CCCTTCCATAAGGTAGGCTTTGCTGATTTCTGGCTGGCGGATCAGCTGAACAGCCTGTCAGTGATACTGATGGAC
CTGGAATATATGATCTGCTTCTACAGTTTGGAGCTCAAATGGGATGAAAGTAAGGGCCTGTTGCCAAATAATTCA
GAAGAATCAGGAATTTGCCACAAATATACATATGGTGTGCGGGCCATTGTTCAGTGCATTCCTGCTTGGCTTCGC
TTCATCCAGTGCCTGCGCCGATATCGAGACACAAAAAGGGCCTTTCCTCATTTAGTTAATGCTGGCAAATACTCC
ACAACTTTCTTCATGGTGACGTTTGCAGCCCTTTACAGCACTCACAAAGAACGAGGTCACTCGGACACTATGGTG
TTCTTTTACCTGTGGATTGTCTTTTATATCATCAGTTCCTGCTATACCCTCATCTGGGATCTCAAGATGGACTGG
GGTCTCTTCGATAAGAATGCTGGAGAGAACACTTTCCTCCGGGAAGAGATTGTATACCCCCAAAAAGCCTACTAC
TACTGTGCCATAATAGAGGATGTGATTCTGCGCTTTGCTTGGACTATCCAAATCTCGATTACCTCTACAACTTTG
TTGCCTCATTCTGGGGACATCATTGCTACTGTCTTTGCCCCACTTGAGGTTTTCCGGCGATTTGTGTGGAACTTC
TTCCGCCTGGAGAATGAACATCTGAATAACTGTGGTGAATTCCGTGCTGTGCGGGACATCTCTGTGGCCCCCCTG
AACGCAGATGATCAGACTCTCCTAGAACAGATGATGGACCAGGATGATGGGGTACGAAACCGCCAGAAGAATCGG
TCATGGAAGTACAACCAGAGCATATCCCTGCGCCGGCCTCGCCTCGCTTCTCAATCCAAGGCTCGTGACACTAAG
GTATTGATAGAAGACACAGATGATGAAGCTAACACTTGAATTTTCTGAAGTCTAGCTTAACATCTTTGGTTTTCC
TACTCTACAATCCTTTCCTCGACCAACGCAACCTCTAGTACCTTTCCAGCCGAAAACAGGAGAAAACACATAACA
CATTTTCCGAGCTCTTCCGGATCGGATCCTATGGACTCCAAACAAGCTCACTGTGTTTCTTTTCTTTTCTTCTGG
TTTAATTTTAATTTTCTATTTTCAAAACAAATATTTACTTCATTTGCCAATCAGAGGATGTTTTAAGAAACAAAA
CATAGTATCTTATGGATTGTTTACAATCACAAGGACATAGATACCTATCAGGATGAAGAACAGGCATTGCAAGGA
CCCTCTGATGGGACGGTACTGAGATATCTCGGCTTCCGCTCAGCCCGGTTTTGACTGGTTGAAACCGGACATTGG
TTTTTAAATTTTTTGTCAGTTTATGTGGAGAATTTTTTTCTTTCCTTCATACCCAGCGCAAAGGCACTGGCCGCA
CTTGCAGGAAAAGTGCAACTTAAAGCAGTACCTTCATTCATGAAGCTACTTTTTAATTTGATGTAACTTTTCTTA
TTTTGGGAAGGGTTGCTGGGTGGGTGGGAAATATGATGTATTTGTTACACATAGTTTTCTCATTATTTATGAAAC
TTAACCATACAGAATGATATAACTCCTGTGCAATGAAGGTGATAACAGTAAAAGAAGGCAGGGGAAACTTACGTT
GGATGACATTTATGAGGGTCAGTCCCACATACCTCTTTCAGGAGACAACTTGCACCAGTTTGACCTTTTCTTTTC
TTTGTTTTTATTTTAAGCCAAAGTTTCATTGCTAACTTCTTAAGTTGCTGCTGCTTTAGAGTCCTGAGCATATCT
CTCATAACAAGGAATCCCACACTTCACACCACCGGCTGAATTTCATGGAAGAGGTTCTGATAATTTTTTTAACTT
TTTAAGGAACAGATGTGGAATACACTGGCCCATATTTCAACCTTAACAGCTGAAGCTATGCCTTATTATGCATCC
ACATGTATGGTCCCTGTAGCGTGACCTTTACTAGCTCTGAATCAGAAGACAGAGCTATTTCAGAGGCTCTGTGTG
CCCTCACTAGATAGTTTTTCTTCTGGGTTCAACCACTTTAGCCAGAATTTGATCAAATTAAAAGTCTGTCATGGG
GAAACTATATTTTTGAGCACATGGAACAAATTATACTTCCTCATTCATATTATGTTGATACAAAAGACCTTGGCA
GCCATTTCTCCCAGCAGTTTTAAAGGATGAACATTGGATTTCATGCCATCCCATAGAAAACCTGTTTTAAAATTT

FIGURE 524B

TAGGGATCTTTACTTGGTCATACATGAAAAGTACACTGCTTAGAAATTATAGACTATTATGATCTGTCCACAGTG
CCCATTGTCACTTCTTTGTCTCATTTCTTCCCTTTGTTCCTTAGTCATCCAAATAAGCCTGAAAACCATAAGAGA
TATTACTTTATTGAATATGGTTGGCATTAAATTTAGCATTTCATTATCTAACAAAATTAATATAAATTCCAGGAC
ATGGTAAAATGTGTTTTAATAACCCCCAGACCCAAATGAAAATTTCAAAGTCAATACCAGCAGATTCATGAAAGT
AAATTTAGTCCTATAATTTTCAGCTTAATTATAAACAAAGGAACAAATAAGTGGAAGGGCAGCTATTACCATTCG
CTTAGTCAAAACATTCGGTTACTGCCCTTTAATACACTCCTATCATCAGCACTTCCACCATGTATTACAAGTCTT
GACCCATCCCTGTCGTAACTCCAGTAAAAGTTACTGTTACTAGAAAATTTTTATCAATTAACTGACAAATAGTTT
CTTTTTAAAGTAGTTTCTTCCATCTTTATTCTGACTAGCTTCCAAAATGTGTTCCCTTTTTGAATCGAGGTTTTT
TTGTTTTGTTTTGTTTTCTGAAAAAATCATACAACTTTGTGCTTCTATTGCTTTTTTGTGTTTTGTTAAGCATGT
CCCTTGGCCCAAATGGAAGAGGAAATGTTTAATTAATGCTTTTTAGTTTAAATAAATTGAATCATTTATAATAAT
CAGTGTTAACAATTTAGTGACCCTTGGTAGGTTAAAGGTTGCATTATTTATACTTGAGATTTTTTTCCCCTAACT
ATTCTGTTTTTTGTACTTTAAAACTATGGGGGAAATATCACTGGTCTGTCAAGAAACAGCAGTAATTATTACTGA
GTTAAATTGAAAAGTCCAGTGGACCAGGCATTTCTTATATAAATAAAATTGGTGGTACTAATGTG

FIGURE 525

AATAAATTATTTTTGTTAAGGCAAGCATTGGTGTGTTCTTTAACTTGCTACTTGGAGACCTAGTGTCCAGTCTGG
ACAGA**ATG**CACAGAGACCAGCCTCACCTGGAATGCAGCCAGACTCGATGTCCCTCAGCACACACAGCTCCTGGCC
ACAGACTGCCCATAGAACTGTCTGCACCCAAACCCCATGGCCTTTTCATGCACGGAGACAGGCCTCTGGATGTGC
AGCCTTGCCACCCCCTGCCCCAATCCTCCCTGAGAGCTCCTGCCTCAGTGCCCTGGGCTGGTGAGGGAGAAGCCT
GTCTGCACCTGCCTAATTCCAGCTCCTCCAGGAAGCAAGGGCTTGTTTGTCAGAGCTGCAGGGTTGGCCACTCGG
TGGGGAGGAGTCAGCCAGGATTAGAGAGCCTGCCCCTAATCCGGCCTGCTGGGTTTTACAAGGATCAGAGCTGC**T**
GATAATGAACCTCATTAAGGGGGAGCAGGAGCCTCAATCCGATTTGGTTTTCTCTTTGACATCTTCACTCTGCTC
AGATGGCCTGGGTGCTATGTGGAGCAGGTGGGATGCCAAGGCCACTCCTGCTATGGGGCAGCTGGGGCTGGGGAG
GGATGGCAGTCTCCCTGCATGTTTCCCTCGACCTCTTTAGCTGCAGCGCCTTGCTGGGCTCCTGGGTTGGACTCC
CTCTCTGTGCCCCTGCTCCAGGCACCCATTGGCTCCATCCTCCTGGTTGTGCTCTGCACCCCCTGCTCCCTTGGG
CTGGCCCTGGCTGGGGGCCTGAGAGACAGACAGGAACCCACAATCAGGAGGCAACCCTGGCCTGCAAGAGGAAGA
CAGAGGCTCCCAGGGCCGGTGCCCTGTGTGCCCACTGCACCAAGGCCGCTGAATAAGCCTGCCCTTCACCCCCTA
AGGGCTCCTTGCCCAATGCCAAGTGCTGGGGATTTCTGTCAGCAAGCCCTGTGGCTCCAGTGACGGTATTTCTAA
AGCCAAACTTAGTTACCTAGAATTAGCGCCATGTTGGAAACACTGTCGCAGCAGCCCGGGCTGCACAGTGTGTAG
CCCAGCCTCCAGGTCCACGGAGTGGTGTGGACCTCCCACCTCACAGCTGCCTCTGGCAGCCAAGCCTCTTTTCGC
CCGGCCCCAGCCCCTCTGGTTGATAAACGGGTGGGCCTCCTCAGCAGCGTGGCTGCCTTTCACCTTGATTTCCCC
AGGGCTCTCGGCAACATCGATAAACCAGCCTCGCCCACCAGCTGGGCCCTCCCCCACCCAGTCTGCCAGGCTGGG
AGCTGGAGCTTGCTGAGTCTTGAATGCCCTTCTAGATGGCTTCTCTAGAGGCTCTCCTGGCAAGAGAGGGTCCCA
AGGGGAGCCCTGCAAAGCAAAGGCTCCTTGTCTGGGGCGGATAGAGAATCTCGCCTCTGTCTGGTGTGTTACCT
ACTGGGGGCACAGGAACAATTTCCTCAAGGAGACAGTGGCATGGAGCTTTGAAAGACGAGTAGGTGTTAGCAAGG
AAATAAGGAGGAACGGGGGTTACGGGCAGAGGAGAAAGCACATGCCAAGTCAGCAAAGAAAAGTAGAATTCGAAA
ACTTTTTAAAAATATTACTAAGGATTTTCACAATGCTGCACTGGGCTAGAAACTGAAGCTAAAACAGATACGTGG
TCCCTGCTGCTATGGGGCTTCCGTTCTAGAGGCAAGGACAGGTTGTGATGAGGGTTCTGAAGGATAGAGACCAAG
CAGGGAGGGTGTTGAGGAGGCTTCTGCGAGACCTGAAGGATGGGAAGCCAGGAAGTGGGAGGGGTGGGGGTCCAG
GCTGGAGGGGCCCAATGTAGGTGTAGAGGGACTACAGCCCTGAGGGGCTGCTCCATGCGGCATTCTTGGAGGTCC
AAGAGGGGCAGCGCCACCTTGGGCCAGGCTCCTCTCCAGCAGCCTTGGTATGGGGTGGGGGTGGGAAGACCCCTG
ATGCAGCCTGTCCTCTGGGTGTGGGGGTGGAGGAGAGGGCTCCAGGGGACCCAGCCAGCCTTGACCCTGGAGGAA
AGTCAGGTGGGCTCAGAGAGAGCCCTCAAATCTGGGCCCTGGGTCAGGGTGGGGTCAAGTCCAGCCTTGAAGAGA
ATGGACTCTGGAATCTGACGTCTGGGTTTGAATCCAGCTTCCAACACTCACTGGCTGTGTGACTTTGGGCAAGAT
AACTTATCCCCTTGTCCCCATGTGTCATTGGAGATAAACTACCCACCTACCAGATTGTTGTACCATGCTGGGCAA
ACACTAAGTGCTTAATAATGGTAGCCCACTGCTC

FIGURE 526

MHRDQPHLECSQTRCPSAHTAPGHRLPIELSAPKPHGLFMHGDRPLDVQPCHPLPQSSLRAPASVPWAGEGEACL
HLPNSSSSRKQGLVCQSCRVGHSVGRSQPGLESLPLIRPAGFYKDQSC

FIGURE 527

AGCCGGATGGTCCCGCAGCTCGGGGCCGGCC**ATG**CTTCGCGGTCCGTGGCGCCAGCTTTGGCTCTTTCTCCTGCT
GCTGCTCCCGGGCGCGCCTGAGCCCCGCGGCGCCTCCAGGCCGTGGGAGGGAACCGACGAGCCGGGCTCGGCCTG
GGCCTGGCCGGGCTTCCAGCGCCTGCAGGAGCAGCTCAGGGCGGCGGGTGCCCTCTCCAAGCGGTACTGGACGCT
CTTCAGCTGCCAGGTGTGGCCCGACGACTGTGACGAGGACGAGGAGGCAGCCACGGGGCCCCTGGGCTGGCGCCT
TCCTCTGTTGGGCCAGCGGTACCTGGACCTCCTGACCACGTGGTACTGCAGCTTCAAAGACTGCTGCCCTAGAGG
GGATTGCAGAATCTCCAACAACTTTACAGGCTTAGAGTGGGACCTGAATGTGCGGCTGCATGGCCAGCATTTGGT
CCAGCAGCTGGTCCTAAGAACAGTGAGGGGCTACTTAGAGACGCCCCAGCCAGAAAAGGCCCTTGCTCTGTCGTT
CCACGGCTGGTCTGGCACAGGCAAGAACTTCGTGGCACGGATGCTGGTGGAGAACCTGTATCGGGACGGGCTGAT
GAGTGACTGTGTCAGGATGTTCATCGCCACGTTCCACTTTCCTCACCCCAAATATGTGGACCTGTACAAGGAGCA
GCTGATGAGCCAGATCCGGGAGACGCAGCAGCTCTGCCACCAGACCCTGTTCATCTTCGATGAAGCGGAGAAGCT
GCACCCAGGGCTGCTGGAGGTCCTTGGGCCACACTTAGAACGCCGGGCCCCTGAGGGCCACAGGGCTGAGTCTCC
ATGGACTATCTTTCTGTTTCTCAGTAATCTCAGGGGCGATATAATCAATGAGGTGGTCCTAAAGTTGCTCAAGGC
TGGATGGTCCCGGGAAGAAATTACGATGGAACACCTGGAGCCCCACCTCCAGGCGGAGATTGTGGAGACCATAGA
CAATGGCTTTGGCCACAGCCGTCTTGTGAAGGAAAACCTGATTGACTACTTCATCCCCTTCCTGCCTTTGGAGTA
CCGTCACGTGAGGCTGTGTGCACGGGATGCCTTCCTGAGCCAGGAGCTCCTGTATAAAGAAGAGACACTGGATGA
AATAGCCCAGATGATGGTGTATGTCCCCAAGGAGGAACAACTCTTTTCTTCCCAGGGCTGCAAGTCTATTTCCCA
GAGGATTAACTACTTCCTGTCA**TGA**AGGCTAGAGGAAGACTTCCTGGAACTGCCTTTCTTCCACTAACAGGACCC
TGGGACCTGTAGGAGCACCCCGTTTGGGACTGTGAGGTGTTTGAGGGTGTGGACTGGCATCCAGCAGCCACTAAC
AAACACACAACTGGTGTGTAAAAGGCAGGCCTTACATTAGAAGCCAAGCCAATCCTTTTTCTTTTTTTGGAGGT
CCCACCGAGATAGATAGGAACTTGGATTGCTGAATTCAAAAACAGAGCCCATTCTTAAGATCACTTGGTGCCTTA
AAGACACGCATTCCAAAGTGGAATGTGGTTGAAGAAAGTGGGCCAGGTGGTTGAAGAAAGCCATGTGGGAGCTCA
GCAAATCCCAAGGGCTTATTATGACACTCCAGATGGTCTCCTTAGCATCTCAGCTCTTCTGCAAGGAAGAGCTTG
GGTGTTAGGCCTCAGAGGCTGTAGGGTCCTTGGGTTACAGAGCCGGGGAGAACGAAGTTCTGTGACCCAGGGGTG
GAGAATACACTCTAGGTTTGCGGGCTGGTGGGCTTTCAAATTGGTACTTCCAGAGGAAAGCCAAGCTGCTTCTGT
TGTGAGCGAATCAGCCAAGAGCCTGAGGCTGAAGGGAAAAGTACACAGAGGAAGATATTTTACAAACCAGGTCAG
TGTAGGCCAAGACTTATGGTCTACAGATTTTGGCGGGGGAGGGGGGACCTTTTCAAAGACAATAGGGGGTCTTGA
CATGTTTGTTGTATGTAAAGATGATAAGATTAAAATTTTTGATTTTTCTAAAAAAAAAAAAAAAAA

FIGURE 528

MLRGPWRQLWLFLLLLLPGAPEPRGASRPWEGTDEPGSAWAWPGFQRLQEQLRAAGALSKRYWTLFSCQVWPDDC
DEDEEAATGPLGWRLPLLGQRYLDLLTTWYCSFKDCCPRGDCRISNNFTGLEWDLNVRLHGQHLVQQLVLRTVRG
YLETPQPEKALALSFHGWSGTGKNFVARMLVENLYRDGLMSDCVRMFIATFHFPHPKYVDLYKEQLMSQIRETQQ
LCHQTLFIFDEAEKLHPGLLEVLGPHLERRAPEGHRAESPWTIFLFLSNLRGDIINEVVLKLLKAGWSREEITME
HLEPHLQAEIVETIDNGFGHSRLVKENLIDYFIPFLPLEYRHVRLCARDAFLSQELLYKEETLDEIAQMMVYVPK
EEQLFSSQGCKSISQRINYFLS

FIGURE 529

ATTTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTTCTCTGCTGGATTAAAGACGGCCCACAGACCAGAAC
TTCCACTATACTACTTAAAATTACATAGGTGGCTTGTCAAATTCAATTGATTAGTATTGTAAAAGGAAAAAGAAG
TTCCTTCTTACAGCTTGGATTCAACGGTCCAAAACAAAAATGCAGCTGCCATTAAAGTCACAGATGAACAAACTT
CTACACTGATTTTAAAATCAAGAATAAGGGCAGCAAGTTTCTGGATTCACTGAATCAACAGACACAAAAAGCTG
GCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAATTAACCCAACGCATAGAAGACTTTTTTTCTCTTCT
AAAAACAACTAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTCAAA**ATG**AAGACTTTTACCTG
GACCCTAGGTGTGCTATTCTTCCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATTCAAAATTAAAAAAAT
AAACCAGAGAAGATACCCTCGTGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATACACATTCCTGGTACC
TGAACAAAGAATAACAGGGCCAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCATTAAAGACATGATCAC
CAGGATGGACCTTGAAAACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGTTCTGCAACTGGTGGT
GGATGTAGATGGAAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACATGAACTCTCGTGTTAC
TCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATAATTCACTTGAACTTTCCCAACTGGAAAA
CAAAATCCTCAATGTCACCACAGAAATGTTGAAGATGGCAACAAGATACAGGGAACTAGAGGTGAAATACGCTTC
CTTGACTGATCTTGTCAATAACCAATCTGTGATGATCACTTTGTTGGAAGAACAGTGCTTGAGGATATTTTCCCG
ACAAGACACCCATGTGTCTCCCCCACTTGTCCAGGTGGTGCCACAACATATTCCTAACAGCCAACAGTATACTCC
TGGTCTGCTGGGAGGTAACGAGATTCAGAGGGATCCAGGTTATCCCAGAGATTTAATGCCACCACCTGATCTGGC
AACTTCTCCCACCAAAAGCCCTTTCAAGATACCACCGGTAACTTTCATCAATGAAGGACCATTCAAAGACTGTCA
GCAAGCAAAAGAAGCTGGGCATTCGGTCAGTGGGATTTATATGATTAAACCTGAAAACAGCAATGGACCAATGCA
GTTATGGTGTGAAAACAGTTTGGACCCTGGGGGTTGGACTGTTATTCAGAAAAGAACAGACGGCTCTGTCAACTT
CTTCAGAAATTGGGAAAATTATAAGAAAGGGTTTGGAAACATTGACGGAGAATACTGGCTTGGACTGGAAAATAT
CTATATGCTTAGCAATCAAGATAATTACAAGTTATTGATTGAATTAGAAGACTGGAGTGATAAAAAAGTCTATGC
AGAATACAGCAGCTTTCGTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAACTTACCAGGGAAATGC
AGGGGATTCTATGATGTGGCATAATGGTAAACAATTCACCACACTGGACAGAGATAAAGATATGTATGCAGGAAA
CTGCGCCCACTTTCATAAAGGAGGCTGGTGGTACAATGCCTGTGCACATTCTAACCTAAATGGAGTATGGTACAG
AGGAGGCCATTACAGAAGCAAGCACCAAGATGGAATTTTCTGGGCCGAATACAGAGGCGGGTCATACTCCTTAAG
AGCAGTTCAGATGATGATCAAGCCTATTGAC**TGA**AGAGAGACACTCGCCAATTTAAATGACACAGAACTTTGTAC
TTTTCAGCTCTTAAAAATGTAAATGTTACATGTATATTACTTGGCACAATTTATTTCTACACATAAAGTTTTTAA
AATGAATTTTACCGTAACTATAAAAGGGAACCTATAAATGT

FIGURE 530

MKTFTWTLGVLFFLLVDTGHCRGGQFKIKKINQRRYPRATDGKEEAKKCAYTFLVPEQRITGPICVNTKGQDAST
IKDMITRMDLENLKDVLSRQKREIDVLQLVVDVDGNIVNEVKLLRKESRNMNSRVTQLYMQLLHEIIRKRDNSLE
LSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQSVMITLLEEQCLRIFSRQDTHVSPPLVQVVPQHIPN
SQQYTPGLLGGNEIQRDPGYPRDLMPPPDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPEN
SNGPMQLWCENSLDPGGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSNQDNYKLLIELEDWS
DKKVYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGGWWYNACAHSNL
NGVWYRGGHYRSKHQDGIFWAEYRGGSYSLRAVQMMIKPID

FIGURE 531

ATGGGGCTGCTCACTGGCACTGGAGGCCGAAAGAAGGTGAGGGCAAGTGAGATGCAGGGACCTCTTCTCACAGCT
GTGCTGACAAGCACAAAAAGGAGCCCCCCACGTCCACACCAGGAAAGGGGGGATGGTGCACAAGATCCAGAGGCG
TCAACAGACACGTCCAGCGAACAAGCACAGGGTGGGCCGTCCGGGAGCCTTGTGCCGCCAGGAGGAAAGCCGCAC
CGAGGGCAGCAGGGAGGCTCTGATGGCTGCCAAGAGGGTCTGATCCAGAAATATGGCCTCAATATGTGCCCCCAG
TGTTTCCGTCAGTACGCGAAGGATATCGGTTTCATTAAATTGGACTAA

FIGURE 532

TAGGTTTCATTTGGAAGCTTGAGTTTTATCATTGGCAACAAATGCCATCAGTTTTTCCAAGCTGACTTGTTCTT
TTTTGAGCAAATCTCTGCCAAAATTACCCCTAAAATATGAATAATCAATTTGTCAGGTTTTTTCAAACTAAAAAT
GTTCTGTGAAAACAAGCAGCTAGTTCAGCTTGTATCTCAAACAATTGTAACTACTTTTTCTAGGGAAAAAAAAAT
CTAGACATCCATACTTTATGGCAG**ATG**TGCTTCATGCATACTTCCCATTTTGTCACACAGAATATCAAAATAACG
TGTACTCAAGGTCAAGATTTACTAACAACTAAAATTCCAAAACTGCTAAACAACAGAATGCTGAATAAGGTGATC
CAATTTTTAATATTTTATTTGAGACAACATCTCACCCTGTCACCCAGGCTGGAATCCAGTGGTGTGACACAGCTC
ACTGCATCCTCAACCTCCTGGGCTCAAGCGATCGTCCCACCTCAGTCTCATGAGTGGTTGGGACTACAGGCATGC
ACCATCATGCCCGGCTCACTTTTTTTTTCTTTTTTTTTT**TAA**TTGTAGACACAGGGTCTCACTATGTTGCCCAGG
CCGGTCTTGAACTCCTGGACTCAAGCAATCCCCCCACCTTGGTTTCCCAAAGTGTTGGGATTACAGGCATGAGCT
ACTACATACAACTGAAATCTTTTAATATGCTTGTCAAAAAGTTTTCTGATTCAGCAAATGGCACTTATATATAAA
AGAGAGAACAAGAAGCTGGATGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTAGGTGGGCAGATCA
CGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACGTGGTGAAACCCCCTCTCTACTAAAAATACAAAAATAGCCAG
GCATGGTGGCCCACGCCTGTAATCCCAGCTACTTGGAAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGTGG
AGGTTGCAGTGAGCCAAGATTGCGCCGCTACATTCCAGCCTGGGCAACACGAGCGAAACTCCGTCTCAAAAAAAA
AAAAAAAAAGAATAGAACTTGGCTGGATGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGGCAGGGCAG
TTGGATCACTTGAGGCCAGGAGTTCAAGACTAGCCTGGCTGACATGGTGAAACTCCATCTCTACTAAAAATACAG
AAAAAAAAATTAGCTGGGAGTGGTGGCACACACCTGTCATCCCAGCTACTCAGGTAGTTGAGGCACAACAATCAC
TTGAGCCTAGGAGGCCCAGGCTGGAGTGAGGTGGCACGATCTTGGTTCACTGCAACCTCCACCTCCAGGGTTCAG
AGTAGCTGGGACTACAGGCCCACACTACCACACCCGGCTAATTTTCGCTTTTTTTCAGTAGAGACCGGGTTTTGC
CATGTTGGCCAGGCTGGTCTCGAAGCCTGAGCCATAACCTGGCGAAAAGATACTTTGAAATGTAACATCGTTTTT
CACTTCAAAATCAAGGTATTTTACCAACTTGTCTTTGGTACCTCCCCAAAAACTGATCTACTACATTTGCAGTTT
CATTCATTTTTCCAACATTAAGGAATAAACTTGAAGCGCTTACATTCTTGTGGGGGAAGTAAGAACAAAACACAT
AATAGGTCATGGTGGTCACATGAAAAGTAAAGGGTAACCGATTGGGGTAGGTGGTGGTAGTTTTGTGTGTGTGTT
TTTTTTTGAGACCAAGTCTCGCCGTTGCCCAGGCTGGAGTGCGGTGGCATGATCTCAGTTCACTGCAACCTCCAC
TTCCTAGGTTCAAGCAATTCTCCTGCCTCAGCTACTCAAGAGGCTGAGGCAGGAGAATTCCTTGAACCTGGGAGG
CAGAGGTTGCAGTGAACTGATAGTGCCGCTGCACTCCATTCTGGGCAAGAGCTAGACTCTTGTCTAAAAAAAAAA
AAAAAATACTTGGAACTGCTATACCTTTGCTTCTTTAAAACTTGCTCCACACAGTGTAGTCAAGCCGACTCTCCA
TACCTGTAGAAATTTAATCTCCTTTACCAATAGGTAGTAATAGGTGGATTTCTAAAAGATTTCCCAACTACTGTT
TCAGTTTAAGATTAATCTCCATTTCTTTCTCAGAGAGATTCCCATCTGCTTTAATTTTAAAATCATCACTAACA
GTAGCTCAATCAATTAACGTTAACATCAATAAAACATGTACCTTTAAAAGGTATGACAGGAACTGTCTTCATGTC
CTTACCCAAGCAAGTCATCCATGGATAAAAACGTTACCAGGAGCTGGAATACAAATGAGGACTTCCATTAAAATG
CTAAACATCATTAAACTCTTTTCAAAGTTGTCTGTC

FIGURE 533

MCFMHTSHFVTQNIKITCTQGQDLLTTKIPKLLNNRMLNKVIQFLIFYLRQHLTLSPRLESSGVTQLTASSTSWA
QAIVPPQSHEWLGLQACTIMPGSLFFSFFF

FIGURE 534

ATCTGTAGATGGGAGTGATTAGCTGTTTAAAAGTTAAAATGTGACTGAGAAGGAAATTGAGTAGGGCAAATTTTA
AATGGGTATTATTTTTCATCTTCAAACAGGCAGACCTGTTATCCTAAACTAGGTGAGTCAGCTTTTGGTACATGT
GATGATTTTCAGTGTAACCAATGATGTAATGATTCTGCCAAATGAAATATAATGATATCACTGTAAAACCGTTCC
ATTTTGATTCTGAGGTTACTCTACTAACAAGCATCACACATTTGTATTTTGCCCTGATTAATATGTTGGCTTCGC
TTTCAGGGTTTTTAATGACCACAACAAGCAAGCATGCAGCTTACTGCTTGAAAGGGTCTTGCCTCACCCAAGCTA
GAGTGCAGTGGCCTTTGAAGCTTACTACAGCCTCAAACTTCTGGGCTCAAGTGATCCTCAGCCTCCCAGTGGTCT
TTGTAGACTGCCTGATGGAGTCTCATGGCACAAGAAGATTAAAACAGTGTCTCCAATTTTAATAAATTTTTGCAA
TCC

FIGURE 535

AGTTAAAACAGCTGAGCTTCTGAATGCCTGCAAGAAGCTGCCCTTTGAAATTAAGAACTTCGTGAAGAAAACAGA
GGCTCTTCGGTTGCAGTATCGCTACTTAGACTTGCGTAGTTTCCAA**ATG**CAGTATAACCTGCGACTGAGGTCCCA
GATGGTCATGAAAATGCGGGAATATCTCTGTAATCTGCATGGGTTTGTGGATATAGAAACCCCCACATTGTTTAA
GAGGACCCCAGGGGGTGCCAAAGAGTTTTTAGTACCATCCAGGGAACCTGGAAAGTTTTGTTCTCTCCCTCAGAG
TCCTCAACAGTTTAAGCAACTTCTGATGGTTGGCGGTTTAGACAGATATTTCAGGTTGCCCGATGTTATCGAGA
TGAAGGTTCAAGACCAGACAGACAGCCTGAGTTTACTCAGATTGACATAGAGATGTCATTTGTAGACCAGACTGG
GATCCAGAGTTTAATTGAGGGTTTGCTCCAGTATTCCTGGCCCAATGACAAAGATCCTGTGGTTGTTCCTTTTCC
TACTATGACTTTTGCTGAGGTGCTGGCCACCTATGGAACTGATAAACCTGACACTCGCTTTGGAATGAAGATTAT
AGATATCAGTGATGTGTTTAGAAACACAGAGATTGGATTTCTTCAAGATGCACTTAGTAAGCCCCATGGAACTGT
GAAAGCCATATGTATCCCTGAAGGAGCAAAATACTTAAAAAGGAAAGACATTGAATCCATTAGAAACTTTGCAGC
TGACCATTTTAATCAGGAAATCTTACCTGTATTCCTTAACGCCAATAGAAACTGGAATTCTCCAGTTGCTAATTT
CATAATGGAGTCACAAAGACTGGAATTAATCAGACTAATGGAGACCCAAGAGGAAGATGTGGTCCTACTAACTGC
TGGAGAGCACAATAAAGCATGCTCTTTGTTAGGAAAATTACGACTGGAATGTGCTGACCTTCTAGAAACAAGAGG
AGTGGTGCTCCGTGACCCCACTCTGTTCTCTTTCCTTTGGGTGGTAGATTTCCCACTCTTCCTGCCCAAGGAGGA
AAGTCCCAGAGAGCTGGAATCGGCCCACCACCCATTTACTGCTCCCCACCCCAGTGACATACATCTCCTGTACAC
TGAGCCCAAAAAGGCCCGTAGCCAACACTATGACTTGGTTTTAAATGGCAATGAAATAGGAGGTGGTTCAATTCG
AATTCACAATGCAGAGCTGCAGCGTTATATCCTGGCAACCTTACTAAAGGAGGATGTGAAAATGCTCTCCCATCT
GCTCCAGGCTTTAGATTATGGGGCACCCCCTCATGGAGGAATTGCCTTAGGGTTAGACAGACTGATATGCCTTGT
CACTGGATCTCCAAGCATCAGAGATGTCATAGCCTTCCCAAAGTCCTTCCGGGGACATGACCTCATGAGCAATAC
CCCAGATTCTGTCCCTCCTGAGGAACTGAAGCCCTATCATATCCGAGTCTCCAAGCCAACAGACTCCAAAGCAGA
AAGAGCTCAT**TGA**ATCATGCATACCATGCAGAAAGTTGAGCTTTTAGGTTTTGTCCTCTTTGCTTCCCCAAGGCT
AAAGTCAGATCTAGAGTTCTGCCACAGGTCTAACAATCAAGTCTTTAGATGGAAGGAATCCAGGCAACATTCTTC
ACCACAACGAAGAAACAGATAAAAGATACCCAATTTTGACTTGATTTCATGCATCATTTGGATTTTTTTGGTTA
GGACTTTTTTTGAAGTTCCTTTTTACTTAGGTGTGAAAGATGGTTCTTTGTTGAAATAATATAGTGGTTTAGTGT
TTTCAAATCATGTTTCTCATACCCAGATAGTAGATTATTCACTTAGGACAGAGGTAATCAAATTATGTGTGAAAT
GTAGGAAAATGCTTGCCCCTGTAAACTAGTGAGTTGATGGAGCATTTGCTTCATCATCCTCATCAAGAGAATCAT
ATAAATTAAGCTTTATAATGACATTTCAACCATCAACATAATATAGTGAGGAGTAGCATAATATTTTTTAATAAT
GCAGAAAACATCACTGAAATGAGAGTCACAAATTTTTCTTCAGTGTTTCAGCCTGAGTAAGTTACATAAACCTCG
CTTAGCCTCCCTTCCTGCTAATGTGTAAAATACATACTTGCCCTGGCTACCTCACCGGGCTGTTATTGCTGGAAT
CAGAGGAGATAACATATATGGAAGATAAAGTGAATAAAAGTACTTTGAAAAACT

FIGURE 536

MQYNLRLRSQMVMKMREYLCNLHGFVDIETPTLFKRTPGGAKEFLVPSREPGKFCSLPQSPQQFKQLLMVGGLDR
YFQVARCYRDEGSRPDRQPEFTQIDIEMSFVDQTGIQSLIEGLLQYSWPNDKDPVVVPFPTMTFAEVLATYGTDK
PDTRFGMKIIDISDVFRNTEIGFLQDALSKPHGTVKAICIPEGAKYLKRKDIESIRNFAADHFNQEILPVFLNAN
RNWNSPVANFIMESQRLELIRLMETQEEDVVLLTAGEHNKACSLLGKLRLECADLLETRGVVLRDPTLFSFLWVV
DFPLFLPKEESPRELESAHHPFTAPHPSDIHLLYTEPKKARSQHYDLVLNGNEIGGGSIRIHNAELQRYILATLL
KEDVKMLSHLLQALDYGAPPHGGIALGLDRLICLVTGSPSIRDVIAFPKSFRGHDLMSNTPDSVPPEELKPYHIR
VSKPTDSKAERAH

FIGURE 537

GCCTGTCTGCATTCTACTATATAAAGCAGCAGAGACGTTGACTAGCGCATATTTGCTAAGAGCACCATGCGCGCA
GCAGCCATCTCCACTCCAAAGTTAGACAAAATGCCAGGAATGTTCTTCTCTGCTAACCCAAAGGAATTGAAAGGA
ACCACTCATTCACTTCTAGACGACAAAATGCAAAAAAGGAGGCCAAAGACTTTTGGAATGGATATGAAAGCATAC
CTGAGATCTATGATCCCACATCTGGAATCTGGAATGAAATCTTCCAAGTCCAAGGATGTACTTTCTGCTGCTGAA
GTAATGCAATGGTCTCAATCTCTGGAAAAACTTCTTGCCAACCAAACTGGTCAAAATGTCTTTGGAAGTTTCCTA
AAGTCTGAATTCAGTGAGGAGAATATTGAGTTCTGGCTGGCTTGTGAAGACTATAAGAAAACAGAGTCTGATCTT
TTGCCCTGTAAAGCAGAAGAGATATATAAAGCATTTGTGCATTCAGATGCTGCTAAACAAATCAATATTGACTTC
CGCACTCGAGAATCTACAGCCAAGAAGATTAAAGCACCAACCCCCACGTGTTTTGATGAAGCACAAAAAGTCATA
TATACTCTTATGGAAAAGGACTCTTATCCCAGGTTCCTCAAATCAGATATTTACTTAAATCTTCTAAATGACCTG
CAGGCTAATAGCCTAAAGTGACTGGTCCCTGGCTGAAGGGAATTAACAGATAGTATCAAGCGCAGAAGGAATGTG
CCAGTATGGCTCCCTGGGTGAACAGCTTGGCCTTTTTTGGGTGTCTTGACAGGCCAAGAAGAACAAATGACTCAG
AATGGATTAACATGAAAGTTATCCAGGCGCAGAGTTGAAGAAGCATAAGCAAGACAAAAACAGAGAGACCGCAGA
AGGAGGAAGATACTGTGGTACTGTCATAAAAAACAGTGGAGCTCTGTATTAGAAAGCCCCTCAGAACTGGGAAGG
CCAGGTAACTCTAGTTACACAGAAACTGTGACTAAAGTCTATGAAACTGATTACAACAGACTGTAAGAATCAAAG
TCAACTGACATCTATGCTACATATTATTATATAGTTTGTACTGAGCTATTGAAGTCCCATTAACTTAAAGTATAT
GTTTTCAAATTGCCATTGCTACTATTGCTTGTCGGTGTTATTTTATTTTATTGTTTTTGACTTTGGAAGAGATGA
ACTGTGTATTTAACTTAAGCTATTGCTCTTAAAACCAGGGAGTCAGAATATATTTGTAAGTTAAATCATTGGTGC
TAATAATAAATGTGGATTTTGTATTAAAATATATAGAAGCAATTTCTGTTTACATGTCCTTGCTACTTTTAAAAA
CTTGCATTTATTCCTCAGATTTTAAAAATAAATAAATAATTCATTT

FIGURE 538

CTTTTCGATCCGCCATCTGCAGTGGAGCCGCCACCAAA**<u>ATG</u>**CAGATTTTCGTGAAAACCCTTATGGGGAAGACCA
TCACCCTCGAGGTTGAACTCTCGGATACAATAGATAATGTAAAGGCCAAGATCCAGGATAAGGAAGGAATTCCTC
CTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGTTGGAAGATGGACGTACTTTGTCTGACTACAATATTCAAA
AGGAGTCTACTCTTCATCTTGTGTTGAGACTTCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACCACTC
CCAGGAAGAATAAGCACAAGAGAAAGAAGGTTAAGCTGGCTCTCCTGAAATATTATAAGGTGGATGAGAATGGCT
TTATGGCAAGCCACTTTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACCAGAAGACA
AG**<u>TAA</u>**CTGTATGACTTAATAA

FIGURE 539

MQIFVKTLMGKTITLEVELSDTIDNVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRG
GAKKRKKKSYTTPRKNKHKRKKVKLALLKYYKVDENGFMASHFDRHYCGKCCLTYCFNKPEDK

FIGURE 540

AAAACAGCCGGGGCTCCAGCGGGAGAACGATA**ATG**CAAAGTGCTATGTTCTTGGCTGTTCAACACGACTGCAGAC
CCATGGACAAGAGCGCAGGCAGTGGCCACAAGAGCGAGGAGAAGCGAGAAAAGATGAAACGGACCCTTTTAAAAG
ATTGGAAGACCCGTTTGAGCTACTTCTTACAAAATTCCTCTACTCCTGGGAAGCCCAAAACCGGCAAAAAAAGCA
AACAGCAAGCTTTCATCAAGCCTTCTCCTGAGGAAGCACAGCTGTGGTCAGAAGCATTTGACGAGCTGCTAGCCA
GCAAATATGGTCTTGCTGCATTCAGGGCTTTTTTAAAGTCGGAATTCTGTGAAGAAAATATTGAATTCTGGCTGG
CCTGTGAAGACTTCAAAAAAACCAAATCACCCCAAAAGCTGTCCTCAAAAGCAAGGAAAATATATACTGACTTCA
TAGAAAAGGAAGCTCCAAAAGAGATAAACATAGATTTTCAAACCAAAACTCTGATTGCCCAGAATATACAAGAAG
CTACAAGTGGCTGCTTTACAACTGCCCAGAAAAGGGTATACAGCTTGATGGAGAACAACTCTTATCCTCGTTTCT
TGGAGTCAGAATTCTACCAGGACTTGTGTAAAAAGCCACAAATCACCACAGAGCCTCATGCTACA**TGA**AATGTAA
AAGGGAGCCCAGAAATGGAGGACATTTCATTCTTTTTCCTGAGGGGAAGGACTGTGACCTGCCATAAAGACTGAC
CTTGAATTCAGCCTGGGTGTTCAGGAAACATCACTCAGAACTATTGATTCAAAGTTGGGTAGTGAATCAGGAAGC
CAGTAACTGACTAGGAGAAGCTGGTATCAGAACAGCTTCCCTCACTGTGTACAGAACGCAAGAAGGGAATAGGTG
GTCTGAACGTGGTGTCTCACTCTGAAAAGCAGGAATGTAAGATGATGAAAGAGACAATGTAATACTGTTGGTCCA
AAAGCATTTAAAATCAATAGATCTGGGATTATGTGGCCTTAGGTAGCTGGTTGTACATCTTTCCCTAAATCGATC
CATGTTACCACATAGTAGTTTTAGTTTAGGATTCAGTAACAGTGAAGTGTTTACTATGTGCAAGGGTATTGAAGT
TCTTATGACCACAGATCATCAGTACTGTTGTCTCATGTAATGCTAAAACTGAAATGGTCCGTGTTTGCATTGTTA
AAAATGATGTGTGAAATAGAATGAGTGCTATGGTGTTGAAAACTGCAGTGTCCGTTATGAGTGCCAAAAATCTGT
CTTGAAGGCAGCTACACTTTGAAGTGGTCTTTGAATACTTTTAATAAATTTATTTTGATAAATAATATTG

FIGURE 541

MQSAMFLAVQHDCRPMDKSAGSGHKSEEKREKMKRTLLKDWKTRLSYFLQNSSTPGKPKTGKKSKQQAFIKPSPE
EAQLWSEAFDELLASKYGLAAFRAFLKSEFCEENIEFWLACEDFKKTKSPQKLSSKARKIYTDFIEKEAPKEINI
DFQTKTLIAQNIQEATSGCFTTAQKRVYSLMENNSYPRFLESEFYQDLCKKPQITTEPHAT

FIGURE 542

TGAAGATGAAAAAGAAGATCATAAAAATGTGCGCCAACAACGGCAGGCGGCATCTAAAGCAGCTTCTAAACAGAG
AGAGATGCTCATGGAAGATGTGGGCAGTGAGGAAGAACAAGAAGAGGAGGATGAGGCACCATTCCAGGAGAAAGA
TTCCGGCAGCGATGAAGATTTCCTAATGGAAGATGATGACGATAGTGACTATGGCAGTTCGAAAAAGAAAAACAA
AAAGATGGTTAAGAAGTCCAAACCTGAAAGAAAAGAAAAGAAAATGCCCAAACCCAGACTAAAGGCTACAGTGAC
GCCAAGTCCAGTGAAAGGCAAAGGGAAAGTGGGTCGCCCCACAGCTTCAAAGGCATCAAAGGAAAAGACTCCTTC
TCCCAAAGAAGAAGATGAGGAACCGGAAAGCCCGCCAGAAAAGAAAACATCTACAAGCCCCCCACCCGAGAAATC
TGGGGATGAAGGGTCTGAAGATGAAGCCCCTTCTGGGGAGGATTAAAAGTGATGATGGTCTGGGGAGAGATTTTA
TTAAAAAAAAAAAGAAAAAAGAGGGAGGAAAAAAAAGAACCTACTTAAGATAGAACATGGTTTTGGCTATGGCTT
GACTCATGGGCTTTCAGTGCTTTTTTCCATTTGTTGAAAGTAACATTTCTCTCTCTCTCTTT

FIGURE 543

AGCCTGAGGAGCTATTTTGAGCAATGGGGAATGCTCACGGACTGTGTGGTAATGAGAGACCCAAACACCAAGTGC
TCCAGGGGCTTTGGGTTTGTCACATATGCCATTGTGGAGGAGGTGGATGCAGCCATGAATGCAAGGCCACACAAG
GTGGATGGAAGAGTTGGAGAACCAAAGAGAGCTGTTTCAAGGGAAGATTCTCAAAGACCAGGTGCTCACTTAACT
GTGAAAAAGATATTTGTTGGCAGCATTAAAGAAGACACTGAAGAACATCACCTAAGAGATAATTTGAACAGTTTG
GAAAAACGGAAGTGATTGAAATCATGACTGACTGAGGCAGTGGCAAGAAAAGGGGCTTTGCCTTTGTAACCTTTG
ATGACCATGACTCTGTGAATAAGACTGCCATTCAGAAATACCATCCTACGAATGGCCATAACTGTGAAGTTAGGA
AAGCCCTGTCAAAGTAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAAGTCGAAGTGGTTCTGGAAACTTTGGTT
TGGTCGTGGAGGTGGTTTCGGTTGGCATGACAGCCGTGGTGGTGGTGGATATGGTGGCAGTGAGGATGGCGA
TAATGGATTTGGTAATGATGGAAGCAATTTTGGAGGTGGTGGAAGCTACAGTGATTTTGGCAACTACAATAATCA
GTCTTCAAATTTTGGACCCATGAAGGGAGGAAACTTTGGAGGCAGAAGCTCTGGGCCCCTATGGCGGTGGAGGCC
AATACTCTGCCAAACCACGAAACCAAGGTGGCTATGGTGGTTTCAGTAGCAGCAGTAGCTATGGCAGTGGCAGAA
GATTTTAATTAGGAAACAAAGCTTAGCTGGAGAGGAGAGCCGGAGAAGTGACAGGGAAGCTACAGGTTACAACAG
ATTTGTGAACTCAGCCAAGCACAGTGGTGGCAGGGCCTAACTGCTACAAAGGAGACATGTTTTAGACAAATACTC
ATGTGTATGGGCAAAAAACTCGAGGACTGTATTTGTGACTAATTGTGTAACAGGTTATTTTAGTTTCTGTTCTGT
GGAAAGCGTAAAGCATTCCAACAAAGGGTTTTAATGCAGATTTTTTTTTTTTGGCACCCATGCTGTTGATTGCT
AAATGTAATAGTCTGATGGTGATGCTGAATAAATGTCTT

FIGURE 544

AGGCAGAGCCCGCGAGGAGGTGACGCGGCTGCGGAGGTGACGCGGGAGGTCGCGCGCCCCTTCCGGCGCGGGGAG
GGCGCTGAAGATCGGGGCCGCTCGGCCGCAGGCCGCCTCCAGCGCCGCGGGATGTAGCGCGGGGGACCGCGGCCC
CCAGCAGAGCCCGCCTGCCCGGCTTTTAGAAGACCAAACTGGACAATGGACTTTGCTCACTATGATGACATGATC
TCCATTGACCTCCATTTGTCTACCATCAGAGGGAGATCTCTGCCCCCTGGGGCTGAGAGACCCCAACCTTTCCCC
AAGCTGAAGCTGCAGGGTATTGAGGTACCAGCCAGATGTCTTCCCACAAAGGATCTGTGGTGGCACAGGGGAATG
GGGCTCCTGCCAGTAACAGGGAAGCTGACACGGTGGAACTGGCTGAACTGGGACCCCTGCTAGAAGAGAAGGGCA
AACGGGTAATCGCCAACCCACCCAAAGCTGAAGAAGAGCAAACATGCCCAGTGCCCCAGGAAGAAGAGGAGGAGG
TGCGGGTACTGACACTTCCCCTGCAAGCCCACCACGCCATGGAGAAGATGGAAGAGTTTGTGTACAAGGTCTGGG
AGGGACGTTGGAGGGTCATCCCATATGATGTGCTCCCTGACTGGCTAAAGGACAACGACTATCTGCTACATGGTC
ATAGACCTCCCATGCCCTCCTTTCGGGCTTGCTTCAAGAGCATCTTCCGCATTCATACAGAAACTGGCAACATCT
GGACCCATCTGCTTGGTTTCGTGCTGTTTCTCTTTTTGGGAATCTTGACCATGCTCAGACCAAATATGTACTTCA
TGGCCCCTCTACAGGAGAAGGTGGTTTTTGGGATGTTCTTTTTGGGTGCAGTGCTCTGCCTCAGCTTCTCCTGGC
TCTTTCACACCGTCTATTGTCATTCAGAGAAAGTCTCTCGGACTTTTTCCAAACTGGACTATTCAGGGATTGCTC
TTCTAATTATGGGGAGCTTTGTCCCCTGGCTCTATTATTCCTTCTACTGCTCCCCACAGCCACGGCTCATCTACC
TCTCCATCGTCTGTGTCCTGGGCATTTCTGCCATCATTGTGGCGCAGTGGGACCGGTTTGCCACTCCTAAGCACC
GGCAGACAAGAGCAGGCGTGTTCCTGGGACTTGGCTTGAGTGGCGTCGTGCCCACCATGCACTTTACTATCGCTG
AGGGCTTTGTCAAGGCCACCACAGTGGGCCAGATGGGCTGGTTCTTCCTCATGGCTGTGATGTACATCACTGGAG
CTGGCCTTTATGCTGCTCGAATTCCTGAGCGCTTCTTTCCTGGAAAATTTGACATATGGTTCCAGTCTCATCAGA
TTTTCCATGTCCTGGTGGTGGCAGCAGCCTTTGTCCACTTCTATGGAGTCTCCAACCTTCAGGAATTCCGTTACG
GCCTAGAAGGCGGCTGTACTGATGACACCCTTCTCTGAGCCTTCCCACCTGCGGGGTGGAGGAGGAACTTCCCAA
GTGCTTTTAAAAATAACTTCTTTGCTGAAGTGAGAGGAAGAGTCTGAGTTGTCTGTTTCTAGAAGAAACCTCTTA
GAGAATTCAGTACCAACCAAGCTTCAGCCCACTTTCACACCCACTGGGCAATAAACTTTCCATTTCCATTCTCCT
AGCTGGGGATGGGGCATGGTCAAACTTAGCCATCCCCTCCTCAGCAAGGCATCTACCGGCCCCTCACAGAGACAG
TACTTTGAAACTCATGTTGAGATTTTACCCTCTCCTCCAACCATTTTGGGAAAATTATGGACTGGGACTCTTCAG
AAATTCTGTCTTTTCTTCTGGAAGAAAATGTCCCTCCCTTACCCCCATCCTTAACTTTGTATCCTGGCTTATAAC
AGGCCATCCATTTTTGTAGCACACTTTTCAAAAACAATTATATACCCTGGTCCCATCTTTCTAGGGCCTGGATCT
GCTTATAGAGCAGGAAGAATAAAGCCACCAACTTTACCTAGCCCGGCTAATCATGGAAGTGTGTCCAGGCTTCA
AGTAACTTGAGTTTTAATTTTTTTTTTTCTTGGCAGAGTAATGTAAAATTTAAATGGGGAAAGATATTTAATAT
TTAATACTAAGCTTTAAAAAGAAACCTGCTATCATTGCTATGTATCTTGATGCAAAGACTATGATGTTAATAAAA
GAAAGTACAGAAGACACTTGGCATTCAAAGATTTC

FIGURE 545

GGCCGCGGAGCCGGGCGGAGCTGGCTTGCGGCTCCCGGGGCCGGCTCTCCGGCCGGAGAC**ATG**GCCCGGGGGCCC
GGCCCGCTAGGCAGGCCTCGCCCCGATACGGTCGCCATGCCCAAGAGAGGAAAGCGACTCAAGTTCCGGGCCCAC
GACGCCTGCTCCGGCCGAGTGACCGTGGCGGATTACGCCAACTCGGATCCGGCGGTCGTGAGGTCTGGACGAGTC
AAGAAAGCCGTAGCCAACGCTGTTCAGCAGGAAGTAAAATCTCTTTGTGGCTTGGAAGCCTCTCAGGTTCCTGCA
GAGGAAGCTCTTTCTGGGGCTGGTGAGCCCTGTGACATCATCGACAGCAGTGATGAGATGGATGCCCAGGAGGAA
AGCATCCATGAGAGAACTGTCTCCAGAAAAAAGAAAAGCAAGAGACACAAAGAAGAACTGGACGGGGCTGGAGGA
GAAGAGTATCCCATGGATATTTGGCTATTGCTGGCCTCCTATATCCGTCCTGAGGACATTGTGAATTTTTCCCTG
ATTTGTAAGAATGCCTGGACTGTCACTTGCACTGCTGCCTTTTGGACCAGGTTGTACCGAAGGCACTACACGCTG
GATGCTTCCCTGCCTTTGCGTCTGCGACCAGAGTCAATGGAGAAGCTGCGCTGTCTCCGGGCTTGTGTGATCCGA
TCTCTGTACCATATGTATGAGCCATTTGCTGCTCGAATCTCCAAGAATCCAGCCATTCCAGAAAGCACCCCCAGC
ACATTAAAGAATTCCAAATGCTTACTTTTCTGGTGCAGAAAGATTGTTGGGAACAGACAGGAACCAATGTGGGAA
TTCAACTTCAAGTTCAAAAAACAGTCCCCTAGGTTAAAGAGCAAGTGTACAGGAGGATTGCAGCCTCCCGTTCAG
TACGAAGATGTTCATACCAATCCAGACCAGGACTGCTGCCTACTGCAGGTCACCACCCTCAATTTCATCTTTATT
CCGATTGTCATGGGAATGATATTTACTCTGTTTACTATCAATGTGAGCACGGACATGCGGCATCATCGAGTGAGA
CTGGTGTTCCAAGATTCCCCTGTCCATGGTGGTCGGAAACTGCGCAGTGAACAGGGTGTGCAAGTCATCCTGGAC
CCAGTGCACAGCGTTCGGCTCTTTGACTGGTGGCATCCTCAGTACCCATTCTCCCTGAGAGCG**TAG**TTACTGCTT
CCCATCCCTTGGGGGCAGCCTCGAGTGTAGTCCATTAGTAATCAGATTCCAGTTTGGACAGGGTGGCTGGATTGT
ATATCTCGTTAGTAATGTACATGCTCTTCAGGTTCTAGGGCTCCTGTTAGGGGAGGGAGAAATGTTGAATCAAGA
GGGAAAACAACTACTATGATTTATAAACATATTTAATGTAAAAATTTGCATTTAAAAGGAGTGGCCCTGTTTTC
TGTGTTAAAACCCCATTTGGTGCTATTGAGTTTGTTCTTTATTCTTTTATCCCAGTGAAAATTGTTGATCTTGCT
GTAGGGAAAAATTAAACTCTTTGAATCTCCAAACAAGGAAGTTTCAGCATTCCCTTATGGATCAGAGGAACCTTA
GAGGCCTGAAATTGTTGCTTCCAGTTTAGCTGCCCCTCAAATTCAAGTGAATATTTTCCCTTCTCCCTTTACCCT
TCTCCAGAAATAAAGCAGGTGACAGGGTTTTCAGAATCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 546

MARGPGPLGRPRPDTVAMPKRGKRLKFRAHDACSGRVTVADYANSDPAVVRSGRVKKAVANAVQQEVKSLCGLEA
SQVPAEEALSGAGEPCDIIDSSDEMDAQEESIHERTVSRKKKSKRHKEELDGAGGEEYPMDIWLLLASYIRPEDI
VNFSLICKNAWTVTCTAAFWTRLYRRHYTLDASLPLRLRPESMEKLRCLRACVIRSLYHMYEPFAARISKNPAIP
ESTPSTLKNSKCLLFWCRKIVGNRQEPMWEFNFKFKKQSPRLKSKCTGGLQPPVQYEDVHTNPDQDCCLLQVTTL
NFIFIPIVMGMIFTLFTINVSTDMRHHRVRLVFQDSPVHGGRKLRSEQGVQVILDPVHSVRLFDWWHPQYPFSLR
A

FIGURE 547

AGTGGAGTGGGACAGGTATATAAAGGAAGTACAGGGCCTGGGGAAGAGGCCCTGTCTAGGTAGCTGGCACCAGGA
GCCGTGGGCAAGGGAAGAGGCCACACCCTGCCCTGCTCTGCTGCAGCCAGAATGGGTGTGAAGGCGTCTCAAACA
GGCTTTGTGGTCCTGGTGCTGCTCCAGTGCTGCTCTGCATACAAACTGGTCTGCTACTACACCAGCTGGTCCCAG
TACCGGGAAGGCGATGGGAGCTGCTTCCCAGATGCCCTTGACCGCTTCCTCTGTACCCACATCATCTACAGCTTT
GCCAATATAAGCAACGATCACATCGACACCTGGGAGTGGAATGATGTGACGCTCTACGGCATGCTCAACACACTC
AAGAACAGGAACCCCAACCTGAAGACTCTCTTGTCTGTCGGAGGATGGAACTTTGGGTCTCAAAGATTTTCCAAG
ATAGCCTCCAACACCCAGAGTCGCCGGACTTTCATCAAGTCAGTACCGCCATTTCTGCGCACCCATGGCTTTGAT
GGGCTGGACCTTGCCTGGCTCTACCCTGGACGGAGAGACAAACAGCATTTTACCACCCTAATCAAGGAAATGAAG
GCCGAATTTATAAAGGAAGCCCAGCCAGGGAAAAAGCAGCTCCTGCTCAGCGCAGCACTGTCTGCGGGGAAGGTC
ACCATTGACAGCAGCTATGACATTGCCAAGATATCCCAACACCTGGATTTCATTAGCATCATGACCTACGATTTT
CATGGAGCCTGGCGTGGGACCACAGGCCATCACAGTCCCCTGTTCCGAGGTCAGGAGGATGCAAGTCCTGACAGA
TTCAGCAACACTGACTATGCTGTGGGGTACATGTTGAGGCTGGGGGCTCCTGCCAGTAAGCTGGTGATGGGCATC
CCCACCTTCGGGAGGAGCTTCACTCTGGCTTCTTCTGAGACTGGTGTTGGAGCCCCAATCTCAGGACCGGGAATT
CCAGGCCGGTTCACCAAGGAGGCAGGGACCCTTGCCTACTATGAGATCTGTGACTTCCTCCGCGGAGCCACAGTC
CATAGAATCCTCGGCCAGCAGGTCCCCTATGCCACCAAGGGCAACCAGTGGGTAGGATACGACGACCAGGAAAGC
GTCAAAAGCAAGGTGCAGTACCTGAAGGACAGGCAGCTGGCGGGCGCCATGGTATGGGCCCTGGACCTGGATGAC
TTCCAGGGCTCCTTCTGTGGCCAGGATCTGCGCTTCCCTCTCACCAATGCCATCAAGGATGCACTCGCTGCAACG
TAGCCCTCTGTTCTGCACACAGCACGGGGGCCAAGGATGCCCCGTCCCCCTCTGGCTCCAGCTGGCCGGGAGCCT
GATCACCTGCCCTGCTGAGTCCCAGGCTGAGCCTCAGTCTCCCTCCCTTGGGGCCTATGCAGAGGTCCACAACAC
ACAGATTTGAGCTCAGCCCTGGTGGGCAGAGAGGTAGGGATGGGGCTGTGGGGATAGTGAGGCATCGCAATGTAA
GACTCGGGATTAGTACACACTTGTTGATTAATGGAAATGTTTACAGATCCCCAAGCCTGGCAAGGGAATTTCTTC
AACTCCCTGCCCCCCAGCCCTCCTTATCAAAGGACACCATTTTGGCAAGCTCTATCACCAAGGAGCCAAACATCC
TACAAGACACAGTGACCATACTAATTATACCCCCTGCAAAGCCCAGCTTGAAACCTTCACTTAGGAACGTAATCG
TGTCCCCTATCCTACTTCCCCTTCCTAATTCCACAGCTGCTCAATAAAGTACAAGAGCTTAACAGTGTGTTGGCG
CTTTGCTTTGGTCTATCTTTGAGCGCCCACTAGACCCACTGGACTCACCTCCCCCATCTCTTCTGGGTTCCTTCC
TCTGAGCCTTGGGACCCCTGAGCTTGCAGAGATGAGGCCGCCATGT

FIGURE 548

CAGGGTAACGCTGTCTTGTGGACCCGCACTTCCCACCCGAGACCTCTCACTGAGCCCGAGCCGCGCGCGAC**ATG**A
GCCACGGGAAGGGAACCGACATGCTCCCGGAGATCGCCGCCGCCGTGGGCTTCCTCTCCAGCCTCCTGAGGACCC
GGGGCTGCGTGAGCGAGCAGAGGCTTAAGGTCTTCAGCGGGGCGCTCCAGGAGGCACTCACAGAGCACTACAAAC
ACCACTGGTTTCCCGAAAAGCCGTCCAAGGGCTCCGGCTACCGCTGCATTCGCATCAACCACAAGATGGACCCCA
TCATCAGCAGGGTGGCCAGCCAGATCGGACTCAGCCAGCCCCAGCTGCACCAGCTGCTGCCCAGCGAGCTGACCC
TGTGGGTGGACCCCTATGAGGTGTCCTACCGCATTGGGGAGGACGGCTCCATCTGCGTCTTGTACGAGGAGGCCC
CACTGGCCGCCTCCTGTGGGCTCCTCACCTGCAAGAACCAAGTGCTGCTGGGCCGGAGCAGCCCCTCCAAGAACT
ACGTGATGGCAGTCTCCAGC**TAG**GCCCTTCCGCCCCCGCCCTGGGCGCCGCCGTGCTCATGCTGCCGTGACAACA
GGCCACCACATACCTCAACCTGGGGAACTGTATTTTTAAATGAAGAGCTATTTATATATATTATTTTTTTTTAAG
AAAGGAGGAAAAGAAACCAAAAGTTTTTTTTAAGAAAAAAAATCCTTCAAGGGAGCTGCTTGGAAGTGGCCTCCC
CAGGTGCCTTTGGAGAGAACTGTTGCGTGCTTGAGTCTGTGAGCCAGTGTCTGCCTATAGGAGGGGGAGCTGTTA
GGGGGTAGACCTAGCCAAGGAGAAGTGGGAGACGTTTGGCTAGCACCCCAGGAAGATGTGAGAGGGAGCAAGCAA
GGTTAGCAACTGTGAACAGAGAGGTCGGGATTTGCCCTGGGGGAGGAAGAGAGGCCAAGTTCAGAGCTCTCTGTC
TCCCCCAGCCAGACACCTGCATCCCTGGCTCCTCTATTACTCAGGGGCATTCATGCCTGGACTTAAACAATACTA
TGTTATCTTTTCTTTTATTTTTCTAATGAGGTCCTGGGCAGAGAGTGAAAAGGCCTCTCCTGATTCCTACTGTCC
TAAGCTGCTTTTCTTGAAATCATGACTTGTTTCTAATTCTACCCTCAGGGGCCTGTAGATGTTGCTTTCCAGCCA
GGAATCTAAAGCTTTGGGTTTTCTGAGGGGGGGAGGAGGGAACTGGAGGTTATTGGGGTTAGGATGGAAGGGAAC
TCTGCACAAAACCTTTGCTTTGCTAGTGCTGCTTTGTGTGTATGTGTGGCAAATAATTTGGGGGTGATTTGCAAT
GAAATTTTGGGACCCAAAGAGTATCCACTGGGGATGTTTTTTGGCCAAAACTCTTCCTTTTGGAACCACATGAAA
GTCTTGATGCTGCTGCCATGATCCCTTTGAGAGGTGGCTCAAAAGCTACAGGGAACTCCAGGTCCTTTATTACTG
CCTTCTTTTCAAAAGCACAACTCTCCTCTAACCCTCCCCTCCCCCTTCCCTTCTGGTCGGGTCATAGAGCTACCG
TATTTTCTAGGACAAGAGTTCTCAGTCACTGTGCAATATGCCCCCTGGGTCCCAGGAGGGTCTGGAGGAAAACTG
GCTATCAGAACCTCCTGATGCCCTGGTGGGCTTAGGGAACCATCTCTCCTGCTCTCCTTGGGATGATGGCTGGCT
AGTCAGCCTTGCATGTATTCCTTGGCTGAATGGGAGAGTGCCCCATGTTCTGCAAGACTACTTGGTATTCTTGTA
GGGCCGACACTAAATAAAAGCCAAACCTTGGGCACTGTTTTTTCTCCCTGGTGCTCAGAGCACCTGTGGGAAAGG
TTGCTGTCTGTCTCAGTACAATCCAAATTTGTCGTAGACTTGTGCAATATATACTGTTGTGGGTTGGAGAAAAGT
GGAAAGCTACACTGGGAAGAAACTCCCTTCCTTCAATTTCTCAGTGACATTGATGAGGGGTCCTCAAAAGACCTC
GAGTTTCCCAAACCGAATCACCTTAAGAAGGACAGGGCTAGGGCATTTGGCCAGGATGGCCACCCTCCTGCTGTT
GCCCCTTAGTGAGGAATCTTCACCCCACTTCCTCTACCCCCAGGTTCTCCTCCCCACAGCCAGTCCCCTTTCCTG
GATTTCTAAACTGCTCAATTTTGACTCAAAGGTGCTATTTACCAAACACTCTCCCTACCCATTCCTGCCAGCTCT
GCCTCCTTTTCAACTCTCCACATTTTGTATTGCCTTCCCAGACCTGCTTCCAGTCTTTATTGCTTTAAAGTTCAC
TTTGGGCCCACAGACCCAAGAGCTAATTTTCTGGTTTGTGGGTTGAAACAAAGCTGTGAATCACTGCAGGCTGTG
TTCTTGCATCTTGTCTGCAAACAGGTCCCTGCCTTTTTAGAAGCAGCCTCATGGTCTCATGCTTAATCTTGTCTC
TCTTCTCTTCTTTATGATGTTCACTTTAAAAACAACAAAACCCCTGAGCTGGACTGTTGAGCAGGCCTGTCTCTC
CTATTAAGTAAAAATAAATAGTAGTAGTATGTTTGTAAGCTATTCTGACAGAAAAGACAAAGGTTACTAATTGTA
TGATAGTGTTTTTATATGGAAGAATGTACAGCTTATGGACAAATGTACACCTTTTGTTACTTTAATAAAAATGT
AGTAGGATAAAAAAAAA

FIGURE 549

MSHGKGTDMLPEIAAAVGFLSSLLRTRGCVSEQRLKVFSGALQEALTEHYKHHWFPEKPSKGSGYRCIRINHKMD
PIISRVASQIGLSQPQLHQLLPSELTLWVDPYEVSYRIGEDGSICVLYEEAPLAASCGLLTCKNQVLLGRSSPSK
NYVMAVSS

FIGURE 550

ATGTCCATGAGGAGCCCCATCTCTGCCCAGCTGGCCCTGGATGGCGTTGGCACCATGGTGAACTGCACCATCAAG
TCAGAGGAGAAGAAAGAGCCTTGCCACGAGGCCCCCCAGGGCTCAGCCACTGCCGCTGAACCTCAGCCTGGAGAC
CCAGCCCGGGCCTCCCAGGATAGTGCTGACCCCCAAGCTCCAGCCCAGGGGAATTTCAGGGGCTCCTGGGACTGT
AGCTCTCCAGAGGGTAATGGGTCCCCAGAACCCAAGAGACCAGGAGCGTCGGAGGCTGCCTCTGGAAGCCAGGAG
AAGCTGGACTTCAACCGAAATTTGAAAGAAGTGGTGCCAGCCATAGAGAAGCTGTTGTCCAGTGACTGGAAGGAG
AGGTTTCTAGGAAGGAACTCTATGGAAGCCAAAGATGTCAAAGGGACCCAAGAGAGCCTAGCAGAGAAGGAGCTC
CAGCTTCTGGTCATGATTCACCAGCTGTCCACCCTGCGGGACCAGCTCCTGACAGCCCACTCGGAGCAGAAGAAC
ATGGCTGCCATGCTGTTTGAGAAGCAGCAGCAGCAGATGGAGCTTGCCCGGCAGCAGCAGGAGCAGATTGCAAAG
CAGCAGCAGCAGCTGATTCAGCAGCAGCATAAGATCAACCTCCTTCAGCAGCAGATCCAGCAGGTTAACATGCCT
TATGTCATGATCCCAGCCTTCCCCCCAAGCCACCAACCTCTGCCTGTCACCCCTGACTCCCAGCTGGCCTTACCC
ATTCAGCCCATTCCCTGCAAACCAGTGGAGTATCCGCTGCAGCTGCTGCACAGCCCCCCTGCCCCAGTGGTGAAG
AGGCCTGGGGCCATGGCCACCCACCACCCCCTGCAGGAGCCCTCCCAGCCCCTGAACCTCACAGCCAAGCCCAAG
GCCCCCGAGCTGCCCAACACCTCCAGCTCCCCAAGCCTGAAGATGAGCAGCTGTGTGCCCCGCCCCCCCAGCCAT
GGAGGCCCCACGCGGGACCTGCAGTCCAGCCCCCCGAGCCTGCCTCTGGGCTTCCTTGGTGAAGGGGACGCTGTC
ACCAAAGCCATCCAGGATGCTCGGCAGCTGCTGCACAGCCACAGTGGGGCCTTGGATGGCTCCCCCAACACCCCC
TTCCGTAAGGACCTCATCAGCCTGGACTCATCCCCAGCCAAGGAGCGGCTGGAGGACGGCTGTGTGCACCCACTG
GAGGAAGCCATGCTGAGCTGCGACATGGATGGCTCCCGCCACTTCCCCGAGTCCCGAAACAGCAGCCACATCAAG
AGGCCCATGAACGCCTTCATGGTGTGGGCCAAGGATGAGCGGAGGAAGATCCTGCAAGCCTTCCCAGACATGCAC
AACTCCAGCATCAGCAAGATCCTTGGATCTCGCTGGAAGTCCATGACCAACCAGGAGAAGCAGCCCTACTATGAG
GAACAGGCGCGGCTGAGCCGGCAGCACCTGGAGAAGTATCCTGACTACAAGTACAAGCCGCGGCCCAAGCGCACC
TGCATCGTGGAGGGCAAGCGGCTGCGCGTGGGAGAGTACAAGGCCCTGATGAGGACCCGGCGTCAGGATGCCCGC
CAGAGCTACGTGATCCCCCCGCAGGCTGGCCAGGTGCAGATGAGCTCCTCAGATGTCCTGTACCCTCGGGCAGCA
GGCATGCCGCTGGCACAGCCACTGGTGGAGCACTATGTCCCTCGTAGCCTGGACCCCAACATGCCTGTGATCGTC
AACACCTGCAGCCTCAGAGAGGAGGGTGAGGGCACAGATGACAGGCACTCGGTGGCTGATGGCGAGATGTACCGG
TACAGCGAGGACGAGGACTCGGAGGGTGAAGAGAAGAGCGATGGGGAGTTGGTGGTGCTCACAGAC**TGA**TCCCGG
CTGGGTGGGCCTGGCCCCTTCTCCTCTGGGGAAGACCTTGTCCCAACTCGATGGGCACAGCCAGCCAACCTAAGA
CTATGTTGGTACTTGGACTTGTTCGTGCCCCAGAGATGGGCAAAGCTGTGCACTTGCAGATACATTCATGAGGGG
AGAGGCGCCCTCCCTTCCTGAGGAGCTGTTGGCCTGGGTGGGCAGGAACTGCAGTATGGCCATGGGCTGAGCAGG
CTGAGCACCTCAGCCTTTAGGGCTTATGGCCAGGGGACACTGTATGACTCTCCTCTCCTGCAGGTGTCTATCCAC
CTGGGGTATGGCATCTACCGACCTGTCTCCCTGGGGTCACATGCTTTGTTTCCATTCTTGTCCTGGCTGGACCAG
CCACTGTGGGACCAACACCCCTCCCACACTCCCCCAGACTGCTCGTCTATCACCAGGATCGCTTTGTACTTTGTG
CAAAAGGGTCTGGCTGTCCCTTGCTGTTTTCATCTCTGCCAAGCCTATTGTGCCTCTGGCTGCTGTATGTGTGCG
CGTGCACGTGTGTGTGTTTCATCTGTTCATTCACTGCACAAGATATTTATTGAGTGCCCACTACGTGCCAGGCAC
TGTTGCTGAGTTCCTGTGGGTGTGTCTCTCGATGCCACTCCTGCTTCTCTGGGGGCCTCTTTCTGTGCTTCTCTT
TGTCCCCAAATTGCTACCTCTTTGTCAGTCTGGGTGTCTCAGGTTCTGTGTGTCCTTGTGTGCATTTCTGTCTCT
CTCTGTCCTCGTCTCTCTGCAAGGCCCTCTATTTCTCTCTTTCTTGGTGTCTGTCCTTTGCCCCCTGTGCCCTCT
GGATTCTCTGGGTCTATGTAGGCCCCTGGTCTGCCCTGGGCTCATCAGCCTTCCTGACCTCCTCCTGCCCTCCCC
TTCACTCCCTCCCTGGCTCTGCCAGTCGGTTCCCACGGAGCCATTTTTAGCTCTGATCAGCATGGGAATGTGCCT
CGGCCTCCAAGGGGCTTTGTCCTGGTGCCCCCGCCCCTGGTCCCAACCTGATCCCACGAGGGAGTTGGGACAGGA
GGATTGATGGTGCTCCCCTTCCTGCCAGCGTCAGAGGCCCTGGAGAGGGGCTGTCCATGGCAGCTGGTCTTTATT
CCTCCCTCATGAGCACAGGGTCGGGGGGGTCCCCATTCTTGGAAGAGGTTGAGAAGACTCCTGGGCTTCAGCCTC
TCCCACCCAGCCCTGCCCCTCACCTGCCTGCCCTCCCCTCCCCCACTCTATACTAGGGACTGGATCTCAGCCTCT
GATCAGTTTCACAAAGTTTGTTCCCTAAGGAAATCAAATCCCATTGTCACCTAACTCTGAAGATCTAAATAGCCC
TTGGATCAGTATGGGAACCCCAAATCCCACAGGGCCAGATGTGGAGTCTGTGTCTGCCCCCGTCTTCTCTCCATC
CTCAAAGCCCCCACTTCTCTCCAGGCTGTTTCTTTTTTTATGACTGTAAACATAGATAGTGCTTTATTTTGTTAA
TAATAAGATAATGATGAGTAACTTAACCAGCACATTTCTCCTGTTTACACTCGGGGGATTTTTTTGTTTTCTGAT
GACATAATAAAGACAGATCATTTCAGAAAAAAAAAAAAAAAAA

FIGURE 551

MSMRSPISAQLALDGVGTMVNCTIKSEEKKEPCHEAPQGSATAAEPQPGDPARASQDSADPQAPAQGNFRGSWDC
SSPEGNGSPEPKRPGASEAASGSQEKLDFNRNLKEVVPAIEKLLSSDWKERFLGRNSMEAKDVKGTQESLAEKEL
QLLVMIHQLSTLRDQLLTAHSEQKNMAAMLFEKQQQQMELARQQQEQIAKQQQQLIQQQHKINLLQQQIQQVNMP
YVMIPAFPPSHQPLPVTPDSQLALPIQPIPCKPVEYPLQLLHSPPAPVVKRPGAMATHHPLQEPSQPLNLTAKPK
APELPNTSSSPSLKMSSCVPRPPSHGGPTRDLQSSPPSLPLGFLGEGDAVTKAIQDARQLLHSHSGALDGSPNTP
FRKDLISLDSSPAKERLEDGCVHPLEEAMLSCDMDGSRHFPESRNSSHIKRPMNAFMVWAKDERRKILQAFPDMH
NSSISKILGSRWKSMTNQEKQPYYEEQARLSRQHLEKYPDYKYKPRPKRTCIVEGKRLRVGEYKALMRTRRQDAR
QSYVIPPQAGQVQMSSSDVLYPRAAGMPLAQPLVEHYVPRSLDPNMPVIVNTCSLREEGEGTDDRHSVADGEMYR
YSEDEDSEGEEKSDGELVVLTD

FIGURE 552

AACTGCCATCTTCCAGTAATTCGCCAAAATGACGAATACAAAGGGAAAGAGGAGAGGCACCCGATGTATGTTCTC
TAGGCCTTTTAGAAAACATGGAGTTGTTCCTTTGGCCACGTATATGCGAGTCTATAAGAAAGGTGATATTGTAGA
CATCAAGGGAATGGGTACTGTTCAAAAAGGAATGCCCCACACGCGTTACCACGGCAAAACTGGAAGAGTCTACAA
TGTTACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAAGGCAAGATTCTTGCCAAGAGAATTAATGT
GCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAATGATCAGAAAAA
GAAAGAAGCCAAAGAGAAAGTTACCTGGATTCAACTAAAGCGCCAGCCTGCTCCACCCAGAGAAGCACACTTTGT
GAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTAAAAAA
AAAAA

FIGURE 553A

GCTTTCAGGCGATCTGGAGAAAGAACGGCAGAACACACAGCAAGGAAAGGTCCTTTCTGGGGATCACCCCATTGG
CTGAAG**ATG**AGACCATTCTTCCTCTTGTGTTTTGCCCTGCCTGGCCTCCTGCATGCCCAACAAGCCTGCTCCCGT
GGGGCCTGCTATCCACCTGTTGGGGACCTGCTTGTTGGGAGGACCCGGTTTCTCCGAGCTTCATCTACCTGTGGA
CTGACCAAGCCTGAGACCTACTGCACCCAGTATGGCGAGTGGCAGATGAAATGCTGCAAGTGTGACTCCAGGCAG
CCTCACAACTACTACAGTCACCGAGTAGAGAATGTGGCTTCATCCTCCGGCCCCATGCGCTGGTGGCAGTCCCAG
AATGATGTGAACCCTGTCTCTCTGCAGCTGGACCTGGACAGGAGATTCCAGCTTCAAGAAGTCATGATGGAGTTC
CAGGGGCCCATGCCCGCCGGCATGCTGATTGAGCGCTCCTCAGACTTCGGTAAGACCTGGCGAGTGTACCAGTAC
CTGGCTGCCGACTGCACCTCCACCTTCCCTCGGGTCCGCCAGGGTCGGCCTCAGAGCTGGCAGGATGTTCGGTGC
CAGTCCCTGCCTCAGAGGCCTAATGCACGCCTAAATGGGGGGAAGGTCCAACTTAACCTTATGGATTTAGTGTCT
GGGATTCCAGCAACTCAAAGTCAAAAAATTCAAGAGGTGGGGGAGATCACAAACTTGAGAGTCAATTTCACCAGG
CTGGCCCCTGTGCCCCAAAGGGGCTACCACCCTCCCAGCGCCTACTATGCTGTGTCCCAGCTCCGTCTGCAGGGG
AGCTGCTTCTGTCACGGCCATGCTGATCGCTGCGCACCCAAGCCTGGGGCCTCTGCAGGCCCCTCCACCGCTGTG
CAGGTCCACGATGTCTGTGTCTGCCAGCACAACACTGCCGGCCCAAATTGTGAGCGCTGTGCACCCTTCTACAAC
AACCGGCCCTGGAGACCGGCGGAGGGCCAGGACGCCCATGAATGCCAAAGGTGCGACTGCAATGGGCACTCAGAG
ACATGTCACTTTGACCCCGCTGTGTTTGCCGCCAGCCAGGGGGCATATGGAGGTGTGTGTGACAATTGCCGGGAC
CACACCGAAGGCAAGAACTGTGAGCGGTGTCAGCTGCACTATTTCCGGAACCGGCGCCCGGGAGCTTCCATTCAG
GAGACCTGCATCTCCTGCGAGTGTGATCCGGATGGGGCAGTGCCAGGGGCTCCCTGTGACCCAGTGACCGGGCAG
TGTGTGTGCAAGGAGCATGTGCAGGGAGAGCGCTGTGACCTATGCAAGCCGGGCTTCACTGGACTCACCTACGCC
AACCCGCAGGGCTGCCACCGCTGTGACTGCAACATCCTGGGGTCCCGGAGGGACATGCCGTGTGACGAGGAGAGT
GGGCGCTGCCTTTGTCTGCCCAACGTGGTGGGTCCCAAATGTGACCAGTGTGCTCCCTACCACTGGAAGCTGGCC
AGTGGCCAGGGCTGTGAACCGTGTGCCTGCGACCCGCACAACTCCCCTCAGCCCACAGTGCAACCAGTTCACAGG
GCAGTGCCCTGTCGGGAAGGCTTTGGTGGCCTGATGTGCAGCGCTGCAGCCATCCGCCAGTGTCCAGACCGGACC
TATGGAGACGTGGCCACAGGATGCCGAGCCTGTGACTGTGATTTCCGGGGAACAGAGGGCCCGGGCTGCGACAAG
GCATCAGGCCGCTGCCTCTGCCGCCCTGGCTTGACCGGGCCCCGCTGTGACCAGTGCCAGCGAGGCTACTGCAAT
CGCTACCCGGTGTGCGTGGCCTGCCACCCTTGCTTCCAGACCTATGATGCGGACCTCCGGGAGCAGGCCCTGCGC
TTTGGTAGACTCCGCAATGCCACCGCCAGCCTGTGGTCAGGGCCTGGGCTGGAGGACCGTGGCCTGGCCTCCCGG
ATCCTAGATGCAAAGAGTAAGATTGAGCAGATCCGAGCAGTTCTCAGCAGCCCCGCAGTCACAGAGCAGGAGGTG
GCTCAGGTGGCCAGTGCCATCCTCTCCCTCAGGCGAACTCTCCAGGGCCTGCAGCTGGATCTGCCCCTGGAGGAG
GAGACGTTGTCCCTTCCGAGAGACCTGGAGAGTCTTGACAGAAGCTTCAATGGTCTCCTTACTATGTATCAGAGG
AAGAGGGAGCAGTTTGAAAAAATAAGCAGTGCTGATCCTTCAGGAGCCTTCCGGATGCTGAGCACAGCCTACGAG
CAGTCAGCCCAGGCTGCTCAGCAGGTCTCCGACAGCTCGCGCCTTTTGGACCAGCTCAGGGACAGCCGGAGAGAG
GCAGAGAGGCTGGTGCGGCAGGCGGGAGGAGGAGGAGGCACCGGCAGCCCCAAGCTTGTGGCCCTGAGGCTGGAG
ATGTCTTCGTTGCCTGACCTGACACCCACCTTCAACAAGCTCTGTGGCAACTCCAGGCAGATGGCTTGCACCCCA
ATATCATGCCCTGGTGAGCTATGTCCCCAAGACAATGGCACAGCCTGTGGCTCCCGCTGCAGGGGTGTCCTTCCC
AGGGCCGGTGGGGCCTTCTTGATGGCGGGGCAGGTGGCTGAGCAGCTGCGGGGCTTCAATGCCCAGCTCCAGCGG
ACCAGGCAGATGATTAGGGCAGCCGAGGAATCTGCCTCACAGATTCAATCCAGTGCCCAGCGCTTGGAGACCCAG
GTGAGCGCCAGCCGCTCCCAGATGGAGGAAGATGTCAGACGCACACGGCTCCTAATCCAGCAGGTCCGGGACTTC
CTAACAGACCCCGACACTGATGCAGCCACTATCCAGGAGGTCAGCGAGGCCGTGCTGGCCCTGTGGCTGCCCACA
GACTCAGCTACTGTTCTGCAGAAGATGAATGAGATCCAGGCCATTGCAGCCAGGCTCCCCAACGTGGACTTGGTG
CTGTCCCAGACCAAGCAGGACATTGCGCGTGCCCGCCGGTTGCAGGCTGAGGCTGAGGAAGCCAGGAGCCGAGCC
CATGCAGTGGAGGGCCAGGTGGAAGATGTGGTTGGGAACCTGCGGCAGGGGACAGTGGCACTGCAGGAAGCTCAG
GACACCATGCAAGGCACCAGCCGCTCCCTTCGGCTTATCCAGGACAGGGTTGCTGAGGTTCAGCAGGTACTGCGG
CCAGCAGAAAAGCTGGTGACAAGCATGACCAAGCAGCTGGGTGACTTCTGGACACGGATGGAGGAGCTCCGCCAC
CAAGCCCGGCAGCAGGGGGCAGAGGCAGTCCAGGCCCAGCAGCTTGCGGAAGGTGCCAGCGAGCAGGCATTGAGT
GCCCAAGAGGGATTTGAGAGAATAAAACAAAAGTATGCTGAGTTGAAGGACCGGTTGGGTCAGAGTTCCATGCTG
GGTGAGCAGGGTGCCCGGATCCAGAGTGTGAAGACAGAGGCAGAGGAGCTGTTTGGGGAGACCATGGAGATGATG
GACAGGATGAAAGACATGGAGTTGGAGCTGCTGCGGGGCAGCCAGGCCATCATGCTGCGCTCGGCGGACCTGACA
GGACTGGAGAAGCGTGTGGAGCAGATCCGTGACCACATCAATGGGCGCGTGCTCTACTATGCCACCTGCAAG**TGA**

FIGURE 553B

TGCTACAGCTTCCAGCCCGTTGCCCCACTCATCTGCCGCCTTTGCTTTTGGTTGGGGGCAGATTGGGTTGGAATG
CTTTCCATCTCCAGGAGACTTTCATGCAGCCTAAAGTACAGCCTGGACCACCCCTGGTGTGTAGCTAGTAAGATT
ACCCTGAGCTGCAGCTGAGCCTGAGCCAATGGGACAGTTACACTTGACAGACAAAGATGGTGGAGATTGGCATGC
CATTGAAACTAAGAGCTCTCAAGTCAAGGAAGCTGGGCTGGGCAGTATCCCCCGCCTTTAGTTCTCCACTGGGGA
GGAATCCTGGACCAAGCACAAAAACTTAACAAAAGTGATGTAAAAATGAAAAGCCAAATAAAAATCTTTGG

FIGURE 554

MRPFFLLCFALPGLLHAQQACSRGACYPPVGDLLVGRTRFLRASSTCGLTKPETYCTQYGEWQMKCCKCDSRQPH
NYYSHRVENVASSSGPMRWWQSQNDVNPVSLQLDLDRRFQLQEVMMEFQGPMPAGMLIERSSDFGKTWRVYQYLA
ADCTSTFPRVRQGRPQSWQDVRCQSLPQRPNARLNGGKVQLNLMDLVSGIPATQSQKIQEVGEITNLRVNFTRLA
PVPQRGYHPPSAYYAVSQLRLQGSCFCHGHADRCAPKPGASAGPSTAVQVHDVCVCQHNTAGPNCERCAPFYNNR
PWRPAEGQDAHECQRCDCNGHSETCHFDPAVFAASQGAYGGVCDNCRDHTEGKNCERCQLHYFRNRRPGASIQET
CISCECDPDGAVPGAPCDPVTGQCVCKEHVQGERCDLCKPGFTGLTYANPQGCHRCDCNILGSRRDMPCDEESGR
CLCLPNVVGPKCDQCAPYHWKLASGQGCEPCACDPHNSPQPTVQPVHRAVPCREGFGGLMCSAAAIRQCPDRTYG
DVATGCRACDCDFRGTEGPGCDKASGRCLCRPGLTGPRCDQCQRGYCNRYPVCVACHPCFQTYDADLREQALRFG
RLRNATASLWSGPGLEDRGLASRILDAKSKIEQIRAVLSSPAVTEQEVAQVASAILSLRRTLQGLQLDLPLEEET
LSLPRDLESLDRSFNGLLTMYQRKREQFEKISSADPSGAFRMLSTAYEQSAQAAQQVSDSSRLLDQLRDSRREAE
RLVRQAGGGGGTGSPKLVALRLEMSSLPDLTPTFNKLCGNSRQMACTPISCPGELCPQDNGTACGSRCRGVLPRA
GGAFLMAGQVAEQLRGFNAQLQRTRQMIRAAEESASQIQSSAQRLETQVSASRSQMEEDVRRTRLLIQQVRDFLT
DPDTDAATIQEVSEAVLALWLPTDSATVLQKMNEIQAIAARLPNVDLVLSQTKQDIARARRLQAEAEEARSRAHA
VEGQVEDVVGNLRQGTVALQEAQDTMQGTSRSLRLIQDRVAEVQQVLRPAEKLVTSMTKQLGDFWTRMEELRHQA
RQQGAEAVQAQQLAEGASEQALSAQEGFERIKQKYAELKDRLGQSSMLGEQGARIQSVKTEAEELFGETMEMMDR
MKDMELELLRGSQAIMLRSADLTGLEKRVEQIRDHINGRVLYYATCK

FIGURE 555

GCGGAGTCTCCAACTGGGAGAGCTGCAGCTGCCGAGAGGAGGAGAACGCTGAGGTCGGTCGGACCAACGGACGCG
CTGACCGCTGCCAACTGCAGCTCGCGCTGCCTCCTGCTCGCGCCGTGCCACTAAGGTCACTCCCGCCTCCGAGAG
CCCAGAGCCGAG<u>ATG</u>GAAACGGTCCAGGAGCTGATCCCCCTGGCCAAGGAGATGATGGCCCAGAAGCGCAAGGGG
AAGATGGTGAAGCTGTACGTGCTGGGCAGCGTGCTGGCCCTCTTCGGCGTGGTGCTCGGCCTGATGGAGACTGTG
TGCAGCCCCTTCACGGCCGCCAGACGTCTGCGGGACCAGGAGGCAGCCGTGGCGGAGCTGCAGGCCGCCCTGGAG
CGACAGGCTCTCCAGAAGCAAGCCCTGCAGGAGAAAGGCAAGCAGCAGGACACGGTCCTCGGCGGCCGGGCCCTG
TCCAACCGGCAGCACGCCTCC<u>TAG</u>GAACTGTGGGAGACCAGCGGAGTGGGAGGGAGACGCAGTAGACAGAGACAG
ACCGAGAAGGAAGGGAGAGACAGAGGGGGCGCGCACAGGAGCCTGACTCCGCTGGGAGAGTGCAGGAGCACGT
GCTGTTTTTTATTTGGACTTAACTTCAGAGAAACCGCTGACATCTAGAACTGACCTACCACAAGCATCCACCAAA
GGAGTTTGGGATTGAGTTTTGCTGCTGTGCAGCACTGCATTGTCATGACATTTCCAACACTGTGTGAATTATCTA
AATGCGTCTACCATTTTGCACTAGGGAGGAAGGATAAATGCTTTTTATGTTATTATTATTAATTATTACAATGAC
CACCATTTTGCATTTTGAAATAAAAAACTTTTTATACCAAAAAAAAAAAAAAAA

FIGURE 556

METVQELIPLAKEMMAQKRKGKMVKLYVLGSVLALFGVVLGLMETVCSPFTAARRLRDQEAAVAELQAALERQAL
QKQALQEKGKQQDTVLGGRALSNRQHAS

FIGURE 557

CCCGCCTCCGAGAGCCCAGAGCCGAGATGGAAACGGTCCAGGAGCTGATCCCCCTGGCCAAGGAGATGATGGCCC
AGAAGCGCAAGGGGAAGATGGTGAAGCTGTACGTGCTGGGCAGCGTGCTGGCCCTCTTCGGCGTGGTGCTCGGCC
TGATGGAGACTGTGTGCAGCGGAGTGGGAGGGAGACGCAGTAGACAGAGACAGACCGAGAGAGGAATGGAGAGAC
AGAGGGGGCGCGCGCACAGGAGCCTGACTCCGCTGGGAGAGTGCAGGAGCACGTGCTGTTTTTTATTTGGACTTA
ACTTCAGAGA

FIGURE 558

CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCC**ATG**ACCGTCG
CGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCC
TGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAA
GTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG
TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGC
TAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGT
GCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAG
CAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG
GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTT
GTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCAC
CACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA
ATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC
CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATG
TTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACAC
GGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAG
GTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT
TGCTGACT**TAG**CCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTA
TCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGG
AATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAG
AACAACTTGCAGAATTGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT
GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGGAA
ATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCTCTTCTAAGCAAAATTGC
TAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAA
TATTTTAAAGGTAAAACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG
AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAAA
AGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATAGTCAA
ATTTGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAA
AACAAGAAAAGTTGAAGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTG
GT

FIGURE 559

MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPALEGRTSFPEDTVITYKCEESFVKIPGE
KDSVICLKGSQWSDIEEFCNRSCEVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLK
WSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYC
PAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPT
TVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVSRTTKHFHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLV
TMGLLT

FIGURE 560A

GTGGATTTGGTCGTCTCCCTGATTCCGAGCTGCGGGCAGGGAGAGGGGCCTCGCGCCGCCCTCAGCAGCCGGCGG
CGGCCGAGGTAGACCGAGCGGGGACGGAAGGACAGACCGACGTCGCCGAGCTGGAATCATGTGAGGGCCAACCGG
GGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCCTCTCAGCATGGAACAGAGGCGGC
CCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCC
CAGCAGCCGGCATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGTCC
ACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCAACCTGACCATCCAGG
TGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTTGTTACCCGCCCCTCATCGTGCAGCCCTGCAGCGAAG
TGCTCACCCTCACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGA
GCCTCTACCAGGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGG
AGCACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGATGGCA
AGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCAGCCGGAAGCTGCCCCGAG
ACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCTCTCATCAAGATCCCTTCAG
ACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTC
TCACTGTCCAGCCCGAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCG
TGCGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGCCGGGGTGG
AATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAGGCCTTCAATATCACCAGCC
AGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAGCAGTATCACCACCCGCCCGATGACTCTGCCCTGT
GTGCCTTCCCTATCCGGGCCATCAACTTGCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACC
TGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGCACCAAGGCGCCTGTCCCCATCGATGATAACTTCTGTG
GACTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCACCAGCAGGGACC
GCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGGACTAAGAGTGGCAAGCTGA
AAAAGATTCGGGCCGACGGTCCCCCCCATGGTGGGGTCCAGTACGAGATGGTCTCTGTGCTCAAGGACGGAAGCC
CCATCCTCCGGGACATGGCCTTCTCCATTGATCAGCGCTACCTGTACGTCATGTCTGAGAGACAGGTCACCAGGG
TCCCCGTGGAGTCATGTGAGCAGTATACGACTTGTGGGGAGTGCCTGAGCTCTGGGGACCCTCACTGTGGCTGGT
GTGCCCTGCACAACATGTGCTCCCGCAGGGACAAATGCCAACAGGCCTGGGAACCTAATCGATTTGCTGCCAGCA
TCAGCCAGTGTGTGAGCCTTGCAGTGCATCCCAGCAGCATCTCAGTATCTGAGCACAGCCGGTTGCTTAGCCTGG
TAGTGAGTGATGCTCCTGATCTATCTGCGGGTATCGCCTGTGCCTTTGGGAACCTGACAGAGGTGGAGGGGCAGG
TGTCCGGGAGCCAGGTCATCTGCATCTCACCTGGGCCCAAGGATGTCCCTGTCATCCCGCTGGATCAAGACTGGT
TTGGGCTGGAGCTACAGCTGAGGTCCAAGGAGACAGGGAAGATATTTGTCAGCACCGAGTTCAAGTTTTACAACT
GCAGTGCCCACCAACTGTGCCTGTCCTGTGTCAACAGCGCCTTCCGCTGCCATTGGTGCAAGTACCGCAACCTCT
GCACTCATGACCCCACCACCTGCTCCTTCCAGGAGGGCCGGATCAATATTTCAGAGGACTGTCCCCAGCTGGTGC
CCACAGAGGAGATCTTGATTCCAGTCGGGGAGGTAAAGCCAATCACCCTTAAGGCGCGAAATCTGCCCCAGCCGC
AGTCCGGCCAGCGAGGCTATGAGTGTGTCCTCAACATACAAGGAGCCATCCACCGGGTCCCCGCTCTGCGCTTCA
ACAGCTCCAGCGTTCAGTGTCAGAACAGCTCGTACCAGTATGATGGCATGGACATCAGCAATCTGGCCGTGGATT
TCGCTGTGGTGTGGAACGGCAATTTCATCATTGACAACCCTCAGGACCTGAAAGTCCATCTCTACAAGTGTGCAG
CCCAGCGGGAGAGCTGCGGCCTCTGCCTCAAGGCCGACCGGAAGTTTGAGTGTGGCTGGTGCAGCGGCGAGCGCA
GGTGCACCCTCCACCAGCACTGTACCAGCCCTTCCAGCCCCTGGCTCGACTGGTCCAGCCACAATGTCAAGTGCT
CCAACCCTCAAATCACCGAGATTTTGACGGTGTCTGGACCGCCGGAAGGAGGGACGCGAGTGACCATCCATGGCG
TGAACCTGGGTCTGGACTTCTCCGAGATCGCCCACCATGTGCAGGTGGCTGGGGTGCCCTGCACGCCCCTCCCAG
GGGAATACATCATCGCTGAGCAGATTGTCTGTGAGATGGGCCATGCCCTCGTGGGAACCACCTCCGGGCCAGTAC
GCCTGTGTATTGGCGAGTGTAAGCCAGAGTTCATGACGAAGTCCCATCAGCAGTACACCTTCGTGAACCCTTCTG
TGCTGTCACTCAACCCAATCCGAGGTCCCGAGTCAGGAGGCACTATGGTGACCATTACCGGCCATTACCTTGGGG
CTGGGAGCAGCGTGGCAGTCTACCTGGGCAACCAGACCTGCGAGTTCTACGGGAGGTCAATGAGTGAGATCGTGT
GTGTCTCACCCCCATCATCCAATGGCCTTGGCCCGGTCCCTGTTTCTGTGAGTGTCGACCGAGCCCATGTGGATA
GCAACCTGCAGTTTGAGTACATAGATGACCCTCGGGTCCAGCGCATCGAGCCAGAGTGGAGCATTGCCAGTGGCC
ACACACCCCTGACCATCACAGGCTTCAACCTGGATGTCATTCAGGAGCCAAGGATCCGAGTCAAATTCAATGGCA
AAGAATCTGTCAATGTGTGTAAAGTTGTGAACACAACCACCCTCACCTGCCTGGCACCCTCTCTGACCACGGACT
ACCGCCCTGGCCTGGACACTGTGGAACGCCCAGATGAGTTTGGATTTGTCTTTAACAATGTCCAATCCTTGCTAA

FIGURE 560B

TTTACAACGACACCAAGTTTATCTACTACCCCAACCCGACCTTTGAACTGCTTAGCCCTACTGGAGTCTTGGATC
AAAAGCCAGGATCGCCCATCATTCTGAAGGGCAAAAACCTCTGCCCTCCTGCCTCTGGAGGGGCCAAACTCAACT
ACACTGTGCTCATCGGAGAGACCCCTTGTGCTGTCACCGTATCTGAGACCCAGCTTCTCTGCGAGCCTCCCAACC
TCACCGGGCAGCACAAGGTCATGGTTCACGTGGGCGGGATGGTGTTCTCGCCTGGCTCGGTGAGTGTCATCTCAG
ACAGCTTGCTGACCCTGCCAGCCATCGTCAGCATCGCGGCCGGCGGCAGCCTCCTCCTCATCATCGTCATCATCG
TCCTCATTGCCTACAAGCGCAAGTCTCGAGAAAATGACCTCACTCTCAAGCGGCTGCAAATGCAGATGGACAATC
TGGAGTCCCGTGTGGCCTTGGAGTGCAAGGAAGCTTTTGCTGAGCTCCAGACGGATATCAATGAGTTGACCAGTG
ACCTGGACCGCTCAGGAATCCCTTACCTGGACTATCGTACCTACGCTATGCGAGTCCTGTTCCCGGGCATCGAGG
ACCACCCCGTCCTGCGGGAGCTGGAGGTACAAGGAAACGGGCAGCAGCACGTGGAGAAGGCCCTGAAGCTCTTTG
CCCAGCTCATCAACAACAAGGTGTTCCTGCTGACCTTCATCCGCACCCTGGAGCTGCAGCGCAGTTTCTCCATGC
GCGACCGGGGCAACGTGGCTTCGCTCATCATGACCGGCCTGCAGGGCCGCCTGGAATATGCCACTGATGTCCTCA
AGCAGCTGCTCTCTGACCTCATCGATAAGAACCTGGAGAACAAGAACCACCCCAAGCTGCTACTCCGGAGGACAG
AGTCTGTGGCTGAAAAGATGCTGACCAATTGGTTCGCCTTCCTCCTGCACAAGTTCCTAAAGGAGTGCGCAGGGG
AGCCACTCTTCATGCTATACTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCATTGATGCCATCACGGGCGAGG
CCCGCTACTCCCTGAGCGAGGACAAGCTCATCCGGCAGCAGATCGAGTACAAGACCCTGATCCTGAACTGCGTCA
ACCCTGACAACGAGAACAGTCCAGAGATCCCAGTGAAGGTGTTAAACTGTGACACCATCACACAGGTCAAGGAGA
AGATTCTTGATGCCGTGTATAAGAATGTGCCCTATTCCCAGCGGCCGAGGGCAGTGGACATGGACTTGGAGTGGC
GCCAAGGCCGGATCGCCCGGGTCGTGCTGCAAGATGAGGACATCACCACCAAGATTGAGGGTGACTGGAAGCGGC
TCAACACACTGATGCATTATCAGGTGTCAGACAGGTCGGTGGTGGCTCTGGTCCCCAAACAGACCTCCTCCTACA
ACATCCCTGCCTCTGCCAGCATCTCCCGGACGTCCATCAGCAGATACGGTGACTCCTCCTTCAGGTATACGGGCA
GCCCCGACAGCCTGCGGTCCCGGGCCCCGATGATCACCCCAGACCTGGAAAGTGGGGTCAAGGTGTGGCATCTGG
TGAAGAACCATGACCACGGTGACCAGAAGGAGGGTGACCGGGGCAGCAAGATGGTGTCCGAGATCTACCTGACCC
GGCTACTGGCCACCAAGGGCACCCTGCAGAAGTTTGTGGACGACTTGTTTGAGACCTTGTTCAGCACTGTGCACC
GGGGCAGCGCTCTCCCCCTGGCCATCAAGTACATGTTTGATTTCCTAGATGAGCAGGCAGACAGGCACAGCATCC
ATGACACAGATGTGCGGCACACCTGGAAAAGCAACTGCCTCCCTCTGCGCTTCTGGGTGAACGTGATTAAGAACC
CCCAGTTCGTGTTTGACATCCACAAGGGCAGCATCACGGACGCCTGCCTCTCTGTGGTGGCCCAGACCTTCATGG
ACTCTTGTTCAACGTCAGAGCACCGGCTGGGCAAGGACTCCCCCTCCAACAAGCTGCTCTATGCCAAGGACATCC
CCAGCTACAAGAGCTGGGTGGAGAGATACTACGCAGACATCGCCAAGCTCCCAGCCATCAGTGACCAGGACATGA
ATGCCTACCTCGCCGAGCAGTCCCGCCTGCACGCCGTGGAGTTCAACATGCTGAGTGCCCTCAATGAGATCTACT
CCTATGTCAGCAAGTATAGTGAGGAGCTCATCGGGGCCCTAGAGCAGGATGAGCAGGCACGGCGGCAGCGGCTGG
CTTATAAGGTGGAGCAGCTCATTAATGCCATGTCCATTGAGAGCTGAGAGGAGGAGCCTCGCATTCCTGGGAAGA
GGGACCTGTCCAAGCTGTCACACTGGGAGTCTCAGATGGAAGGACAAGTGATGGGGATCAGGCCCCAGAGCTTGC
TGTCCCCTGAGACCCCATCCTGGGGAGAGGGGAGGACTCCTCTCCCTACGCCAGCCAAGTTTCGTCATAGCCAGT
TCCAGCTGGGAGAGACAGTGGGCGTCGTCCATCCTCAGTGAGAACACCAGAGAACCCGGGGCCGGGAGAAGGTGG
TTCTTCAAGCCGAGAGGCACGAGCTGGGGACAGTTCTGCCTCTGTGACTGCTGCTTTGCATGAAAACTCATTTGA
TGTATATTGGGGAAATAATGAGAACTTTATTTAATTTTTTTAAGAAAAAGGGAAAAAAACAGAAATAAAACAAAA
AGCCGCCCTGTTAATCCAAATTAAAAAAAAAAAAAAAA

FIGURE 561

ACTGAATTCAACAATTATTTATTGAGTGTCTATTATGTGCTAGATACTGAGACACATCAGAGAACAAAACCAAAA
GCCCTGCCCTCGTCGGGCTTACAGTCTAGCACTTACTGCCAGTTAACCTGGAGGCTACCTGGAACCCCGGGCAAG
TCACCGCACCTCTGTGCCTCGGTCCTCAGCTGCCTAATGGGAGAATAAGCAGACCTGGCTCAGACATGAATCATG
TGCTTGGTGTACTGCAGATGCCAAACTGCATCCCCATAACCCACCACCCAGACAGTAGATAGGGCTGGAAGTTGA
TTTTTAATGATCAAGTACAATGGAGGGAGGGCAGAGGGGCTAAGCCTAGCTGTCTGGGGTGCTGTGGTGGTGGTG
GGCTGGCTACACAAACTGTTGCTGCTGCTGCTGCTTCTTGGTGGCTGCCTTGCTGGCGAGGTCCTTGGCCTTCTC
TGTAGCTGCCAGTGCTGTCTCCTTTGCCTTCTCCTTGGCTTCCTTGGCTGTCTCAACAAGTGTTTTGGAAGGGGC
CTCGCCTTGCAGCTTTGCCAAGATATATTCAAAACCCTTCATAGTCTTGGTCACATTGCTTTTGAACCAGGCAAG
ACCAAATTCCTGGACAGCTCTGGAGACACCAAATAAGCTAGAGGAGACCCAGGCTTCCCGGCGGATTTCGGTCCG
GCCACTGTTGTCAGAGTTCACACAGTAAACACATCGTTCCTCCACCACC

FIGURE 562

TTTCGGCCGGAACCGCCATCTTCCAGTAATTCGCCAAAATGACAAACACAAAGGGAAAGAGGAGAGGCACCCGAT
ATATGTTCTCTAGGCCTTTTAGAAAACATGGAGTTGTTCCTTTGGCCACATATATGCGAATCTATAAGAAAGGTG
ATATTGTAGACATCAAGGGAACGGGTACTGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAAACTGGAA
GAGTCTACAATGTTACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGA
GAATTAATGTGCGTATTGAGCACATTAAGCATTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAATG
ATCCTCCACCCAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCCCTATG
AATTCATGGCATAATAGGTGTT

FIGURE 563

MTNTKGKRRGTQYMFSRPFRKHGVVALATYMQIYKKGDIVDIKGMGTVQKGMPHKCYHGKTGRVYNVPQHAVGIV
VNTQVKGKILAKRINVRIEHIKHSKS

FIGURE 564

ATGAAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCCAGCTGAAGCCAACAAGAGTTCTGAA
GATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACATTTACAACCAGAATGTATCCCAG
AAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCAGTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTG
TGCGAGTGCAGGTACGAGGAGCGCAGCACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGT
GCCCTGTTGCTCTACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATATACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCCGAGCA
AACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTC
TTCGATCGGCACAAGATGCTCAGC**TAG**

FIGURE 565

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPMPVPGHDVEAYCLL
CECRYEERSTTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

FIGURE 566

ACCTGCACTGACTTTTTTCTCCTTTTGGAGGGAGAGCAGAGACCATGTCTGACATAGAAGAGGTGGTGGAAGAGT
ACGAGGAGGAGGAGCAGGAAGAAGCAGCTGTTGAAGAGCAGGAGGAGGCAGCGGAAGAGGATGCTGAAGCAGAGG
CTGAGACCGAGGAGACCAGGGCAGAAGAAGATGAAGAAGAAGAGGAAGCAAAGGAGGCTGAAGATGGCCCAATGG
AGGAGTCCAAACCAAAGCCCAGGTCGTTCATGCCCAACTTGGTGCCTCCCAAGATCCCCGATGGAGAGAGAGTGG
ACTTTGATGACATCCACCGGAAGCGCATGGAGAAGGACCTGAATGAGTTGCAGGCGCTGATCGAGGCTCACTTTG
AGAACAGGAAGAAAGAGGAGGAGGAGCTCGTTTCTCTCAAAGACAGGATCGAGAGACGTCGGGCAGAGCGGGCCG
AGCAGCAGCGCATCCGGAATGAGCGGGAGAAGGAGCGGCAGAACCGCCTGGCTGAAGAGAGGGCTCGACGAGAGG
AGGAGGAGAACAGGAGGAAGGCTGAGGATGAGGCCCGGAAGAAGAAGGCTTTGTCCAACATGATGCATTTTGGGG
GTTACATCCAGAAGXXXXXXXXXACAGAGCGGAAAAGTGGGAAGAGGCAGACTGAGCGGGAAAAGAAGAAGAAGA
TTCTGGCTGAGAGGAGGAAGGTGCTGGCCATTGACCACCTGAATGAAGATCAGCTGAGGGAGAAGGCCAAGGAGC
TGTGGCAGAGCATCTATAACTTGGAGGCAGAGAAGTTCGACCTGCAGGAGAAGTTCAAGCAGCAGAAATATGAGA
TCAATGTTCTCCGAAACAGGATCAACGATAACCAGAAAGTCTCCAAGACCCGCGGGAAGGCTAAAGTCACCGGGC
GCTGGAAATAGAGCCTGGCCTCCTTCACCAAAGATCTGCTCCTCGCTCGCACCTGCCTCCGGCCTGCACTCCCCC
AGTTCCCGGGCCCTCCTGGGCACCCCAGGCAGCTCCTGTTTGGAAATGGGGAGCTGGCCTAGGTGGGAGCCACCA
CTCCTGCCTGCCCCCACACCCACTCCACACCAGTAATAAAAAGCCACCACACACTG

FIGURE 567

CCAGCCTTGCCCGGCAGAGGACTCTGGAGGATGAGGAGGAACAGGAGCGCGCGAXGGCGGCGGCACCGCAACCTG
AGCTCCACCACGGACGATGAGGCTCCCAGGCTCAGCAGAATGGAGACCGGCAGCCTCTGCTTCTGAGAGACTACC
GAGCGTGGAAGAAGCAGAGGTGCCCAAGCCACTGCCCCCAGCCTCCAAAGATGAGGACGAGGACATCCAGAGCAT
CCTCAGAACACGGCAGGAGCGGAGGCAGAGGCGGCAGGTGGTGGAGGCTGCACAGGCCCCCATCCAGGAGAGGCT
GGAGGCAGAGGAGGGGAGGAACAGCTTGAGCCCTGTGCAGGCCACACAGAAACCCCTAGTCTCCAAGAAGGAACT
GGAAATCCCACCTCGCCGGAGACTGAGTCGGGAACAGCGGGGCCCCTGCGCTGGAGGAGGAGAGCTTGGTGGGCA
GGGAGCCAGAAGAGAGGAAGAAAGGGGTTCCAGAAAAGTCCCCAGTCTTGGAGAAATCCTCCATGCCAAAGAAGA
CGGCACCTGAAAAGAGCCTGGTCTCCGATAAAACCTCCATCTCTGAGAAGGTGCTGGCCTCAGAGAAGACATCTC
TATCAGAGAAGATAGCAGTGTCAGAGAAAAGAAACAGCTCAGAGAAGAAGTCTGTTCTAGAAAAAAACCAGTGTCT
CTGAGAAGTCGCTGGCCCCAGGGATGGCACTGGGCTCAGGAAGGAGGCTGGTGTCTGAGAAAGCTTCCATCTTTG
AGAAGGCACTGGCCTCAGAGAAGAGCCCAACTGCAGATGCTAAGCCGGCCCCAAAGAGGCCACAGCCTCAGAGCA
GCCCCTGGCGCAGGAGCCGCCAGCCTCTGGGGGAAGCCCAGCCACCACCAAGGAGCAGAGAGGAAGGGCCCTCCC
TGGGAAGAACCTGCCCTCTTTGGCAGAGCAGGGGGCTTCAGACCCTCCGACTGTGGCCTCCCGCCTCCCACCCGT
CACACTCCAGGTGAAAATCCCCAGCAAGGAGGAAGAGGCAGATATGTCCTCACCCACACAGCGAACCTACAGCAG
CTCCCTCAAACGCTCCAGCCCCAGGACCATCTCCTTTCGGATGAAACCCAAGAAAGAAAACTCGGAAACAACCCT
AACTCGCAGTGCCAGCATGAAGCTCCCAGACAACACAGTGAAGTTGGGAGAGAAGCTGGAGAGATACCACACGGC
CATACGGAGATCAGAATCTGTCAAGTCTCGGGGTCTGCCTTGCACTGAGTTATTCGTGGCTCCTGTGGGTGTAGC
CAGCAAGCGCCACCTCTTTGAGAAGGAACTGGCGGGCCAGAGCCGAGCAGAACCAGCCTCCAGCCGGAAGGAGAA
CTTGAGGCTCTCAGGGGTTGTGACATCAAGGCTCAACCTGTGGATCAGCAGGACCCAGGAATCTGGAGATCAGGA
CCCCCAGGAGGCACAGAAAGCATCATCTGCAACCGAGAGGACTCAGTGGGGACAGAAATCTGACTCCTCGCTGGA
CGCTGAGGTGTGACAAGCCCCGCCAAGACAGACCTGCAAGTCTTCGTCTCAAGGGACCTCCCTCATGCCAGGCCC
CTGCCTCTCACAGCAGCACCCTTTCCTCTCATTGTCCCTGTTCCCTTTTTGCCTGTGGATCTGTTTGGCCAGGGT
CCCTGGGGTCAGGAATATTTGCAAGACTCAGCCAGCTCCTTCCCAGCCCAGCCTCTTGGGGCTGGGACTTTCTCA
CCCTGCGGCAGGCACAACAGATGCTGGGACCCAGTCTCTGCCCAGGTCACAGCACAAGTGCACATCAGCACTATG
GGGCCTATGTCCTGCCCAGAGACCTCTGCTCCTTCCTGCTCACATCCACAGTCAGGGCACGGCGCCCCTCAAGAA
CTCCAGAGTCACCTGTCTCATCGGCTCCCAGCAAGTGCCTCTTTGTCTATGATGTCCCCCTTCTCTGAGGCCTGG
ACCCACCCATCTTTGTCCCTGGGGCCTGCTCCCAGCCACTGAGGCCCGCTCTGGCCAGGGGAGAAGGAGCTGCCG
TGCGTCTTCCCTGTGCCCCGTCTCCCTGCTTGGTTCTCCCCTCCCTTCCCTGGCCGGCTGCCATGGCCAGGAGCT
AAGTGCCTTTTTGTGTGCAACCACTTACCCTTTCTCTGAAAAACCTGTTCTCAGGAAGGATCTGATAAACTCATT
TACTCTCAGGTGTAAGAGACTGATGAGACCTTAGAAGCGAATTCCTCTCTGGAGGCCTTGCTTTCTAGCAGAGTC
ACCTGAAGTGTGTGAGGAGGATCATCATTTTCCTCATCCCCCCTCTTCTCACATTAAGGTGGTGGCTTGCCACTC
AGCAGTCCTAGCTTGGTGACTGGGAACTGCCACATACAGGGCCAGGCCTACCCTCCTTCCCCACAAGCCCCCTCC
AACCCCCACCCCCATGCTCTGGACCTCATGGCTCCTATGAGCTTGGAGCATGGTGAACCATCAGAGAATCTAGAA
CCAACCAAGCTAGGAACATCAGCCTGGTGCCTGTTAACCCCTTAAAGCTGTGGTTTACAACTTTTCAAAAATTTA
AATCATTAG

FIGURE 568

ATTCAAGGCCTGGGGGAGCTGCGGTTCCGAGAAGCGGCAGACGGCAGCCAGAAGGCTTGGGCTGTTGAGTAAGCA
GCCCCCTCTCAGTCCCGGCCCTCCCCGCCCCGCGCCCTGCGCCTCCAGTGAGTGACTGAGCCCCCGCTGCGGCCC
CGCCCCCGGGGCCCTGCCGGAGCTGGTGCGCGGCGCGGAGGGGAGGGCCGGCCAGGGTAGGAATGCGCTGCGGGC
GGGCGGCGCAGGAGGCGAGCGGCGGAACATGTAAGGGCACATCCCGCGAGCTGCCGCCCAGCGCGCAGACAGAGC
CCAGGGGAGCAAGAGAACGGGCGGGCGGTGGGGCTCACGGCCTAGGGAGGCGCGGAGGCATCTGGCAGAGGCGGG
TCGGGCTGGGCCAGCTGGGGTAGAGCGGAGGAGCGGGTGCCGGCTGAAGCGGGGCGGTGGGCGCGGAGCGCGCTG
GGGGCACCGACACCACCTCACCGGCAGCCGGGTGCTGAGGGCCGCGGTGTGGGTGCGCGGAGCAGTCAGGGCGCA
GGTGGGCAGCGCGCACGGCCTGCCAGCCCGGGGCGCCAGAATCCTGCGCTGCGGGGCCGAGAGGGGCGCCGCGCC
CGCCGCAGCCTGGAGCTTTCCGCGAACCTCGGGGCGCCCATGACGGCGGCGGCGACGGCTACCGTGCTCAAGGAG
GGCGTGCTGGAGAAGCGCAGCGGCGGGCTGCTGCAGCTGTGGAAGCGGAAGCGCTGCGTCCTCACCGAACGCGGG
CTGCAGCTCTTCGAGGCCAAGGGCACGGGCGGCCGGCCCAAGGAGCTCAGCTTCGCCCGCATCAAGGCCGTGGAG
TGCGTGGAGAGCACCGGGCGCCACATCTACTTCACGCTGGTGACCGAAGGGGGCGGCGAGATCGACTTCCGCTGC
CCCCTGGAAGATCCCGGCTGGAACGCCCAGATCACCCTAGGCCTGGTCAAGTTCAAGAACCAGCAGGCCATCCAG
ACAGTGCGGGCCCGGCAGAGCCTCGGGACCGGGACCCTCGTGTCCTAAACCACCGGGCGCACCATCTTTCCTTCA
TGCTACCCACCACCTCAGTGCTGAGGTCAAGGCAGCTTCGTTGTTCCCTCTGGCTTGTGGGGGCACGGCTGTGCT
CCATGTGGCAAGGTGGAAGGAATGGACGAGCCCTGGGAGGAGGGCAGAAGGCTACGCAGGGCTGAGGATGAAGAT
GCAGCCCCTGGATGGTCCCAGACTCTCAGGACATGCCCAGCTCAGGGGCTTCGAGCCACAGGCCTGGCCTCATAT
GGCATGAGGGGGAGCTGGCATAGGAGCCCCCTCCCTGCTGTGGTCCTGCCCTCTGTCCTGCAGACTGCTCTTAGC
CCCCTGGCTTTGTGCCAGGCCTGGAGGAGGGCAGTCCCCCATGGGGTGCCGAGCCAACGCCTCAGGAATCAGGAG
GCCAGCCTGGTACCAAAAGGAGTACCCAGGGCCTGGTACCCAGGCCCACTCCAGAATGGCCTCTGGACTCACCTT
GAGAAGGGGGAGCTGCTGGGCCTAAAGCCCACTCCTGGGGGTCTCCTGCTGCTTAGGTCCTTTTGGGACCCCCAC
CCATCCAGGCCCTTTCTTTGCACACTTCTTCCCCCACCTCTACGCATCTTCCCCCCACTGCGGTGTTCGGCCTGA
AGGTGGTGGGGGTGAGGGGGGGTTTGGCCATTAGCATTTCATGTCTTTCCCCAA

FIGURE 569

ATGGCGGCGGCGGCGGCAGCTGGTGCGGCCTCCGGGCTGCCGGGTCCAGTGGCACAAGGATTAAAGGAAGCGTTA
GTGGATACGCTCACCGGGATCCTATCCCCAGTACAGGAGGTGCGGGCGGCTGCTGAAGAACAGATTAAGGTGCTG
GAGGTGACGGAGGAATTTGGTGTTCACTTGGCAGAACTGACTGTAGATCCCCAGGGGGCACTGGCAATCCGTCAG
CTGGCATCAGTCATCTTGAAACAATATGTGGAGACTCACTGGTGTGCCCAATCAGAGAAATTTAGGCCTCCTGAA
ACTACAGAAAGGGCAAAAATTGTTATCCGGGAGCTATTGCCTAATGGGTTGAGAGAATCGATAAGCAAAGTGCGC
TCCAGTGTGGCCTATGCAGTGTCAGCCATTGCCCACTGGGACTGGCCTGAAGCTTGGCCCCAACTCTTCAACCTG
CTCATGGAGATGTTGGTGAGCGGAGACTTAAATGCCGTCCATGGAGCCATGCGTGTGCTGACAGAATTCACTCGT
GAAGTTACAGACACACAGATGCCACTTGTTGCTCCTGTCATTCTCCCAGAGATGTATAAGATCTTCACCATGGCT
GAGGTGTATGGTATTCGAACCCGTTCCCGAGCCGTGGAGATTTTTACCACTTGTGCCCATATGATCTGTAACATG
GAGGAGCTGGAAAAGGGTGCAGCCAAAGTCCTGATCTTTCCCGTGGTACAGCAGTTCACAGAGGCCTTTGTTCAG
GCCCTCCAGATACCAGATGGCCCCACATCTGACAGTGGGTTTAAGATGGAGGTCCTAAAGGCAGTGACAGCCCTA
GTGAAAAACTTCCCAAAGCACATGGTGTCCTCCATGCAGCAGATTCTGCCTATTGTTTGGAACACCCTAACCGAG
AGTGCAGCTTTTTATGTGAGGACAGAAGTAAATTACACAGAAGAAGTAGAAGATCCTGTGGATTCTGATGGTGAA
GTCCTGGGCTTTGAAAATCTCGTCTTTAGCATTTTTGAATTTGTCCATGCTCTACTAGAAAATAGCAAATTCAAA
AGCACTGTTAAGAAAGCCTTGCCTGAATTGATTTATTATATTATCCTGTACATGCAAATCACTGAGGAGCAGATT
AAAGTATGGACAGCCAACCCCCAACAATTTGTAGAAGATGAAGATGATGATACATTCTCCTATACTGTTAGAATA
GCAGCTCAAGACTTGTTGCTGGCTGTGGCCACAGATTTCCAGAATGAAAGTGCAGCAGCCCTGGCTGCTGCAGCC
ACTCGACATTTACAAGAAGCTGAGCAAACCAAAAACAGTGGCACTGAGCACTGGTGGAAGATCCATGAGGCATGC
ATGCTTGCCCTAGGCTCAGTGAAGGCCATCATCACTGACAGTGTGAAAAATGGCAGGATTCATTTTGACATGCAT
GGGTTCCTGACCAATGTCATCCTTGCAGACCTCAACCTCTCAGTGTCTCCTTTCCTCTTGGGCCGGGCACTTTGG
GCTGCCAGTCGGTTCACTGTTGCTATGTCCCCTGAACTGATCCAGCAGTTCCTACAGGCAACAGTTAGTGGTCTT
CACGAGACACAGCCCCCATCAGTTCGAATTTCTGCAGTGAGAGCCATCTGGGGTTATTGTGACCAACTGAAAGTC
TCAGAGAGTACCCACGTGCTCCAGCCCTTCCTCCCCAGCATCCTTGATGGCTTAATTCACCTAGCAGCCCAGTTC
AGCTCAGAGGTCCTCAACCTGGTGATGGAGACCCTGTGCATCGTTTGTACAGTAGACCCCGAATTCACAGCAAGC
ATGGAAAGCAAAATCTGCCCCTTCACCATCGCCATTTTCCTAAAGTACAGTAATGATCCCGTCGTCGCCTCACTG
GCTCAGGACATCTTCAAGGAGCTGTCCCAGATTGAAGCCTGTCAGGGCCCAATGCAAATGAGGCTGATTCCCACT
CTGGTCAGCATAATGCAGGCCCCAGCAGACAAGATTCCTGCAGGGCTTTGTGCGACAGCCATTGATATCCTGACA
ACAGTAGTACGAAATACAAAGCCTCCCCTTTCCCAGCTTCTCATCTGCCAAGCTTTCCCTGCTGTGGCACAGTGT
ACCCTTCACACAGATGACAATGCCACCATGCAGAATGGCGGAGAGTGCTTGCGGGCCTATGTGTCAGTGACCCTG
GAACAAGTAGCCCAGTGGCATGATGAGCAGGGCCACAATGGACTGTGGTATGTGATGCAAGTGGTGAGCCAGCTC
CTGGACCCCCGCACCTCAGAGTTCACTGCGGCCTTTGTGGGCCGCCTTGTTTCCACCCTCATCTCCAAGGCAGGG
CGGGAACTCGGGGAGAATCTAGACCAGATTCTTCGTGCCATCCTCAGTAAGATGCAGCAGGCAGAGACGCTCAGT
GTCATGCAGTCCCTGATCATGGTGTTCGCTCATCTGGTGCACACTCAGCTAGAACCTCTCTTGGAGTTCCTGTGT
AGCCTCCCAGGACCTACTGGCAAACCTGCTCTAGAGTTTGTGATGGCTGAGTGGACAAGCCGACAGCACCTGTTC
TATGGACAGTATGAAGGCAAAGTCAGCTCTGTGGCACTCTGTAAGCTGCTCCAGCATGGCATCAATGCAGATGAC
AAACGGCTACAGGATATCCGTGTGAAGGGAGAGGAGATCTACAGCATGGATGAGGGCATCCGCACCCGCTCTAAG
TCAGCCAAAAACCCAGAACGCTGGACAAACATTCCTTTGCTGGTCAAGATCCTAAAGCTGATCATCAACGAGCTC
TCCAACGTCATGGAGGCTAATGCCGCTCGCCAGGCCACTCCTGCAGAGTGGAGTCAAGATGACTCCAATGATATG
TGGGAGGACCAGGAGGAGGAAGAGGAGGAGGAGGAGGATGGTTTAGCTGGCCAACTTTTATCTGACATTCTTGCT
ACAAGTAAATATGAGGAGGATTACTACGAGGATGATGAGGAAGATGACCCTGATGCCCTGAAGGATCCTCTCTAT
CAGATTGATCTGCAGGCATATCTCACAGATTTCCTCTGCCAGTTTGCTCAGCAGCCCTGCTACATAATGTTTTCA
GGCCACCTTAATGACAATGAGAGGCGAGTTCTACAGACCATCGGCATC**TAA**

FIGURE 570

MAAAAAAGAASGLPGPVAQGLKEALVDTLTGILSPVQEVRAAAEEQIKVLEVTEEFGVHLAELTVDPQGALAIRQ
LASVILKQYVETHWCAQSEKFRPPETTERAKIVIRELLPNGLRESISKVRSSVAYAVSAIAHWDWPEAWPQLFNL
LMEMLVSGDLNAVHGAMRVLTEFTREVTDTQMPLVAPVILPEMYKIFTMAEVYGIRTRSRAVEIFTTCAHMICNM
EELEKGAAKVLIFPVVQQFTEAFVQALQIPDGPTSDSGFKMEVLKAVTALVKNFPKHMVSSMQQILPIVWNTLTE
SAAFYVRTEVNYTEEVEDPVDSDGEVLGFENLVFSIFEFVHALLENSKFKSTVKKALPELIYYIILYMQITEEQI
KVWTANPQQFVEDEDDTFSYTVRIAAQDLLLAVATDFQNESAAALAAAATRHLQEAEQTKNSGTEHWWKIHEAC
MLALGSVKAIITDSVKNGRIHFDMHGFLTNVILADLNLSVSPFLLGRALWAASRFTVAMSPELIQQFLQATVSGL
HETQPPSVRISAVRAIWGYCDQLKVSESTHVLQPFLPSILDGLIHLAAQFSSEVLNLVMETLCIVCTVDPEFTAS
MESKICPFTIAIFLKYSNDPVVASLAQDIFKELSQIEACQGPMQMRLIPTLVSIMQAPADKIPAGLCATAIDILT
TVVRNTKPPLSQLLICQAFPAVAQCTLHTDDNATMQNGGECLRAYVSVTLEQVAQWHDEQGHNGLWYVMQVVSQL
LDPRTSEFTAAFVGRLVSTLISKAGRELGENLDQILRAILSKMQQAETLSVMQSLIMVFAHLVHTQLEPLLEFLC
SLPGPTGKPALEFVMAEWTSRQHLFYGQYEGKVSSVALCKLLQHGINADDKRLQDIRVKGEEIYSMDEGIRTRSK
SAKNPERWTNIPLLVKILKLIINELSNVMEANAARQATPAEWSQDDSNDMWEDQEEEEEEEEDGLAGQLLSDILA
TSKYEEDYYEDDEEDDPDALKDPLYQIDLQAYLTDFLCQFAQQPCYIMFSGHLNDNERRVLQTIGI

FIGURE 571

AGTCAAGATGGAGGAGTACGCGCGAGAGCCTTGCCCATGGCGAATTGTGGATGACTGTGGTGGGGCCTTTACGAT
GGGTACCATTGGTGGTGGTATCTTTCAAGCAATCAAAGGTTTTCGCAATTCTCCAGTGGGAGTAAACCACAGACT
ACGAGGGAGTTTGACAGCTATTAAAACCAGGGCTCCACAGTTAGGAGGTAGCTTTGCAGTTTGGGGAGGGCTGTT
TTCCATGATTGACTGTAGTATGGTTCAAGTCAGAGGAAAGGAAGATCCCTGGAACTCCATCACAAGTGGTGCCTT
AACGGGAGCCATACTGGCAGCAAGAAATGGACCAGTGGCCATGGTTGGGTCAGCCGCAATGGGTGGCATTCTCCT
AGCTTTAATTGAAGGAGCTGGTATCTTGTTGACAAGATTTGCCTCTGCACAGTTTCCCAATGGTCCTCAGTTTGC
AGAAGACCCCTCCCAGTTGCCTTCAACTCAGTTACCTTCCTCACCTTTTGGAGACTATCGACAATATCAGTAGGA
CTTCTTTCCTAGGATTTCTTTAACAGAACGAGTTGTGGTTCGAGAAGGATTTCAGAAGATCAAGTTACAGTCTGT
TTTTAAAACCATAGGTGGGACAGCTATGGCCAATAGGCTATAAAGAGACATTTAGCACTTTTTTCTATTTAAAGG
AACAAGCGGGGAAGGGTGCTAAAAGATAATACGTTTATTTATTCACACTTGAATTGCATTTGTGATCAAAATAAA
TGTTTAAATCGCTAAAGGAAAATACAGTAAGTGCTTGAAAGATGAAGGACCAAAAGGCCAAAAAACAGTGAAATA
TGATCATCATCTCTTGCGGACTTCTCTGCCTGGTTTGTGTGTTCTGTTATTCAAACAATAAAAAGCTGGTGGAA
CTTACTCTTTCTTTTAAGATAAGTTGTAGACTTCGATGTTTCATGCTCATGTACTTCAAATAATGCATGTTTTAT
AGTTAGTCCCTCATCACTTGAAGTGACTTCTGAGAATTATGCAGAGTCAACATGGATCATTTCACAGTGAGATGC
TTTATGGATTGAAGGATATGGTAAAATGTTTATAGTTTACTTTGAAAGTAAAATATACTATGTCTTGGTTTTGAG
GATATTGGATACAAAACTCTCTTCCTTTAGGGCTACTGAGTCTTGATTCCTGATCATCAGAAATTTCACCAGAAA
CAACTTGCTTCCAATATACCCAATTCTATATGAAGAATTCATGGAGAGTGTACTGGCACTGGAAGAGTTTAGTGT
TTCTTGTATGCTTGAAAATAAAGTATGTACTGTTTTGAATGTGTTCCAAGTCCTCTGCATAAACGATGTATTTTG
GGGTCTGGTTGGGCCTGGAAAATGGATGAGCACTTCAGAACAGGTCATTTTCCTGATATTGGAAGTGACATGTGG
CCCTATAGGAGGCATGATGTTAGTTAATTACACATTTGCCTACATCTGTGGGAAATGGAGAACAAAGCCATGTGG
GTACTGTAAACACACGTTTATCTTTTGGCCCAATGCCATACATATGGTAGGCATTTAATTACTGATTGTGTTTGG
ATAATTTGGGAATTTTCGACTGTGGTAAAATATACATAAAATAATACTTATTAAAAAAAAAAAAAAAAAA

FIGURE 572

MEEYAREPCPWRIVDDCGGAFTMGTIGGGIFQAIKGFRNSPVGVNHRLRGSLTAIKTRAPQLGGSFAVWGGLFSM
IDCSMVQVRGKEDPWNSITSGALTGAILAARNGPVAMVGSAAMGGILLALIEGAGILLTRFASAQFPNGPQFAED
PSQLPSTQLPSSPFGDYRQYQ

FIGURE 573

GGCCATGGCGAGCGGCGAGCATTCCCCCGGCAGCGGCGCGGCCCGGCGGCCGCTGCACTCCGCGCAGGCTGTGGA
CGTGGCCTCGGCCTCCAACTTCCGGGCCTTTGAGCTGCTGCACTTGCACCTGGACCTGCGGGCTGAGTTCGGGCC
TCCAGGGCCCGGCGCAGGGAGCCGGGGGCTGAGCGGCACCGCGGTCCTGGACCTGCGCTGCCTGGAGCCCGAGGG
CGCCGCCGAGCTGCGGCTGGACTCGCACCCGTGCCTGGAGGTGACGGCGGCGGCGCTGCGGCGGGAGCGGCCCGG
CTCGGAGGAGCCGCCTGCGGAGCCCGTGAGCTTCTACACGCAGCCCTTCTCGCACTATGGCCAGGCCCTGTGCGT
GTCCTTCCCGCAGCCCTGCCGCGCCGCCGAGCGCCTCCAGGTGCTGCTCACCTACCGCGTCGGGGAGGGACCCGG
GGTTTGCTGGTTGGCTCCCGAGCAGACAGCAGGAAAGAAGAAGCCCTTCGTGTACACCCAGGGCCAGGCTGTCCT
AAACCGGGCCTTCTTCCCTTGCTTCGACACGCCTGCTGTTAAATACAAGTATTCAGCTCTTATTGAGGTCCCAGA
TGGCTTCACAGCTGTGATGAGTGCTAGCACCTGGGAGAAGAGAGGTCCAAATAAGTTCTTCTTCCAGATGTGTCA
GCCCATCCCCTCCTATCTGATAGCTTTGGCCATCGGAGATCTGGTTTCGGCTGAAGTTGGACCCAGGAGCCGGGT
GTGGGCTGAGCCCTGCCTGATTGATGCTGCCAAGGAGGAGTACAACGGGGTGATAGAAGAATTTTTGGCAACAGG
AGAGAAGCTTTTTGGACCTTATGTTTGGGGAAGGTATGACTTGCTCTTCATGCCACCGTCCTTTCCATTTGGAGG
AATGGAGAACCCTTGTCTGACCTTTGTCACCCCCTGCCTGCTAGCTGGGGACCGCTCCTTGGCAGATGTCATCAT
CCATGAGATCTCCCACAGTTGGTTTGGGAACCTGGTCACCAACGCCAACTGGGGTGAATTCTGGCTCAATGAAGG
TTTCACCATGTACGCCCAGAGGAGGATCTCCACCATCCTCTTTGGCGCTGCGTACACCTGCTTGGAGGCTGCAAC
GGGGCGGGCTCTGCTGCGTCAGCACATGGACATCACTGGAGAGGAAAACCCACTCAACAAGCTCCGCGTGAAGAT
TGAACCAGGCGTTGACCCGGACGACACCTATAATGAGACCCCCTACGAGAAAGGTTTCTGCTTTGTTTCATACCT
GGCCCACTTGGTGGGTGATCAGGATCAGTTTGACAGTTTTCTCAAGGCCTATGTGCATGAATTCAAATTCCGAAG
CATCTTAGCCGATGACTTTCTGGACTTCTACTTGGAATATTTCCCTGAGCTTAAGAAAAAGAGAGTGGATATCAT
TCCAGGTTTTGAGTTTGATCGATGGCTGAATACCCCCGGCTGGCCCCCGTACCTCCCTGATCTCTCCCCTGGGGA
CTCACTCATGAAGCCTGCTGAAGAGCTAGCCCAACTGTGGGCAGCCGAGGAGCTGGACATGAAGGCCATTGAAGC
CGTGGCCATCTCTCCCTGGAAGACCTACCAGCTGGTCTACTTCCTGGATAAGATCCTCCAGAAATCCCCTCTCCC
TCCTGGGAATGTGAAAAAACTTGGAGACACATACCCAAGTATCTCAAATGCCCGGAATGCAGAGCTCCGGCTGCG
ATGGGGCCAAATCGTCCTTAAGAACGACCACCAGGAAGATTTCTGGAAAGTGAAGGAGTTCCTGCATAACCAGGG
GAAGCAGAAGTATACACTTCCGCTGTACCACGCAATGATGGGTGGCAGTGAGGTGGCCCAGACCCTCGCCAAGGA
GACTTTTGCATCCACCGCCTCCCAGCTCCACAGCAATGTTGTCAACTATGTCCAGCAGATCGTGGCACCCAAGGG
CAGTTAGAGGCTCGTGTGCATGGCCCCTGCCTCTTCAGGCTCTCCAGGCTTTCAGAATAATTGTTTGTTCCCAAA
TTCCTGTTCCCTGATCAACTTCCTGGAGTTTATATCCCCTCAGGATAATCTATTCTCTAGCTTAGGTATCTGTGA
CTCTTGGGCCTCTGCTCTGGTGGGAACTTACTTCTCTATAGCCCACTGAGCCCCGAGACAGAGAACCTGCCCACA
GCTCTCCCCGCTACAGGCTGCAGGCACTGCAGGGCAGCGGGTATTCTCCTCCCCACCTAAGTCTCTGGGAAGAAG
TGGAGAGGACTGATGCTCTTCTTTTTCTCTTTCTGTCCTTTTCTTGCTGATTTTATGCAAAGGGCTGGCATTC
TGATTGTTCTTTTTCAGGTTTAATCCTTATTTAATAAAGTTTTCAAGCAAAAATT

FIGURE 574

MASGEHSPGSGAARRPLHSAQAVDVASASNFRAFELLHLHLDLRAEFGPPGPGAGSRGLSGTAVLDLRCLEPEGA
AELRLDSHPCLEVTAAALRRERPGSEEPPAEPVSFYTQPFSHYGQALCVSFPQPCRAAERLQVLLTYRVGEGPGV
CWLAPEQTAGKKKPFVYTQGQAVLNRAFFPCFDTPAVKYKYSALIEVPDGFTAVMSASTWEKRGPNKFFFQMCQP
IPSYLIALAIGDLVSAEVGPRSRVWAEPCLIDAAKEEYNGVIEEFLATGEKLFGPYVWGRYDLLFMPPSFPFGGM
ENPCLTFVTPCLLAGDRSLADVIIHEISHSWFGNLVTNANWGEFWLNEGFTMYAQRRISTILFGAAYTCLEAATG
RALLRQHMDITGEENPLNKLRVKIEPGVDPDDTYNETPYEKGFCFVSYLAHLVGDQDQFDSFLKAYVHEFKFRSI
LADDFLDFYLEYFPELKKKRVDIIPGFEFDRWLNTPGWPPYLPDLSPGDSLMKPAEELAQLWAAEELDMKAIEAV
AISPWKTYQLVYFLDKILQKSPLPPGNVKKLGDTYPSISNARNAELRLRWGQIVLKNDHQEDFWKVKEFLHNQGK
QKYTLPLYHAMMGGSEVAQTLAKETFASTASQLHSNVVNYVQQIVAPKGS

FIGURE 575

AGGCTCTATTTAGAGCCGGGTAGGGGAGCGCAGCGGCCAGATACCTCAGCGCTACCTGGCGGAACTGGATTTCTC
TCCCGCCTGCCGGCCTGCCTGCCACAGCCGGACTCCGCCACTCCGGTAGGATTCCCCGCCTGTCATTCCCTAGCC
CAGCTCTTGGGAAACTGCAGAGGGGTCCAGAGGATTTGCAGTTCTGAACCTGCACACTCCAGTCTAGGATCTCCG
AGCAAGAGCGTAGCCTCATGGCTGCAACCTGTGAGATTAGCAACATTTTTAGCAACTACTTCAGTGCGATGTACA
GCTCGGAGGACTCCACCCTGGCCTCTGTTCCCCCTGCTGCCACCTTTGGGGCCGATGACTTGGTACTGACCCTGA
GCAACCCCCAGATGTCATTGGAGGGTACAGAGAAGGCCAGCTGGTTGGGGGAACAGCCCCAGTTCTGGTCGAAGA
CGCAGGTTCTGGACTGGATCAGCTACCAAGTGGAGAAGAACAAGTACGACGCAAGCGCCATTGACTTCTCACGAT
GTGACATGGATGGCGCCACCCTCTGCAATTGTGCCCTTGAGGAGCTGCGTCTGGTCTTTGGGCCTCTGGGGGACC
AACTCCATGCCCAGCTGCGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGGATCATTGAGCTGCTGGAGA
AGGATGGCATGGCCTTCCAGGAGGCCCTAGACCCAGGGCCCTTTGACCAGGGCAGCCCCTTTGCCCAGGAGCTGC
TGGACGACGGTCAGCAAGCCAGCCCCTACCACCCCGGCAGCTGTGGCGCAGGAGCCCCCTCCCCCGGCAGCTCTG
ACGTCTCCACCGCAGGGACTGGTGCTTCTCGGAGCTCCCACTCCTCAGACTCCGGTGGAAGTGACGTGGACCTGG
ATCCCACTGATGGCAAGCTCTTCCCCAGCGATGGTTTCGTGACTGCAAGAAGGGGGATCCCAAGCACGGGAAGC
GGAAACGAGGCCGGCCCCGAAAGCTGAGCAAAGAGTACTGGGACTGTCTCGAGGGCAAGAAGAGCAAGCACGCGC
CCAGAGGCACCCACCTGTGGGAGTTCATCCGGGACATCCTCATCCACCCGGAGCTCAACGAGGGCCTCATGAAGT
GGGAGAATCGGCATGAAGGCGTCTTCAAGTTCCTGCGCTCCGAGGCTGTGGCCCAACTATGGGGCCAAAAGAAAA
AGAACAGCAACATGACCTACGAGAAGCTGAGCCGGGCCATGAGGTACTACTACAAACGGGAGATCCTGGAACGGG
TGGATGGCCGGCGACTCGTCTACAAGTTTGGCAAAAACTCAAGCGGCTGGAAGGAGGAAGAGGTTCTCCAGAGTC
GGAACTGAGGGTTGGAACTATACCCGGGACCAAACTCACGGACCACTCGAGGCCTGCAAACCTTCCTGGGAGGAC
AGGCAGGCCAGATGGCCCCTCCACTGGGGAATGCTCCCAGCTGTGCTGTGGAGAGAAGCTGATGTTTTGGTGTAT
TGTCAGCCATCGTCCTGGGACTCGGAGACTATGGCCTCGCCTCCCCACCCTCCTCTTGGAATTACAAGCCCTGGG
GTTTGAAGCTGACTTTATAGCTGCAAGTGTATCTCCTTTTATCTGGTGCCTCCTCAAACCCAGTCTCAGACACTA
AATGCAGACAACACCTTCCTCCTGCAGACACCTGGACTGAGCCAAGGAGGCCTGGGGAGGCCCTAGGGGAGCACC
GTGATGGAGAGGACAGAGCAGGGGCTCCAGCACCTTCTTTCTGGACTGGCGTTCACCTCCCTGCTCAGTGCTTGG
GCTCCACGGGCAGGGGTCAGAGCACTCCCTAATTTATGTGCTATATAAATATGTCAGATGTACATAGAGATCTAT
TTTTTCTAAAACATTCCCCTCCCCACTCCTCTCCCACAGAGTGCTGGACTGTTCCAGGCCCTCCAGTGGGCTGAT
GCTGGGACCCTTAGGATGGGGCTCCCAGCTCCTTTCTCCTGTGAATGGAGGCAGAGACCTCCAATAAAGTGCCTT
CTGGGCTTTTTCTAACCTTTGTCTTAGCTACCTGTGTACTGAAATTTGGGCCTTTGGATCGAATATGGTCAAGAG
GTTGGAGGGGAGGAAAATGAAGGTCTACCAGGCTGAGGGTGAGGGCAAAGGCTGACGAAGAGGGGAGTTACAGAT
TTCCTGTAGCAGGTGTGGGCTTACAGACACATGGACTGGGCTGGGAGGCGAGCAAAGGAAGCAGCTGAGACTGTT
GGAGAACGCTTACAAGACTTCATGCAAGCAAGGACATGAACTCAGAACACTGAGGTCAGAAGCATCCTGCTGTCA
TGACACCGCTCGAGTGACCTTGACCTTGACCAAGTCTGTCCTGTTTAGGACTGATTTTTCCTATTAGGCTAGGGT
TTGGACCTGATGTTCTCAAGATGTCTAGAATTGCATGGCTGGCCTTGTGGAATAGATGGTTTTGCATTCCAGCCA
AGTGTGCTGTAAACTGTATATCTGTAATATGAATCCCAGCTTTTGAGTCTGACAAAATCAGAGTTAGGATCTTGT
AAAGGA

FIGURE 576

CGGGTACAGGGGGCCCAAGAGCTGGGCTGGCTGTCTCCTGCTCATCCAGCC**ATG**CGGTGGCTGTGGCCCCTGGCT
GTCTCTCTTGCTGTGATTTTGGCTGTGGGGCTAAGCAGGGTCTCTGGGGGTGCCCCCCTGCACCTGGGCAGGCAC
AGAGCCGAGACCCAGGAGCAGCAGAGCCGATCCAAGAGGGGCACCGAGGATGAGGAGGCCAAGGGCGTGCAGCAG
TATGTGCCTGAGGAGTGGGCGGAGTACCCCCGGCCCATTCACCCTGCTGGCCTGCAGCCAACCAAGCCCTTGGTG
GCCACCAGCCCTAACCCCGACAAGGATGGGGGCACCCCAGACAGTGGGCAGGAACTGAGGGGCAATCTGACAGGG
GCACCAGGGCAGAGGCTACAGATCCAGAACCCCCTGTATCCGGTGACCGAGAGCTCCTACAGTGCCTATGCCATC
ATGCTTCTGGCGCTGGTGGTGTTTGCGGTGGGCATTGTGGGCAACCTGTCGGTCATGTGCATCGTGTGGCACAGC
TACTACCTGAAGAGCGCCTGGAACTCCATCCTTGCCAGCCTGGCCCTCTGGGATTTTCTGGTCCTCTTTTTCTGC
CTCCCTATTGTCATCTTCAACGAGATCACCAAGCAGAGGCTACTGGGTGACGTTTCTTGTCGTGCCGTGCCCTTC
ATGGAGGTCTCCTCTCTGGGAGTCACGACTTTCAGCCTCTGTGCCCTGGGCATTGACCGCTTCCACGTGGCCACC
AGCACCCTGCCCAAGGTGAGGCCCATCGAGCGGTGCCAATCCATCCTGGCCAAGTTGGCTGTCATCTGGGTGGGC
TCCATGACGCTGGCTGTGCCTGAGCTCCTGCTGTGGCAGCTGGCACAGGAGCCTGCCCCCACCATGGGCACCCTG
GACTCATGCATCATGAAACCCTCAGCCAGCCTGCCCGAGTCCCTGTATTCACTGGTGATGACCTACCAGAACGCC
CGCATGTGGTGGTACTTTGGCTGCTACTTCTGCCTGCCCATCCTCTTCACAGTCACCTGCCAGCTGGTGACATGG
CGGGTGCGAGGCCCTCCAGGGAGGAAGTCAGAGTGCAGGGCCAGCAAGCACGAGCAGTGTGAGAGCCAGCTCAAC
AGCACCGTGGTGGGCCTGACCGTGGTCTACGCCTTCTGCACCCTCCCAGAGAACGTCTGCAACATCGTGGTGGCC
TACCTCTCCACCGAGCTGACCCGCCAGACCCTGGACCTCCTGGGCCTCATCAACCAGTTCTCCACCTTCTTCAAG
GGCGCCATCACCCCAGTGCTGCTCCTTTGCATCTGCAGGCCGCTGGGCCAGGCCTTCCTGGACTGCTGCTGCTGC
TGCTGCTGTGAGGAGTGCGGCGGGGCTTCGGAGGCCTCTGCTGCCAATGGGTCGGACAACAAGCTCAAGACCGAG
GTGTCCTCTTCCATCTACTTCCACAAGCCCAGGGAGTCACCCCCACTCCTGCCCCTGGGCACACCTTGC**TGA**GGC
CCCAGTAGGGGTGGGGAGGGAGGGAGAGGCCGCCACCCCCGCCGGTGTCTGCTGTTCTTTCCCCATAGGTCTTGC
TTTGTTGCCTGTCTTGCTGTCTAGGGATGGACTTGGTTCCTCTTGTCAAGGTTTGGGAATCCG

FIGURE 577

MRWLWPLAVSLAVILAVGLSRVSGGAPLHLGRHRAETQEQQSRSKRGTEDEEAKGVQQYVPEEWAEYPRPIHPAG
LQPTKPLVATSPNPDKDGGTPDSGQELRGNLTGAPGQRLQIQNPLYPVTESSYSAYAIMLLALVVFAVGIVGNLS
VMCIVWHSYYLKSAWNSILASLALWDFLVLFFCLPIVIFNEITKQRLLGDVSCRAVPFMEVSSLGVTTFSLCALG
IDRFHVATSTLPKVRPIERCQSILAKLAVIWVGSMTLAVPELLLWQLAQEPAPTMGTLDSCIMKPSASLPESLYS
LVMTYQNARMWWYFGCYFCLPILFTVTCQLVTWRVRGPPGRKSECRASKHEQCESQLNSTVVGLTVVYAFCTLPE
NVCNIVVAYLSTELTRQTLDLLGLINQFSTFFKGAITPVLLLCICRPLGQAFLDCCCCCCCEECGGASEASAANG
SDNKLKTEVSSSIYFHKPRESPPLLPLGTPC

FIGURE 578

GCGCGCAGCGCTGGTACCCCGTTGGTCCGCGCGTTGCTGCGTTGTGAGGGGTGTCAGCTCAGTGCATCCCAGGCA
GCTCTTAGTGTGGAGCAGTGAACTGTGTGTGGTTCCTTCTACTTGGGGATC<u>ATG</u>CAGAGAGCTTCACGTCTGAAG
AGAGAGCTGCACATGTTAGCCACAGAGCCACCCCCAGGCATCACATGTTGGCAAGATAAAGACCAAATGGATGAC
CTGCGAGCTCAAATATTAGGTGGAGCCAACACACCTTATGAGAAAGGTGTTTTTAAGCTAGAAGTTATCATTCCT
GAGAGGTACCCATTTGAACCTCCTCAGATCCGATTTCTCACTCCAATTTATCATCCAAACATTGATTCTGCTGGA
AGGATTTGTCTGGATGTTCTCAAATTGCCACCAAAAGGTGCTTGGAGACCATCCCTCAACATCGCAACTGTGTTG
ACCTCTATTCAGCTGCTCATGTCAGAACCCAACCCTGATGACCCGCTCATGGCTGACATATCCTCAGAATTTAAA
TATAATAAGCCAGCCTTCCTCAAGAATGCCAGACAGTGGACAGAGAAGCATGCAAGACAGAAACAAAAGGCTGAT
GAGGAAGAGATGCTTGATAATCTACCAGAGGCTGGTGACTCCAGAGTACACAACTCAACACAGAAAAGGAAGGCC
AGTCAGCTAGTAGGCATAGAAAAGAAATTTCATCCTGATGTT<u>TAG</u>GGGACTTGTCCTGGTTCATCTTAGTTAATG
TGTTCTTTGCCAAGGTGATCTAAGTTGCCTACCTTGAATTTTTTTTAAATATATTTGATGACATAATTTTTGTG
TAGTTTATTTATCTTGTACATATGTATTTTGAAATCTTTTAAACCTGAAAAATAAATAGTCATTTAATGTTGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 579

MQRASRLKRELHMLATEPPPGITCWQDKDQMDDLRAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIY
HPNIDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSEPNPDDPLMADISSEFKYNKPAFLKNARQWTEKH
ARQKQKADEEEMLDNLPEAGDSRVHNSTQKRKASQLVGIEKKFHPDV

FIGURE 580A

ATGCTGCAAATGCCGAAGTTAAATGAAATACCTCCGGGGAGGGCAGGCCGCAGGGAGGCTCGGGGGGAGGGAAGA
TGGCCTGGACAAACAGGTCCTGAAGCTGCGAGGCTGGAGTGGAGGGCGCAGGGGCAGGCGGGCGGCGCCAGAGCT
CCATGGGACAGCTGGGGAAGCTCCAGGCTACCTACACAACCTGGCCCAGGCTGGTCACGGTGTCCCCCCTCCCTG
CTCTGTGCCCTCTCCTTCCAGAAATCCACCATGGAGAGTAAGGATGAGGTCAGCGACACCGACAGTGGCATCATC
CTGCAGTCTGGCCCCGACAGCCCGGTCTCCCCAATGAAGGAGCTGACCCATGCAGTGCACAAGCAGCAGAGGGCC
CTGGAAGCGAGGCTGGAGGCCTGCCTGGAGGAGCTGAGGAGACTCTGCCTTCGGGAAGCGGAGCTGACGGGCACC
TTGCCAGCGGAGTATCCCCTCAAACCAGGGGAAAAGGCCCCCAAGGTTCGCCGCAGGATCGGAGCGGCTTACAAA
CTGGATGACTGGGCCTTGCACAGAGAGGACCCCCTAAGCAGCCTGGAGCGCCAGCTGGCCCTGCAGCTGCAGATC
ACAGAGGCAGCCCGTCGGCTGTGCCTGGAGGAGAACCTCAGCAGGCAGGCTCGGCGGCAGCGGAAGCACTCCATG
CTGCAGGAGGAGAAGAAGCTGCAGGAGCTCCAGCGCTGCCTGGTCGAGCGGCGGCGCAATAGCGAGCCACCTCCG
GCTGCTGCTCTCCCCCTGGGCCGAGAGCTCAGTGCCTCTGATGACAGCTCCCTGTCAGATGGGCTCCTCCTGGAG
GAAGAGGAATCCCAAGTGCCAAAACCTCCTCCAGAGTCTCCAGCCCCACCTTCTCGGCCTCTCCCACCCCAAACC
CTTGAGGGTCTGCAGCCAACAGGACCTGAGGCTGGGAGCCCAGAACGGGCTCCAGTCCAGAACAGCCCCTGGAAG
GAAACCAGCCTGGACCACCCCTATGAGAAGCCCAGGAAGTCTTCTGAGCCCTGGAGCGAGTCCAGCAGCCCAGCC
ACCACACCACAGGATGGGCCCAGTGCCTCCAGCCTGTGGCTTCTGGAGCCTGCCTCCTACCACGTGGTTCCCATC
CGTGGTGTTCCTGGCCAGTGGCAGGGCCGCACCAGTGCCCCAGCCACCCCTGAGATACAGGGGAGGAGGGGCCAG
TCGCAGTCTCTGAGGGTGGATTCCTTCCGGGCGGGTCCTGAGGGCCGAGGTCGCAGCGCCTTTCCCCGCCGCCGC
CCCACTCACTACACGGTGACAGTGCCAGATTCCTGCTTTCCCGCGACCAAGCCCCCGCTGCCCCACGCCGCCTGC
CACTCCTGCTCAGAAGACAGTGGCTCTGACGTCTCCAGCATCTCCCACCCCACTTCGCCGGGCAGCAGCAGCCCC
GACATCTCCTTTCTGCAGCCTCTCTCCCCTCCCAAGACCCATCGTCACCGCGGGGCCTGGGTCCCAGCCGGCAGC
AGAGAGCTGGTCGCCCACCACCCCAAGCTACTGCTGCCGCCTGGCTATTTCCCGGCGGGGCGGTACGTGGTGGTG
GCTGAGAGCCCCCTGCCGCCTGGCGAGTGGGAGCTGCGCCGCGCAGCCCCGGGCCCTGCTTACGAGGAGGAGGGC
ACTCCCCTGCGCTACCAGCGTCTGGTGCCCTCCCGCAGCCGCATCGTGCGGACGCCCTCCCTGAAGGACAGCCCG
GCAGGCCGGGGGCTCAGCAAGGCCGCCGTGTCCGAGGAGCTCAAGTGGTGGCACGAGCGTGCACGCCTCCGGAGC
ACCCGCCCCCACTCACTGGACCGCCAAGGAGCTTTCCGGGTCAGGAGCCTGCCCCTTGGGAGAGAGGGCTTCGGA
CGAGCCCTGGGACCCCGGGCACAGGTGCCCACAGTTTGTGTGCTGCGGAGATCGCCTGATGGGGCCCCTGTGCAA
GTCTTTGTACCTGAAAAAGGAGAGATCATCAGCCAGGTGTAACTCTGCGCCCCACGCTGGAAAAAACTGTTTCAT
AGAGGGGCTGGGCTGAGACCCCCCCACCCCTGAGTGCCTCTTTCAGCTCCCCCATCCCCATCGCAGGCCGATGAC
CTGGAGCTGAGACCTTTTATTATTTTTTTTTACACGACTTTTTTCAGAAGCCCTGACCTAAGGATTTATATATG
TGGATTGTCCTCAATACCCCTGTGATATGATTATGTTTTATCCCCCAGAGTTTGGCCTACTGGACTTAAGGCCTT
GCCTGTCTGACTGACAGCCTCTATCTCCTTATATAAGACAAGTGGCAGGGGACGAGTGAAGCAGAGTGAGCCACC
TTGGGAGTTCTCCAACGCTCTGTGCTCTGGTTCTAAGAAATTCCCTGGGGAACTGCCCCTGGCCCTCCTGTCCCA
CTATTGCTGGAGGCTGGACATGGTACATACTCATGCACATGACTCTCCCCCATTTCCCAGGTCTCTGGGTACCCC
AGCCTGGGCTGGGGGAGAATCTCTTCCCCCTTTTCTAATGTGCTCTGTGATGCACACACCAAGTGGTAGGTCAAA
GGTCAGTATATCCCGGTGGTGTATTGTCTTGCTAGACCCTGCTATTTCCTGACCCCCTAAATCCTCTTTAGGGA
CCCAGTCACTATACCCTGTCTATGCCCTGTGGGCTCCCAGACCCCTGAGCTTTGAGTCAGTGGCATCACAGTTTG
TAGCCTCAGGGGGTCTGGCTGGGGGCTGGTCCATGCTTGTGGTTAGTGGACAGCAGCCACCCTTTGACAGCTACC
TCTGGGCATCTCAAGGGCTTGCAGCCCCACTGCTCCTTCTAACATTTTGTTTGTTTTTGAGATGGAGTCTCGCTC
TGTCGCCCAGGCTGGAATGCTGTAGCAAGATTTCGGCTCACTGCAACCCCCGTCTCCCGGGTTCAAGCGAATCTC
CTGCCTCAGCCTTCCGAGTAGCTGGGATTACAGGCAAGCACCACCATGCCTGCTAATTTTTTATTTTTAGTAGAG
ATGGGGTTTCATCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAAGTGATCCACCTGCCTTGGCCTTTCAA
AGTGCTGGGATTACAGGCATGAGCCACCGCACCTGGCCCTTCTAACGTTTTTCATCATAGTCCCAAAAACCAAT
ACTTTACAAGTGGTTTTGGAAAGGCACCACTTTTGTGGCATGTTCTGGTTGGGAGAGGGAGTCACAGTTCCTACT
CCCCCCACCAGCTATGCTTCTGCTCTGAGAAGGTGGTTATTTATACAAACATGGACATACTCACTCCCAAGGGCT
GATGAGATGCTGAATTTTCTTTGGGGGCATTCATTAATTGTCCCAGCTGCAGCGACTGGAGCAAGTCTGGAAGCT
GCCTGTGCTAAGACCACCCAGCTGTCCCTGGGTTCTCATCCTAGGGCCTTCTTTGCTTCCAGGTCAGGGGACCTG
CTTCAATGAGAAAGCAACTGAATTGAGGCTAGGAGAGGTAGGGAGAGCTGAGTTCTGACTTCACCTGTGCAGAAC
TCTCTGCCCCCATGTTACCTGGACTGGAACAGACTGTGAATATAGCAGAAGGTTCCAAGAACTCTGGTGTCTGAC

FIGURE 580B

CTAGAAGAGGCACAGTTCTCTCTACTGGAAAGAAAACGATGTAGCCGATTGCACAAGGGTGCCAAGGGAAGACCC
AGGATGGCCCATCAAAGGAACCTGGGGGAGGATGCAGGAGGCTGAAGGGATGCACCTGGCATTTCTCTCACTGTG
CTCTTACCGCATCAGCAACCCCCAACTTTTGGGCCTACTCTGCCCCCCATGCGTGAATACCCTGCTTGGATGCTG
TGCTTTTCCGGTTTGTCTCTAAGCCCCTTTCTCCAGGGCATGTTGGTTTCCCTGGCCTCTCAGTGTCCTAACTGG
AGCCCAGAGTGCCTTGTTCTGAGCCAGGAGACGGCTGAGCACTGGCCCTCCACACCTAAGCGTCCTTTACATTAA
CTTATTGGTCTTGTATAACACCTGGTGCCATTGCCAAGTGGCTGTGTCCTCAGCTACAGAGCTGGAATTGTGTGG
GGTTTAGTGCTAAATACTTCAATAAAGTCTGTTTTTTGTGATTGGCTG

FIGURE 581

TCCCGGGCCGGGAGCCCAGCAGGCCGGGAGCGGCTGAGGCCACACCCCGCGGGCCGGGCCGCTTCCCTCCGGTGA
ATCATCGCTCGCAGCGGCGGCGCCCGCAGTGGCCGCAGCAGCGCGCCGGGCCCTGGCCGCGCCCCAGCCGAGCGC
AGCGCGGAGTCGCCCCGACCTTTCTCTGCGCAGTACGGCCGCCGGGACCGCAGCATGGCGGCATCGCGGCCAAG
CTGGCGAAGGACCGGGAGGCGGCCGAGGGGCTGGGCTCCCACGACAGGGCCATCAAGTACCTCAACCAGGACTAC
GAGGCGCTGCGGAACGAGTGCCTGGAGGCCGGGACGCTCTTCCAGGACCCGTCCTTCCCGGCCATCCCCTCGGCC
CTGGGCTTCAAGGAGTTGGGGCCCTACTCCAGCAAAACCCGGGGCATCGAGTGGAAGCGCCCCACGGAGATCTGC
GCTGACCCCCAGTTTATCATTGGAGGAGCCACCCGCACAGACATCTGCCAAGGAGCCCTGGGTGACTGCTGGCTG
CTGGCAGCCATTGCCTCCCTCACCTTGAATGAAGAAATCCTGGCTCGAGTCGTCCCCCTAAACCAGAGCTTCCAG
GAAAACTATGCAGGGATCTTTCACTTCCAGTTCTGGCAATACGGCGAGTGGGTGGAGGTGGTGGTGGATGACAGG
CTGCCCACCAAGGACGGGGAGCTGCTCTTTGTGCATTCAGCCGAAGGGAGCGAGTTCTGGAGCGCCCTGCTGGAG
AAGGCATACGCCAAGATCAACGGATGCTATGAAGCGCTATCAGGGGGTGCCACCACTGAGGGCTTCGAAGACTTC
ACCGGAGGCATTGCTGAGTGGTATGAGTTGAAGAAGCCCCCTCCCAACCTGTTCAAGATCATCCAGAAAGCTCTG
CAAAAAGGCTCTCTCCTTGGCTGCTCCATCGACATCACCAGCGCCGCGGACTCGGAGGCCATCACGTTTCAGAAG
CTGGTGAAGGGGCACGCGTACTCGGTCACCGGAGCCGAGGAGGTTGAAAGTAACGGAAGCCTACAGAAACTGATC
CGCATCCGAAATCCCTGGGGAGAAGTGGAGTGGACAGGGCGGTGGAATGACAACTGCCCAAGCTGGAACACTATA
GACCCAGAGGAGAGGGAAAGGCTGACCAGACGGCATGAAGATGGAGAATTCTGGATGTCTTTCAGTGACTTCCTG
AGGCACTATTCCCGCCTGGAGATCTGTAACCTGACCCCAGACACTCTCACCAGCGATACCTACAAGAAGTGGAAA
CTCACCAAAATGGATGGGAACTGGAGGCGGGGCTCCACCGCGGGAGGTTGCAGGAACTACCCGAACACATTCTGG
ATGAACCCTCAGTACCTGATCAAGCTGGAGGAGGAGGATGAGGACGAGGAGGATGGGGAGAGCGGCTGCACCTTC
CTGGTGGGGCTCATTCAGAAGCACCGACGGCGGCAGAGGAAGATGGGCGAGGACATGCACACCATCGGCTTTGGC
ATCTATGAGGTTCCAGAGGAGTTAAGTGGGCAGACCAACATCCACCTCAGCAAAAACTTCTTCCTGACGAATCGC
GCCAGGGAGCGCTCAGACACCTTCATCAACCTCCGGGAGGTGCTCAACCGCTTCAAGCTGCCGCCAGGAGAGTAC
ATTCTCGTGCCTTCCACCTTCGAACCCAACAAGGATGGGGATTTCTGCATCCGGGTCTTTTCTGAAAAGAAAGCT
GACTACCAAGCTGTCGATGATGAAATCGAGGCCAATCTTGAAGAGTTCGACATCAGCGAGGATGACATTGATGAT
GGATTCAGGAGACTGTTTGCCCAGTTGGCAGGAGAGGATGCGGAGATCTCTGCCTTTGAGCTGCAGACCATCCTG
AGAAGGGTTCTAGCAAAGCGCCAAGATATCAAGTCAGATGGCTTCAGCATCGAGACATGCAAAATTATGGTTGAC
ATGCTAGATTCGGACGGGAGTGGCAAGCTGGGGCTGAAGGAGTTCTACATTCTCTGGACGAAGATTCAAAAATAC
CAAAAAATTTACCGAGAAATCGACGTTGACAGGTCTGGTACCATGAATTCCTATGAAATGCGGAAGGCATTAGAA
GAAGCAGGTTTCAAGATGCCCTGTCAACTCCACCAAGTCATCGTTGCTCGGTTTGCAGATGACCAGCTCATCATC
GATTTTGATAATTTTGTTCGGTGTTTGGTTCGGCTGGAAACGCTATTCAAGATATTTAAGCAGCTGGATCCCGAG
AATACTGGAACAATAGAGCTCGACCTTATCTCTTGGCTCTGTTTCTCAGTACTTTGAAGTTATAACTAATCTGCC
TGAAGACTTCTCATGATGGAAAATCAGCCAAGGACTAAGCTTCCATAGAAATACACTTTGTATCTGGACCTCAAA
ATTATGGGAACATTTACTTAAACGGATGATCATAGCTGAAAATAATGATACTGTCAATTTGAGATAGCAGAAGTT
TCACACATCAAAGTAAAAGATTTGCATATCATTATACTAAATGCAAATGAGTCGCTTAACCCTTGACAAGGTCAA
AGAAAGCTTTAAATCTGTAAATAGTATACACTTTTTACTTTTACACACTTTCCTGTTCATAGCAATATTAAATCA
GGAAAAAAAAATGCAGGGAGGTATTTAACAGCTGAGCAAAAACATTGAGTCACTCTCAAAGGACACGAGGCCCTT
GGCAGGGAATATTTAAAGCAACTTCAAGTTTAAAATGCAGCTGTTGATTCTACCAAACAACAGTCCAAGATTACC
ATTTCCCATGAGCCAACTGGGAAACATGGTATATCATGAAGTAATCTTGTCAAGGCATCTGGAGAGTCCAGGAGA
GAAGACTCACCTCTGTCGCTTGGGTTAAACAAGAGACAGGTTTTGTAGAATATTGATTGGTAATAGTAAATCGTT
CTCCTTACAATCAAGTTCTTGACCCTATTCGGCCTTATACATCTGGTCTTACAAAGACCAAAGGGATCCTGCGCT
TGATCAACTGAACCAGTATGCCAAAACCAGGCATCCAATTTGTAAACCAATTATGATAAAGGACAAAATAAGCTG
TTTGCCACCTCAAAACTTTATGAACTTCACCACCACTAGTGTCTGTCCATGGAGTTAGAGGGGACATCACTTAGA
AGTTCTTATAGAAAGGACACAAGTTTGTTTCCTGGCTTTACCTTGGGAAAATGCTAGCAACATTATAGAAATTTT
GCCTTGTTGCCTTATCTTCTTCCAAATGTACTGTTAAATAAAAATAAAGGGTTACCCCATGCAATCACACCATGC
CATGTTTTCCTTCCTGGAGGGCAGCCCCACAGGACGGTTTATGAGCACACAATTATAGCTTGTTTCTACTTTAAC
AAGGTATGCTGCCTCTGTAAATTCATGTATTCAAAGGAAAAGACACCTTGCCTATAATTAAAATGTGGAACTATA
AAATTTTTTAAAATCC

FIGURE 582

TCTAATACCTATTGATCTGTTACTTTCTCCCATCACGCTCAGGTGGGAACATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCACTGATTCTACATTATGGTGAGTTCCATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCTCAATGGCCTATTTAGGCCCATACCCTACGTCAC
GGCAGCCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTTGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CAGCCTCTACAGTCCCAACGTCTGCCTCACAGCAGATTCTTCACGCCCAGCTTCTACCTCACTTGGACCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCAGCCTCTGC
CTCACAGCGGACTCTC

FIGURE 583

GGTATTTCAGGACAGCCAGGAGGGGGCGCACATCCGCCGAGAAACTGTGAGCAAGAGCGTCTGTGCTGAACCATG
GCGCCACCAGAGGGCGCGCGATCCCGCCCCAACCAACTTCCCGCTGAGGTGCCAGAAGCAGCGAGGAGCTTCAGC
TTCCTCAGGGCAGCACGAGGGTCGTGTTAACTTGGTGTTCTTCATTGATGATGATTATTCCCCACCTTCTAAGAG
ACAAAGACCAACGAGCCACCACAGCCACCAGTCCCAGAACCTGCCAATGCTGGGGAACGGAAA<u>ATG</u>AGGGAGTTC
AACTCTGGCCCTCACAATCCAGTGGAGGAGACGAAACTCATCTGCCTCTGTCCCTCTGGGCACGCCTCATGCCAG
GTGCATCTGTGGACAGGGGCCATGCCCCTGGGCTTCCAAAGTTGGAGAGAGCTGCCAGGCTCAGGTCTGAAGGCC
AGAATTCTACAGTAAGTCCTACTGAGTCAAGGTGGGAGCAGGGTCGGTAGCTTCCGAGGCTCTGCGGGAGAATCC
GTTTCCTGGCCGTAGAGGTGGCCTGCACTCCGCAGCTTGTGCTGCCCGTCTCGAATGACTGGAGTTTCCTGCTTC
TGTCACTACACCTCCCACCCTCTCCATCACCTGCTCTGCTCTTACAAGGATCCGAAGAAATGGAATCATCGTATC
GCTGATCTACGTAAACAAACTGAAGAATTGTCTGAAAGAAAATATGACATGAACTTATGAATTCAACAGGTGAAG
ATTTACAACTTGATAAATCAACTTTGTCAGCTCGAGCTGTAAAAGCCAAAGGTCCGGTGATGATCCCATACCCTT
TTTTCCAGTCTCATGTTGAAGATTTTTATGTAGAAGGCCTTCCCAAAGGAATTTTTTTTTTTTTTTTTTTTTGA
GATGGAGTTTTCACTCTTATCGCCCAGGCTGGGGTGCAATGGCGCAACCTTGCTGGTCACTGCAACCTCTGCCTC
CTGGGTTCAAGAAATTCTCCTGCCTTAGCCTCCCAAGTCACTGGGATTACAGGTGCCCACCACCATACCAGGCTA
ATTTTTGTATTTTTAGTGGAGATGCGGTTTCACCATGTTGGCCGGGCCAGTCTCGAACTCCTGACGTCAAGTGAT
CTTCCCGCCTCGACTCCTGATATCAAGTGATCTTCCCGCCTCGGCCTCCCAGAGTGCTGAGATTACAGACGTGAA
CCCATGCCTGGCCAGGAATTTTGTTTTTTAGGAAGGCTTTCTACTAATGGAATTCCTGGCCTTGAGAGGATGTTA
CTTTAGAAGGAAAGGATTTTTTTGTTATTAAAAGCTGGACCTACCATGAAAGACTTCTGAATCCAGGAAGAGAAA
CTGACTGGGCAACATGTTATTCAGAAACAGGACCTTGCCCTGTCACTCAGGATGGAGTTCAGTGGTCCTATCATG
GCTCATTATAGCCTCAAACTCCCAGGCTCAAGCAATCCTACCATGTCAGCCTTCCCAGTAGCTGGGACTACAGAT
ACCGGGTCTCACACTGTCACCCAGGCTGGAGTACAGTGGCACAACCTCTGCTCACTGCAGCCTCCACCTGCCAGG
CTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGTGATTTCCAGGATGTGAGCTCACAATGACTCAAGCT
GCCACATACTGTTGATTGTGAAATGCCAGTTGAAGCATATGTCCTGCGAGCTTAGGGGTGCTACAAGTTGACCAC
TGCAGCAGTAAAGATGACTCTGAAGAATGGCGTGGGTTGGTTCCTTTCAAATGCACTTGAGCAGCGGTCTCCAAC
CACAGGGCCACAGAGCTGGAGCTGGATCTACCATGAAAGACTTGTGAATCCAGGAAGAGAGACTGACTGGGCAAC
ATGTTATTCAGAATCTTCCTGTGCCATCCAGGCTGGAGTGCAGTGATGTGATCATAGCTCACTATAGCTTTGGCC
TTCTGAGATCAAGCAATCCTCCCATCTCAACCTCCCAAGTAGCTAGGACTACACACGCATGTCACCCATGCCCAG
ATCATTTTTGTAGAGTCAGAGTTTCACCGTGGTGGCCAGGTTGGCCATGTTGGCCAGATGGGGTCTTCTTTTGTT
GCCCAGGCTGGCCACAAATTCCTGGGCTCAAGTGATCCTCCCACCTCGTCCTTGTAGAGATGAGATTTAGTTATG
TCGTCCAGGCTGATCTCAAACTCCTGGGCTAAATCGATTGTCTCACCTCAGCCTCTCAAGTATGTTATGAAGGTT
ATATGTTAGGAAGGGTCCCAGGAGGTAAACCCACACAGATGGGATTTGGGCATAGGTTTGGTTTCCCAGGGGGCA
GTGCTGAGCTCTTTGCCAGTGGGAAATGGGATGCTGGTGATTTCCAGTAGGTGACCTCACAGTGACTCAAGCTAC
CACTTACTGTTGATTGTGACGAAATGCCAGCTGAGGCACATGCCTTGGGAGCTAAGTGGTTGCTGCCCTTGACCA
CTGTGAAGACTGGTGTGGGAAGGGTCGTTTTGGATGCACTTGAGCAGGGGTCCCCAACCCCTGAGCCATGGAGCC
GCAAGGAGCCACACAGCAGGAGGTGGGAACATCCAGTTGCAGGAAAACAAGCTTAACACGCCCACTGATTCTACA
TTATGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGA
CTCTCAATGGCCTATTTAGGCCCATACCCTACGTCACGGCAGCCTCCGCAGATGAGGCTACTGCCTCACAACAGC
CTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCC
CTGAACTTTCTCAAGTTGACCTCACCAGGCCCAGCTCATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCAT
CTTGGTGGCCCCTCCAGGCCCAGCCTCTGCCTCCCGTCAGCCTCTACAGTCCCAACGTCTGCCTCACAGCAGATT
CTTCACGCCCAGCTTCTACCTCACTGTGGACCCCCCAAGCCAAGCTCCCAACCTTTCAGCAGCTTCTACACACCC
AGCTCCTGCCACCCAGTGGCCTCTTTAGGCCAAGCTCATGCTTCACAAGGGCCTTTCCAGGCCCAACTTTTGTCT
CATGGCAACCTTCCCTGGCCAGATTCCTGCCTGTCTCCCAGCAGCCTAGACAGGCCCAGGTCTTGCCTCACACTG
GCCTCTCTACATCCAGCTTATGCCTCACGGTGGCCTCTCCA

FIGURE 584

MMIIPHLLRDKDQRATTATSPRTRQCWGTENEGVQLWPSQSSGGDETHLPLSLWARLMPGASVDRGHAPGLPKLE
KAARLRSEGQNSTVSPTESRWEQGR

FIGURE 585

GGACGGAAGGAGCGGCGGCGACGGAGGAGGAGG**ATG**GAGGCGGTGGTGTTCGTCTTCTCTCTCCTCGATTGTTGC
GCGCTCATCTTCCTCTCGGTCTACTTCATAATTACATTGTCTGATTTAGAATGTGATTACATTAATGCTAGATCA
TGTTGCTCAAAATTAAACAAGTGGGTAATTCCAGAATTGATTGGCCATACCATTGTCACTGTATTACTGCTCATG
TCATTGCACTGGTTCATCTTCCTTCTCAACTTACCTGTTGCCACTTGGAATATATATCGATACATTATGGTGCCG
AGTGGTAACATGGGAGTGTTTGATCCAACAGAAATACACAATCGAGGGCAGCTGAAGTCACACATGAAAGAAGCC
ATGATCAAGCTTGGTTTCCACTTGCTCTGCTTCTTCATGTATCTTTATAGTATGATCTTAGCTTTGATAAATGAC
TGAAGCTGGAGAAGCCGTGGTTGAAGTCAGCCTACACTACAGTGCACAGTTGAGGAGCCAGAGACTTCTTAAATC
ATCCTTAGAACCGTGACCATAGCAGTATATATTTTCCTCTTGGAACAAAAAACTATTTTTGCTGTATTTTTACCA
TATAAAGTATTTAAAAAACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 586

MEAVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWVIPELIGHTIVTVLLLMSLHWFIFLLNL
PVATWNIYRYIMVPSGNMGVFDPTEIHNRGQLKSHMKEAMIKLGFHLLCFFMYLYSMILALIND

FIGURE 587

CCCTAATCAAGTACCCCCTCCTCCTCCACCACCTCCTGCCCCACCCCTCCCTGCATCTGGATTCTTTTTGGCATC
CATGTCAGAAGACAATCGCCCTTTAACTGGACTTGCAGCTGCAATTGCCGGAGCAAAACTTAGGAAAGTGTCACG
GATGGAGGATACCTCTTTCCCAAGTGGAGGGAATGCTATTGGTGTGAACTCCGCCTCATCTAAAACAGATACAGG
CCGTGGAAATGGACCCCTTCCTTTAGGGGGTAGTGGTTTAATGGAAGAAATGAGTGCCCTGCTGGCCAGGAGGAG
AAGAATTGCTGAAAAGGGATCAACAATAGAAACAGAACAAAAAGAGGACAAAGGTGAAGATTCAGAGCCTGTAAC
TTCTAAGGCCTCTTCAACAAGTACACCTGAACCAACAAGAAAACCTTGGGAAAGAACAAATACAATGAATGGCAG
CAAGTCACCTGTTATCTCCAGACCAAAATCCACACCCTTATCACAGCCCAGTGCCAATGGAGTCCAGACGGAAGG
ACTTGACTATGACAGGCTGAAGCAGGACATTTTAGATGAAATGAGAAAAGAATTAACAAAGCTAAAAGAAGAGCT
CATTGATGCAATCAGGCAGGAACTGAGCAAGTCAAATACTGCATAGAGGAACAGACTAAGGAGAGATAGGACTTT
AATCTGGAGGAAAAAATATCCTACAAACAACAACTGTTCACAACAGCAAACCCCTACATTTATGAGCTGTAAGAAG
AAAATGGAGACAAACAGAAGGAGGGAAAAACCAACCTACTCTGAAAGCCTTCAGACATTATGACTCTGGTGATAA
GCTCTTTCCCTCTCCGTTTGCTGCTTTTTTCTGGCCTTTACAACAGAATGGAAGAGAATCATTTAAGAGTTCCTG
TAACAGTTATGCAGAAAATACTAAAACCCATCAGGCAAGATCACCACGCATTGAAATATTTTCATATCAAGATAA
AGTCGCACATTTTCCACAATACATTGCTAAAATAAAGAGGAGAAAGGCTTAGGAAGTTTTTCTGCAGAGAGTGCT
GGTAAAGAATTGAGCAAGTTTGCTATTGTATTGTAATGTTTCTCTCAGGTTTGTTCTTCCTATCATGTTTGATAT
TCCATGAATAATTGAGATCAGCCCTATGTAAGTTAAGATCATAATATGTGGAACAAATGGAATTGTAAGTGCTTT
CAAAGGGTAATATTTATAAGAAAGTGTCCGAAAAATGTTTCTTCAGCTTGAGAAATTTTAGAATGATAGGAAGTT
TCTCGAGTTAGCCTTCATGCAATTTTGTAGATTAAAACATAAAATTTGTCCAGAACTTAAAGATTTAGATGCCTT
CCTAAATTGTTACAATGCTTTACCAAATCTATGACTTCTACATAACACAAACCAGTGGTCAAATGTAAACACTAT
ATTGTAGATTTACTGTAGGTTTTCAACCTTTTTTAGATTTATGCATGTGGACATTTTTATAATGTAATTACAATC
ACCACAAGGTTAGCTTTTTTAATTGCAGACAGTAATGCATGTCACACTAATATGTAGTGGCCTTTTCAAGGCCTA
GTCCCAGGGAAAACATTTTGTAGAGTATAGGGGAGTGGGAGGAAGGGGAGGAATAATTTTTTATTTAAAGTTGAT
TTCTGCACTATCTTTTTCTCAGTTACCTGCATGAATAAATAATGAGAAATATTTTGTGACTTTAATTGGTAAATA
TGTTACAAAACCAAGTACTTAATCTTTTACATCATGTCTTCAGCTATTTGTATTTTAACCAGTAATTTCAATGGT
CTGAAACATGATTCTGAGCTTCACATAATATCTTAACTGTGGAACTCAAAAGTTTGATCACTGAATTTGGCAGTT
ATTATTACCTAGGTACCCCCGCTGTTACACAGGTGTTTAGATACGTGTTCCTGAATGAAGCTGCTTTTGAATTTT
GTTATGTTGAAATGCAAGAAATAACAATGATGGCAGCAATTAAGGTCACAGAAATCATTAGGTAAAGGAAAACCA
ATGAGGAGTTCTGCAGTTTTCTTTTAATAAGTAAAGTGAGACTTGGGTGGTGGGAAGAAGGAAGGTGGGAAGAAG
GAATTAGACACTCTGCCTGCCACTCTGCGTGTGTGTGCTCTCGCGCACGTGCTGTCTATATGGAAGCCACTCCCT
TTTCTTTCCTTTGAAACTGGTAAGGTTAAAATAGGGGAGAAATCCTACATGTTGGAATGATAGCTTTTTGGAAAA
TTTAAGAAACTCTCCAGGCTCTCCATCTTGATTTATGCTTGAGTTGTTATGTGCCATATTTGCTTTGAACTCTGA
TTATCAGAAGTTTTACTAAAACTTTGAAATAATTCACTTTCATCTGCTTTCTAGATTTTGTACATCTCAGTCCAT
AAAGCAAAGCTTGTTGATAGTGTAGTTTTCTAAACGCTGCAAATTTGCAGCCTTTACCACTACAAAGAAGTTTGG
ATGAGGGATTTTTTTTTTCTTTGTCAAAATAGTTCCTGTTTCTGTAGAAATTTCATTTTTAGATTAAACTGTGAT
GGATGGGCTATCATAATTCAAGTATACATTTCTTTTTTCTATCAGATATTCATTGTCATGCAGTAGTAGTAAAAA
CATCAAAGATGCAGCAAGCTTATTAAGTATTATTTTCTAAAAGAAATAGGAGGCATTTTCATCTTTATTATTGTA
CTTTTGGTTATGCAAACACTTTGATAATATAAACAGTTATGTCCCCTATAAATCTGGTCAGCAACCTCTTTTGAT
TTTGTTGGGTAAGTTAAATAGTCTGTAGTAGGTAGAGTACTGGGTACAAGTGGTCCAAACTAAGATAAGAGACTA
AAATAAAATGCTAAATCTTAAAAGAAACTGGGTTTATGCACTAAACGTTTTGTGCCTTGGTCTAATATTAACATG
ATGTATGTGTAAACTGAC

FIGURE 588

MSEDNRPLTGLAAAIAGAKLRKVSRMEDTSFPSGGNAIGVNSASSKTDTGRGNGPLPLGGSGLMEEMSALLARRR
RIAEKGSTIETEQKEDKGEDSEPVTSKASSTSTPEPTRKPWERTNTMNGSKSPVISRPKSTPLSQPSANGVQTEG
LDYDRLKQDILDEMRKELTKLKEELIDAIRQELSKSNTA

FIGURE 589

GGGGCTGCTGGGACTCGCGTCGGTTGGCGACTCCCGGACGTAGGTAGTTTGTTGGGCCGGGTTCTGAGGCCTTGC
TTCTCTTTACTTTTCCACTCTAGGCCACG**ATG**CCGCAGTACCAGACCTGGGAGGAGTTCAGCCGCGCTGCCGAGA
AGCTTTACCTCGCTGACCCTATGAAGGCACGTGTGGTTCTCAAATATAGGCATTCTGATGGGAACTTGTGTGTTA
AAGTAACAGATGATTTAGTTTGTTTGGTGTATAAAACAGACCAAGCTCAAGATGTAAAGAAGATTGAGAAATTCC
ACAGTCAACTAATGCGACTTATGGTAGCCAAGGAAGCCCGCAATGTTACCATGGAAACTGAG**TGA**ATGGTTTGAA
ATGAAGACTTTGTCGTGTACTTAGGAAGTAAATATCTTTTGAATTAGAGAAAGTGTTGGGACAGAAAGTACTTTA
TGTAACTAAGTGGGCTGTTCAGAAGCTTAGAGGTCATTTTTTGTAATTTTCTTTTTAATTACTTTAGAGAGCTAG
GGATGCAAATGTTTTCAGTTAGAAAGCCTTTATTTACTTTTGGAAATTGAACAAGAAATGCATCTGTCTTAGAAA
CTGGAGATTATTTGATGTTAGGTAAAACATGTAATTGTTTCTCTGGCAAATTTGTATCAGTAATTTGAAAATGAG
ATATTAGGAAAAACCAATTCTTCTTAAATTTAGTTCATCTTTCTTTAAAAGAACATTAAATGTAACCATTTTGTC
AGATCCATGTATTTTGGAGCATAAAATGTATGCTGTTGTGACCAATAAATATAAAATATGGTAATTGGAATTAAC
TCCACACCATAGTATGCATTGTTATACATACTGTGTACCTAATTATGTATAGCAGTGTAGTCTCAATTATATCTG
AAAGTAATTGTGACTAACAAGTATGCTTTGCCTTATTTCCACATTTAAACTACCTGTTAATATAAGGGATTTGTA
GTATCAGCTTGTTGAGCAATGACTTTGAATCTAGTTTTCAGTGATCAGAAGCAGCAGTTATTTGAGTGTATGAAT
GGAATGATGATCACTGTGCTATAATGTACTGAAACCACCATATTACAGAAATATTTACTACATATTTTCCATCTG
TAGTTTCTCAGAAGGGCTATGGATTAGTTTGAACTGTCAAATCCTTGCATACTTCTGTGACACCCCTGCCCATTT
TCTGTCTTTAATTAACCAAGGTGTTAGGTGTGACTGTCACAACTGTTATGTTTTCCAGTAAACTAGAAGTACGAT
ATTTGATAATTATATTTGTATTTCACCACCTAAATGTAATGTTGATTCCTCAAGAATGAAATGAAGGCACTACAT
TGAAATATGTTTTGTATAAATTTGTCATGTTGAACAGCATTTTAGCATGGTAAGTTCCCTTAGCTATATGAATTT
TGGCATGTTTCAGAGAGATCAGTAAATAAAATATTAGAT

FIGURE 590

MPQYQTWEEFSRAAEKLYLADPMKARVVLKYRHSDGNLCVKVTDDLVCLVYKTDQAQDVKKIEKFHSQLMRLMVA
KEARNVTMETE

FIGURE 591

GCGGCTCCCAGGAGGCGTGAACCGCGGACCATGAGCGTGGGCTTCATCGGGGCCGGCCAGCTGGCCTATGCTCTG
GCGCGGGGCTTCACGGCCGCAGGCATCCTGTCGGCTCACAAGATAATAGCCAGCTCCCCAGAAATGAACCTGCCC
ACGGTGTCCGCGCTCAGGAAGATGGGTGTGAACCTGACACGCAGCAACAAGGAGACGGTGAAGCACAGCGACGTC
CTGTTTCTGGCTGTGAAGCCACATATCATCCCCTTCATCCTGGATGAGATTGGGGCCGACGTGCAAGCCAGACAC
ATCGTGGTCTCCTGTGCGGCTGGTGTCACCATCAGCTCTGTGGAGAAGAAGCTGATGGCATTCCAGCCAGCCCCC
AAAGTGATTCGCTGCATGACCAACACACCTGTGGTAGTGCAGGAAGGCGCTACAGTGTACGCCACGGGCACCCAT
GCCCTGGTGGAGGATGGGCAGCTCCTGGAGCAGCTCATGAGCAGCGTGGGCTTCTGCACTGAGGTGGAAGAGGAC
CTCATCGATGCCGTCACGGGGCTCAGTGGCAGCGGGCCTGCCTATGCATTCATGGCTCTGGACGCATTGGCTGAT
GGTGGGGTGAAGATGGGTTTGCCACGGCGCCTGGCAATCCAACTCGGGGCCCAGGCTTTGCTGGGAGCTGCCAAG
ATGCTGCTGGACTCGGAGCAGCATCCATGCCAGCTTAAGGACAATGTCTGCTCCCCTGGGGGAGCCACCATCCAC
GCCCTGCACTTTCTAGAGAGTGGGGGCTTCCGCTCTCTGCTCATCAATGCAGTTGAGGCCTCCTGTATCCGAACA
CGAGAGCTACAGTCCATGGCCGACCAAGAAAAGATCTCCCCAGCTGCCCTTAAGAAGACCCTCTTAGACAGAGTG
AAGCTGGAATCCCCCACAGTCTCCACACTGACCCCCTCCAGCCCAGGGAAGCTCCTCACAAGAAGCCTGGCCCTG
GGAGGCAAGAAGGACTAAGGCAGCATC

FIGURE 592

TTTTCTTTTGACTTGTTTGTGGATGGAATGTTTACAGACATTTCTAATTACTGCTTTAATTAAATAAATTGGATC
AAAGGCCGTTCGAGGTATTTTTGTTTTGCCGTTTGTCGCTCAGAATTGGCATTTTGAGAGGTGATTGATACTGCT
AACAATTTTCTAGTACTCTAGTTTGTTTCAAGAAGAGATTTTGGGTAGACGTAATCTTCACCCTTTCAAATTATA
TAACAATACGAACATTATTTTTTATACTGATCATAATTTCCAGATTTGGGGAGGGGGTGATCGTGGCAGGAAAAG
TTGTATGTTTGGTAGTTGCATATGGTGATTTTTGATTTTTCAATGCTGGTAGGTAAGTAAGGAGGTCTCTGTACC
ATGGCTCGTACAAAGCAGACTGCCCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCC
GCTCGCAAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTGGCGCTCCGT
GAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTCGCAAACTTCCCTTCCAGCGTCTGGTGCGAGAAATT
GCTCAGGACTTTAAAACAGATCTGCGCTTCCAGAGCGCAGCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTAT
CTGGTTGGCCTTTTTGAAGACACCAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATC
CAGCTAGCACGCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTCATTCTCAAAAAAA
AAAAAAAAAATTTCTCTTCTTCCTGTTATTGGTAGTTCTGAACGTTAGATATTTTTTTTCCATGGGGTCAAAAGG
TACCTAAGTATATGATTGCGAGTGGAAAAATAGGGGACAGAAATCAGGTATTGGCAGTTTTTCCATTTTCATTTG
TGTGTGAATTTTTAATATAAATGCGGAGACGTAAAGCATTAATGCAAGTTAAAATGTTTCAGTGAACAAGTTTCA
GCGGTTCAACTTTATAATAATTATAAATAAACCTGTTAAATTTTTCTGGACAATGCCAGCATTTGGATTTTTTTA
AAACAAGTAAATTTCTTATTGATGGCAACTAAATGGTGTTTGTAGCATTTTTATCATACAGTAGATTCCATCCAT
TCACTATACTTTTCTAACTGAGTTGTCCTACATGCAAGTACATGTTTTTAATGTTGTCTGTCTTCTGTGCTGTTC
CTGTAAGTTTGCTATTAAAATACATTAAACTAT

FIGURE 593A

AATCTATCAGGGAACGGCGGTGGCCGGTGCGGCGTGTTCGGTGGCGGCTCTGGCCGCTCAGGCGCCTGCGGCTGG
GTGAGCGCACGCGAGGCGGCGAGGCGGCAGCGTGTTTCTAGGTCGTGGCGTCGGGCTTCCGGAGCTTTGGCGGCA
GCTAGGGGAGGATGGCGGAGTCTTCGGATAAGCTCTATCGAGTCGAGTACGCCAAGAGCGGGCGCGCCTCTTGCA
AGAAATGCAGCGAGAGCATCCCCAAGGACTCGCTCCGGATGGCCATCATGGTGCAGTCGCCCATGTTTGATGGAA
AAGTCCCACACTGGTACCACTTCTCCTGCTTCTGGAAGGTGGGCCACTCCATCCGGCACCCTGACGTTGAGGTGG
ATGGGTTCTCTGAGCTTCGGTGGGATGACCAGCAGAAAGTCAAGAAGACAGCGGAAGCTGGAGGAGTGACAGGCA
AAGGCCAGGATGGAATTGGTAGCAAGGCAGAGAAGACTCTGGGTGACTTTGCAGCAGAGTATGCCAAGTCCAACA
GAAGTACGTGCAAGGGGTGTATGGAGAAGATAGAAAAGGGCCAGGTGCGCCTGTCCAAGAAGATGGTGGACCCGG
AGAAGCCACAGCTAGGCATGATTGACCGCTGGTACCATCCAGGCTGCTTTGTCAAGAACAGGGAGGAGCTGGGTT
TCCGGCCCGAGTACAGTGCGAGTCAGCTCAAGGGCTTCAGCCTCCTTGCTACAGAGGATAAAGAAGCCCTGAAGA
AGCAGCTCCCAGGAGTCAAGAGTGAAGGAAAGAGAAAAGGCGATGAGGTGGATGGAGTGGATGAAGTGGCGAAGA
AGAAATCTAAAAAAGAAAAAGACAAGGATAGTAAGCTTGAAAAAGCCCTAAAGGCTCAGAACGACCTGATCTGGA
ACATCAAGGACGAGCTAAAGAAAGTGTGTTCAACTAATGACCTGAAGGAGCTACTCATCTTCAACAAGCAGCAAG
TGCCTTCTGGGGAGTCGGCGATCTTGGACCGAGTAGCTGATGGCATGGTGTTCGGTGCCCTCCTTCCCTGCGAGG
AATGCTCGGGTCAGCTGGTCTTCAAGAGCGATGCCTATTACTGCACTGGGGACGTCACTGCCTGGACCAAGTGTA
TGGTCAAGACACAGACACCCAACCGGAAGGAGTGGGTAACCCCAAAGGAATTCCGAGAAATCTCTTACCTCAAGA
AATTGAAGGTTAAAAAACAGGACCGTATATTCCCCCCAGAAACCAGCGCCTCCGTGGCGGCCACGCCTCCGCCCT
CCACAGCCTCGGCTCCTGCTGCTGTGAACTCCTCTGCTTCAGCAGATAAGCCATTATCCAACATGAAGATCCTGA
CTCTCGGGAAGCTGTCCCGGAACAAGGATGAAGTGAAGGCCATGATTGAGAAACTCGGGGGGAAGTTGACGGGGA
CGGCCAACAAGGCTTCCCTGTGCATCAGCACCAAAAAGGAGGTGGAAAAGATGAATAAGAAGATGGAGGAAGTAA
AGGAAGCCAACATCCGAGTTGTGTCTGAGGACTTCCTCCAGGACGTCTCCGCCTCCACCAAGAGCCTTCAGGAGT
TGTTCTTAGCGCACATCTTGTCCCCTTGGGGGGCAGAGGTGAAGGCAGAGCCTGTTGAAGTTGTGGCCCCAAGAG
GGAAGTCAGGGGCTGCGCTCTCCAAAAAAAGCAAGGGCCAGGTCAAGGAGGAAGGTATCAACAAATCTGAAAAGA
GAATGAAATTAACTCTTAAAGGAGGAGCAGCTGTGGATCCTGATTCTGGACTGGAACACTCTGCGCATGTCCTGG
AGAAAGGTGGGAAGGTCTTCAGTGCCACCCTTGGCCTGGTGGACATCGTTAAAGGAACCAACTCCTACTACAAGC
TGCAGCTTCTGGAGGACGACAAGGAAAACAGGTATTGGATATTCAGGTCCTGGGGCCGTGTGGGTACGGTGATCG
GTAGCAACAAACTGGAACAGATGCCGTCCAAGGAGGATGCCATTGAGCACTTCATGAAATTATATGAAGAAAAAA
CCGGGAACGCTTGGCACTCCAAAAATTTCACGAAGTATCCCAAAAAGTTCTACCCCCTGGAGATTGACTATGGCC
AGGATGAAGAGGCAGTGAAGAAGCTGACAGTAAATCCTGGCACCAAGTCCAAGCTCCCCAAGCCAGTTCAGGACC
TCATCAAGATGATCTTTGATGTGGAAAGTATGAAGAAAGCCATGGTGGAGTATGAGATCGACCTTCAGAAGATGC
CCTTGGGGAAGCTGAGCAAAAGGCAGATCCAGGCCGCATACTCCATCCTCAGTGAGGTCCAGCAGGCGGTGTCTC
AGGGCAGCAGCGACTCTCAGATCCTGGATCTCTCAAATCGCTTTTACACCCTGATCCCCCACGACTTTGGGATGA
AGAAGCCTCCGCTCCTGAACAATGCAGACAGTGTGCAGGCCAAGGTGGAAATGCTTGACAACCTGCTGGACATCG
AGGTGGCCTACAGTCTGCTCAGGGGAGGGTCTGATGATAGCAGCAAGGATCCCATCGATGTCAACTATGAGAAGC
TCAAAACTGACATTAAGGTGGTTGACAGAGATTCTGAAGAAGCCGAGATCATCAGGAAGTATGTTAAGAACACTC
ATGCAACCACACACAATGCGTATGACTTGGAAGTCATCGATATCTTTAAGATAGAGCGTGAAGGCGAATGCCAGC
GTTACAAGCCCTTTAAGCAGCTTCATAACCGAAGATTGCTGTGGCACGGGTCCAGGACCACCAACTTTGCTGGGA
TCCTGTCCCAGGGTCTTCGGATAGCCCCGCCTGAAGCGCCCGTGACAGGCTACATGTTTGGTAAAGGGATCTATT
TCGCTGACATGGTCTCCAAGAGTGCCAACTACTGCCATACGTCTCAGGGAGACCCAATAGGCTTAATCCTGTTGG
GAGAAGTTGCCCTTGGAAACATGTATGAACTGAAGCACGCTTCACATATCAGCAAGTTACCCAAGGGCAAGCACA
GTGTCAAAGGTTTGGGCAAAACTACCCCTGATCCTTCAGCTAACATTAGTCTGGATGGTGTAGACGTTCCTCTTG
GGACCGGGATTTCATCTGGTGTGAATGACACCTCTCTACTATATAACGAGTACATTGTCTATGATATTGCTCAGG
TAAATCTGAAGTATCTGCTGAAACTGAAATTCAATTTTAAGACCTCCCTGTGGTAATTGGGAGAGGTAGCCGAGT
CACACCCGGTGGCTCTGGTATGAATTCACCCGAAGCGCTTCTGCACCAACTCACCTGGCCGCTAAGTTGCTGATG
GGTAGTACCTGTACTAAACCACCTCAGAAAGGATTTTACAGAAACGTGTTAAAGGTTTTCTCTAACTTCTCAAGT
CCCTTGTTTTGTGTTGTGTCTGTGGGGAGGGGTTGTTTTGGGGTTGTTTTTGTTTTTTCTTGCCAGGTAGATAAA
ACTGACATAGAGAAAAGGCTGGAGAGAGATTCTGTTGCATAGACTAGTCCTATGGAAAAAACCAAGCTTCGTTAG
AATGTCTGCCTTACTGGTTTCCCCAGGGAAGGAAAAATACACTTCCACCCTTTTTTCTAAGTGTTCGTCTTTAGT

FIGURE 593B

TTTGATTTTGGAAAGATGTTAAGCATTTATTTTTAGTTAAAAATAAAAACTAATTTCATACTATTTAGATTTTCT
TTTTTATCTTGCACTTATTGTCCCCTTTTTAGTTTTTTTGTTTGCCTCTTGTGGTGAGGGGTGTGGGAAGACCA
AAGGAAGGAACGCTAACAATTTCTCATACTTAGAAACAAAAAGAGCTTTCCTTCTCCAGGAATACTGAACATGGG
AGCTCTTGAAATATGTAGTATTAAAAGTTGCATTTG

FIGURE 594

CGAGCGGCGGCGGAGCAGGCATTTCCAGCAGTGAGGAGACAGCCAGAAGCAAGCTATTGGAGCTGAAGGAACCTG
AGACAGAAGCTAGTCCCCCCTCTGAATTTTACTGATGAAGAAACTGAGGCCACAGAGCTAAAGTGACTTTTCCCA
AGGTCGCCCAGCGAGGACGTGGGACTTCTCAGACGTCAGGAGAGTGATGTGAGGGAGCTGTGTGACCATAGAAAG
TGACGTGTTAAAAACCAGCGCTGCCCTCTTTGAAAGCCAGGGAGCATCATTCATTTAGCCTGCTGAGAAGAAGAA
ACCAAGTGTCCGGGATTCAGACCTCTCTGCGGCCCCAAGTGTTCGTGGTGCTTCCAGAGGCAGGGCT**ATG**CTCAC
ATTCATGGCCTCTGACAGCGAGGAAGAAGTGTGTGATGAGCGGACGTCCCTAATGTCGGCCGAGAGCCCCACGCC
GCGCTCCTGCCAGGAGGGCAGGCAGGGCCCAGAGGATGGAGAGAACACTGCCCAGTGGAGAAGCCAGGAGAACGA
GGAGGACGGTGAGGAGGACCCTGACCGCTATGTCTGTAGTGGGGTTCCCGGGCGGCCGCCAGGCCTGGAGGAAGA
GCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTGTCACTCTGTGCATGATCGTGGTGGT
AGCCACCATCAAGTCTGTGCGCTTCTACACAGAGAAGAATGGACAGCTCATCTACACGACATTCACTGAGGACAC
ACCCTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGAC
CATCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCATGTCTTCACTGAT
GCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGACCTACAATGTGGCCATGGACTACCCCAC
CCTCTTGCTGACTGTCTGGAACTTCGGGGCAGTGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCA
GCAGGCCTACCTCATCATGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTG
GGTCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTCTGAGAATGCTGGT
AGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATATACTCATCTGCCATGGTGTGGACGGTTGG
CATGGCGAAGCTGGACCCCTCCTCTCAGGGTGCCCTCCAGCTCCCCTACGACCCGGAGATGGAAGAAGACTCCTA
TGACAGTTTTGGGGAGCCTTCATACCCCGAAGTCTTTGAGCCTCCCTTGACTGGCTACCCAGGGGAGGAGCTGGA
GGAAGAGGAGGAAAGGGGCGTGAAGCTTGGCCTCGGGGACTTCATCTTCTACAGTGTGCTGGTGGGCAAGGCGGC
TGCCACGGGCAGCGGGGACTGGAATACCACGCTGGCCTGCTTCGTGGCCATCCTCATTGGCTTGTGTCTGACCCT
CCTGCTGCTTGCTGTGTTCAAGAAGGCGCTGCCCGCCCTCCCCATCTCCATCACGTTCGGGCTCATCTTTTACTT
CTCCACGGACAACCTGGTGCGGCCGTTCATGGACACCCTGGCCTCCCATCAGCTCTACATC**TGA**GGGACATGGTG
TGCCACAGGCTGCAAGCTGCAGGGAATTTTCATTGGATGCAGTTGTATAGTTTTACACTCTAGTGCCATATATTT
TTAAGACTTTTCTTTCCTTAAAAAATAAAGTACGTGTTTACTTGGTGAGGAGGAGGCAGAACCAGCTCTTTGGTG
CCAGCTGTTTCATCACCAGACTTTGGCTCCCGCTTTGGGGAGCGCCTCGCTTCACGGACAGGAAGCACAGCAGGT
TTATCCAGATGAACTGAGAAGGTCAGATTAGGGCGGGGAGAAGAGCATCCGGCATGAGGGCTGAGATGCGCAAAG
AGTGTGCTCGGGAGTGGCCCCTGGCACCTGGGTGCTCTGGCTGGAGAGGAAAAGCCAGTTCCCTACGAGGAGTGT
TCCCAATGCTTTGTCCATGATGTCCTTGTTATTTTATTGCCTTTAGAAACTGAGTCCTGTTCTTGTTACGGCAGT
CACACTGCTGGGAAGTGGCTTAATAGTAATATCAATAAATAGATGAGTCCTGTTAGAAAAA

FIGURE 595

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVPGRPPGL
EEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTTFTEDTPSVGQRLLNSVLNTLIMISVIV
VMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPL
VLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVW
TVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEERGVKLGLGDFIFYSVLVG
KAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI

FIGURE 596

CGAGCGGCGGCGGAGCAGGCATTTCCAGCAGTGAGGAGACAGCCAGAAGCAAGCTATTGGAGCTGAAGGAACCTG
AGACAGAAGCTAGTCCCCCCTCTGAATTTTACTGATGAAGAAACTGAGGCCACAGAGCTAAAGTGACTTTTCCCA
AGGTCGCCCAGCGAGGACGTGGGACTTCTCAGACGTCAGGAGAGTGATGTGAGGGAGCTGTGTGACCATAGAAAG
TGACGTGTTAAAAACCAGCGCTGCCCTCTTTGAAAGCCAGGGAGCATCATTCATTTAGCCTGCTGAGAAGAAGAA
ACCAAGTGTCCGGGATTCAGACCTCTCTGCGGCCCCAAGTGTTCGTGGTGCTTCCAGAGGCAGGGCT**ATG**CTCAC
ATTCATGGCCTCTGACAGCGAGGAAGAAGTGTGTGATGAGCGGACGTCCCTAATGTCGGCCGAGAGCCCCACGCC
GCGCTCCTGCCAGGAGGGCAGGCAGGGCCCAGAGGATGGAGAGAACACTGCCCAGTGGAGAAGCCAGGAGAACGA
GGAGGACGGTGAGGAGGACCCTGACCGCTATGTCTGTAGTGGGGTTCCCGGGCGGCCGCCAGGCCTGGAGGAAGA
GCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTGTCACTCTGTGCATGATCGTGGTGGT
AGCCACCATCAAGTCTGTGCGCTTCTACACAGAGAAGAATGGACAGCTCATCTACACGACATTCACTGAGGACAC
ACCCTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGAC
CATCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCATGTCTTCACTGAT
GCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGACCTACAATGTGGCCATGGACTACCCCAC
CCTCTTGCTGACTGTCTGGAACTTCGGGGCAGTGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCA
GCAGGCCTACCTCATCATGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTG
GGTCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTCTGAGAATGCTGGT
AGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATATACTCATCTGCCATGGTGTGGACGGTTGG
CATGGCGAAGCTGGACCCCTCCTCTCAGGGTGCCCTCCAGCTCCCCTACGACCCGGAGATGGAAGACTCCTATGA
CAGTTTTGGGGAGCCTTCATACCCCGAAGTCTTTGAGCCTCCCTTGACTGGCTACCCAGGGGAGGAGCTGGAGGA
AGAGGAGGAAAGGGGCGTGAAGCTTGGCCTCGGGGACTTCATCTTCTACAGTGTGCTGGTGGGCAAGGCGGCTGC
CACGGGCAGCGGGGACTGGAATACCACGCTGGCCTGCTTCGTGGCCATCCTCATTGGCTTGTGTCTGACCCTCCT
GCTGCTTGCTGTGTTCAAGAAGGCGCTGCCCGCCCTCCCCATCTCCATCACGTTCGGGCTCATCTTTTACTTCTC
CACGGACAACCTGGTGCGGCCGTTCATGGACACCCTGGCCTCCCATCAGCTCTACATC**TGA**GGGACATGGTGTGC
CACAGGCTGCAAGCTGCAGGGAATTTTCATTGGATGCAGTTGTATAGTTTTACACTCTAGTGCCATATATTTTTA
AGACTTTTCTTTCCTTAAAAAATAAAGTACGTGTTTACTTGGTGAGGAGGAGGCAGAACCAGCTCTTTGGTGCCA
GCTGTTTCATCACCAGACTTTGGCTCCCGCTTTGGGGAGCGCCTCGCTTCACGGACAGGAAGCACAGCAGGTTTA
TCCAGATGAACTGAGAAGGTCAGATTAGGGCGGGGAGAAGAGCATCCGGCATGAGGGCTGAGATGCGCAAAGAGT
GTGCTCGGGAGTGGCCCCTGGCACCTGGGTGCTCTGGCTGGAGAGGAAAAGCCAGTTCCCTACGAGGAGTGTTCC
CAATGCTTTGTCCATGATGTCCTTGTTATTTTATTGCCTTTAGAAACTGAGTCCTGTTCTTGTTACGGCAGTCAC
ACTGCTGGGAAGTGGCTTAATAGTAATATCAATAAATAGATGAGTCCTGTTAGAAAAA

FIGURE 597

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVPGRPPGL
EEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTTFTEDTPSVGQRLLNSVLNTLIMISVIV
VMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPL
VLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVW
TVGMAKLDPSSQGALQLPYDPEMEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEERGVKLGLGDFIFYSVLVGK
AAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI

FIGURE 598A

TATACTTCGCTACTTGGCTAGAGTTGCAACTACAGCTGGGTTATATGGCTCTAATCTGATGGAACATACTGAGAT
TGATCACTGGTTGGAGTTCAGTGCTACAAAATTATCTTCATGTGATTCCTTTACTTCTACAATTAATGAACTCAA
TCATTGCCTGTCTCTGAGAACATACTTAGTTGGAAACTCCTTGAGTTTAGCAGATTTATGTGTTTGGGCCACCCT
AAAAGGAAATGCTGCCTGGCAAGAACAGTTGAAACAGAAGAAAGCTCCAGTTCATGTAAAACGTTGGTTTGGCTT
TCTTGAAGCCCAGCAGGCCTTCCAGTCAGTAGGTACCAAGTGGGATGTTTCAACAACCAAAGCTCGAGTGGCACC
TGAGAAAAAGCAAGATGTTGGGAAATTTGTTGAGCTTCCAGGTGCGGAGATGGGAAAGGTTACCGTCAGATTTCC
TCCAGAGGCCAGTGGTTACTTACACATTGGGCATGCAAAAGCTGCTCTTCTGAACCAGCACTACCAGGTTAACTT
TAAAGGGAAACTGATCATGAGATTTGATGACACAAATCCTGAAAAAGAAAAGGAAGATTTTGAGAAGGTTATCTT
GGAAGATGTTGCAATGTTGCATATCAAACCAGATCAATTTACTTATACTTCGGATCATTTTGAAACTATAATGAA
GTATGCAGAGAAGCTAATTCAAGAAGGGAAGGCTTATGTGGATGATACTCCTGCTGAACAGATGAAAGCAGAACG
TGAGCAGAGGATAGAATCTAAACATAGAAAAAACCCTATTGAGAAGAATCTACAAATGTGGGAAGAAATGAAAAA
AGGGAGCCAGTTTGGTCAGTCCTGTTGTTTGCGAGCAAAAATTGACATGAGTAGTAACAATGGATGCATGAGAGA
TCCAACCCTTTATCGCTGCAAAATTCAACCACATCCAAGAACTGGAAATAAATACAATGTTTATCCAACATATGA
TTTTGCCTGCCCCATAGTTGACAGCATCGAAGGTGTTACACATGCCCTGAGAACAACAGAATACCATGACAGAGA
TGAGCAGTTTTACTGGATTATTGAAGCTTTAGGCATAAGAAAACCATATATTTGGGAATATAGTCGGCTAAATCT
CAACAACACAGTGCTATCCAAAAGAAAACTCACATGGTTTGTCAATGAAGGACTAGTAGATGGATGGGATGACCC
AAGATTTCCTACGGTTCGTGGTGTACTGAGAAGAGGGATGACAGTTGAAGGACTGAAACAGTTTATTGCTGCTCA
GGGCTCCTCACGTTCAGTCGTGAACATGGAGTGGGACAAAATCTGGGCGTTTAACAAAAAGGTTATTGACCCAGT
GGCTCCACGATATGTTGCATTACTGAAGAAAGAAGTGATCCCAGTGAATGTACCTGAAGCTCAGGAGGAGATGAA
AGAAGTAGCCAAACACCCAAAGAATCCTGAGGTTGGCTTGAAGCCTGTGTGGTATAGTCCCAAAGTTTTCATTGA
AGGTGCTGATGCAGAGACTTTTTCGGAGGGTGAGATGGTTACATTTATAAATTGGGGCAACCTCAACATTACAAA
AATACACAAAAATGCAGATGGAAAAATCATATCTCTTGATGCAAAGTTGAATTTGGAAAACAAAGACTACAAGAA
AACCACTAAGGTCACTTGGCTTGCAGAGACTACACATGCTCTTCCTATTCCAGTAATCTGTGTCACTTATGAGCA
CTTGATCACAAAGCCAGTGCTAGGAAAAGACGAGGACTTTAAGCAGTATGTCAACAAGAACAGTAAGCATGAAGA
GCTAATGCTAGGGGATCCCTGCCTTAAGGATTTGAAAAAAGGAGATATTATACAACTCCAGAGAAGAGGATTCTT
CATATGTGATCAACCTTATGAACCTGTTAGCCCATATAGTTGCAAGGAAGCCCCGTGTGTTTTGATATACATTCC
TGATGGGCACACAAAGGAAATGCCAACATCAGGGTCAAAGGAAAAGACCAAAGTAGAAGCCACAAAAAAATGAGAC
CTCTGCTCCTTTTAAGGAAAGACCAACACCTTCTCTGAATAATAATTGTACTACATCTGAGGATTCCTTGGTCCT
TTACAATAGAGTGGCTGTTCAAGGAGATGTGGTTCGTGAATTAAAAGCCAAGAAAGCACCAAAGGAAGATGTAGA
TGCAGCTGTAAAACAGCTTTTGTCTTTGAAAGCTGAATATAAGGAGAAAACTGGCCAGGAATATAAACCTGGAAA
CCCTCCTGCTGAAATAGGACAGAATATTTCTTCTAATTCCTCAGCAAGTATTCTGGAAAGTAAATCTCTGTATGA
TGAAGTTGCTGCACAAGGGGAGGTGGTTCGTAAGCTAAAAGCTGAAAAATCCCCTAAGXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXCTTCTCAAGGGGAAGTAGTTCGGAAACTTAAAACTGAAAAAGCCCCTAAGGATCAAGT
AGATATAGCTGTTCAAGAACTCCTTCAGCTAAAGGCACAGTACAAGTCTTTGATAGGAGTAGAGTATAAGCCTGT
GTCGGCCACTGGAGCTGAGGACAAAGATAAGAAGAAGAAAGAAAAAGAAAATAAATCTGAAAAGCAGAATAAGCC
TCAGAAACAAAATGATGGCCAAAGGAAAGACCCTTCTAAAAACCAAGGAGGTGGGCTCTCATCAAGTGGAGCAGG
AGAAGGGCAGGGGCCTAAGAAACAGACCAGGTTGGGTCTTGAGGCAAAAAAAGAAGAAAATCTTGCTGATTGGTA
TTCTCAGGTCATCACAAAGTCAGAAATGATTGAATACCATGACATAAGTGGCTGTTATATTCTTCGTCCCTGGGC
CTATGCCATTTGGGAAGCCATCAAGGACTTTTTTGATGCTGAGATCAAGAAACTTGGTGTTGAAAACTGCTACTT
CCCCATGTTTGTGTCTCAAAGTGCATTAGAGAAAGAGAAGACTCATGTTGCTGACTTTGCCCCAGAGGTTGCTTG
GGTTACAAGATCTGGCAAAACCGAGCTGGCAGAACCAATTGCCATTCGTCCTACTAGTGAAACAGTAATGTATCC
TGCATATGCAAAATGGGTACAATCACACAGAGACCTGCCCATCAAGCTCAATCAGTGGTGCAATGTGGTGCGTTG
GGAATTCAAGCATCCTCAGCCTTTCCTACGTACTCGTGAATTTCTTTGGCAGGAAGGGCACAGTGCTTTTGCTAC
CATGGAAGAGGCAGCGGAAGAGGTCTTGCAGATACTTGACTTATATGCTCAGGTATATGAAGAACTCCTGGCAAT
TCCTGTTGTTAAAGGAAGAAAGACGGAAAAGGAAAAATTTGCAGGAGGAGACTATACAACTACAATAGAAGCATT
TATATCTGCTAGTGGAAGAGCTATCCAGGGAGGAACATCACATCATTTAGGGCAGAATTTTTCCAAAATGTTTGA

FIGURE 598B

AATCGTTTTTGAAGATCCAAAGATACCAGGAGAGAAGCAATTTGCCTATCAAAACTCCTGGGGCCTGACAACTCG
AACTATTGGTGTTATGACCATGGTTCATGGGGACAACATGGGTTTAGTATTACCACCCCGTGTAGCATGTGTTCA
GGTGGTGATTATTCCTTGTGGCATTACCAATGCACTTTCTGAAGAAGACAAAGAAGCGCTGATTGCAAAATGCAA
TGATTATCGAAGGCGATTACTCAGTGTTAACATCCGCGTTAGAGCTGATTTACGAGATAATTATTCTCCAGGTTG
GAAATTCAATCACTGGGAGCTCAAGGGAGTTCCCATTAGACTTGAAGTTGGGCCACGTGATATGAAGAGCTGTCA
GTTTGTAGCCGTCAGACGAGATACTGGAGAAAAGCTGACAGTTGCTGAAAATGAGGCAGAGACTAAACTTCAAGC
TATTTTGGAAGACATCCAGGTCACCCTTTTCACAAGGGCTTCTGAAGACCTTAAGACTCATATGGTTGTGGCTAA
TACAATGGAAGACTTTCAGAAGATACTAGATTCTGGAAAGATTGTTCAGATTCCATTCTGTGGGGAAATTGACTG
TGAGGACTGGATCAAAAAGACCACTGCCAGGGATCAAGATCTTGAACCTGGTGCTCCATCCATGGGAGCTAAAAG
CCTTTGCATCCCCTTCAAACCACTCTGTGAACTGCAGCCTGGAGCCAAATGTGTCTGTGGCAAGAACCCTGCCAA
GTACTACACCTTATTTGGTCGCAGCTACTGAGGGATGAACGAAAGCCCCCTCTTCAACTCCTCTCACTTTTTAAA
GCATTGATATTAGTATCTTCTCAGATACAGACCGTTTTATGATTTTTTAAAAAGTAAAAGTTCTAAAATGAAGTC
ACACAGGACAATTATTCTTATGCCTAAGTTAACAGTGGATAAAAGACTTTTCTGTAAACAACTCCAGTAATAAAT
ATCATGAACTA

FIGURE 599A

AGTAGCTGCGGCGCAGGGGCGGAGCGAAGGCTGCGGCGGCGTCGGGTACGCGCACACGTTGCATCTTCTTCCTTT
CGCGGGGTCCTCCGTAGTTCTGGCACGAGCCAGGCGTACTGACAGGTGGACCAGCGGACTGGTGGAGATGGCGAC
GCTCTCTCTGACCGTGAATTCAGGAGACCCTCCGCTAGGAGCTTTGCTGGCAGTAGAACACGTGAAAGACGATGT
CAGCATTTCCGTTGAAGAAGGGAAAGAGAATATTCTTCATGTTTCTGAAAATGTGATATTCACAGATGTGAATTC
TATACTTCGCTACTTGGCTAGAGTTGCAACTACAGCTGGGTTATATGGCTCTAATCTGATGGAACATACTGAGAT
TGATCACTGGTTGGAGTTCAGTGCTACAAAATTATCTTCATGTGATTCCTTTACTTCTACAATTAATGAACTCAA
TCATTGCCTGTCTCTGAGAACATACTTAGTTGGAAACTCCTTGAGTTTAGCAGATTTATGTGTTTGGGCCACCCT
AAAAGGAAATGCTGCCTGGCAAGAACAGTTGAAACAGAAGAAAGCTCCAGTTCATGTAAAACGTTGGTTTGGCTT
TCTTGAAGCCCAGCAGGCCTTCCAGTCAGTAGGTACCAAGTGGGATGTTTCAACAACCAAAGCTCGAGTGGCACC
TGAGAAAAAGCAAGATGTTGGGAAATTTGTTGAGCTTCCAGGTGCGGAGATGGGAAAGGTTACCGTCAGATTTCC
TCCAGAGGCCAGTGGTTACTTACACATTGGGCATGCAAAAGCTGCTCTTCTGAACCAGCACTACCAGGTTAACTT
TAAAGGGAAACTGATCATGAGATTTGATGACACAAATCCTGAAAAAGAAAAGGAAGATTTTGAGAAGGTTATCTT
GGAAGATGTTGCAATGTTGCATATCAAACCAGATCAATTTACTTATACTTCGGATCATTTTGAAACTATAATGAA
GTATGCAGAGAAGCTAATTCAAGAAGGGAAGGCTTATGTGGATGATACTCCTGCTGAACAGATGAAAGCAGAACG
TGAGCAGAGGATAGACTCTAAACATAGAAAAAACCCTATTGAGAAGAATCTACAAATGTGGGAAGAAATGAAAAA
AGGGAGCCAGTTTGGTCAGTCCTGTTGTTTGCGAGCAAAAATTGACATGAGTAGTAACAATGGATGCATGAGAGA
TCCAACCCTTTATCGCTGCAAAATTCAACCACATCCAAGAACTGGAAATAAATACAATGTTTATCCAACATATGA
TTTTGCCTGCCCCATAGTTGACAGCATCGAAGGTGTTACACATGCCCTGAGAACAACAGAATACCATGACAGAGA
TGAGCAGTTTTACTGGATTATTGAAGCTTTAGGCATAAGAAAACCATATATTTGGGAATATAGTCGGCTAAATCT
CAACAACACAGTGCTATCCAAAAGAAAACTCACATGGTTTGTCAATGAAGGACTAGTAGATGGATGGGATGACCC
AAGATTTCCTACGGTTCGTGGTGTACTGAGAAGAGGGATGACAGTTGAAGGACTGAAACAGTTTATTGCTGCTCA
GGGCTCCTCACGTTCAGTCGTGAACATGGAGTGGGACAAAATCTGGGCGTTTAACAAAAAGGTTATTGACCCAGT
GGCTCCACGATATGTTGCATTACTGAAGAAAGAAGTGATCCCAGTGAATGTACCTGAAGCTCAGGAGGAGATGAA
AGAAGTAGCCAAACACCCAAAGAATCCTGAGGTTGGCTTGAAGCCTGTGTGGTATAGTCCCAAAGTTTTCATTGA
AGGTGCTGATGCAGAGACTTTTTCGGAGGGTGAGATGGTTACATTTATAAATTGGGGCAACCTCAACATTACAAA
AATACACAAAAATGCAGATGGAAAAATCATATCTCTTGATGCAAAGTTGAATTTGGAAAACAAAGACTACAAGAA
AACCACTAAGGTCACTTGGCTTGCAGAGACTACACATGCTCTTCCTATTCCAGTAATCTGTGTCACTTATGAGCA
CTTGATCACAAAGCCAGTGCTAGGAAAAGACGAGGACTTTAAGCAGTATGTCAACAAGAACAGTAAGCATGAAGA
GCTAATGCTAGGGGATCCCTGCCTTAAGGATTTGAAAAAAGGAGATATTATACAACTCCAGAGAAGAGGATTCTT
CATATGTGATCAACCTTATGAACCTGTTAGCCCATATAGTTGCAAGGAAGCCCCGTGTGTTTTGATATACATTCC
TGATGGGCACACAAAGGAAATGCCAACATCAGGGTCAAAGGAAAAGACCAAAGTAGAAGCCACAAAAAATGAGAC
CTCTGCTCCTTTTAAGGAAAGACCAACACCTTCTCTGAATAATAATTGTACTACATCTGAGGATTCCTTGGTCCT
TTACAATAGAGTGGCTGTTCAAGGAGATGTGGTTCGTGAATTAAAAGCCAAGAAAGCACCAAAGGAAGATGTAGA
TGCAGCTGTAAAACAGCTTTTGTCTTTGAAAGCTGAATATAAGGAGAAAACTGGCCAGGAATATAAACCTGGAAA
CCCTCCTGCTGAAATAGGACAGAATATTTCTTCTAATTCCTCAGCAAGTATTCTGGAAAGTAAATCTCTGTATGA
TGAAGTTGCTGCACAAGGGGGAGGTGGTTCGTAAGCTAAAAGCTGAAAAATCCCCTAAGGCTAAAATAAATGAAGC
TGTAGAATGCTTACTGTCCCTGAAGGCTCAGTATAAAGAAAAAACTGGGAAGGAGTACATACCTGGTCAGCCCCC
ATTATCTCAAAGTTCGGATTCAAGCCCAACCAGAAATTCTGAACCTGCTGGTTTAGAAACACCAGAAGCGAAAGT
ACTTTTTGACAAAGTAGCTTCTCAAGGGGAAGTAGTTCGGAAACTTAAAACTGAAAAAGCCCCTAAGGATCAAGT
AGATATAGCTGTTCAAGAACTCCTTCAGCTAAAGGCACAGTACAAGTCTTTGATAGGAGTAGAGTATAAGCCTGT
GTCGGCCACTGGAGCTGAGGACAAAGATAAGAAGAAGAAAGAAAAAGAAAATAAATCTGAAAAGCAGAATAAGCC
TCAGAAACAAAATGATGGCCAAAGGAAAGACCCTTCTAAAAACCAAGGAGGTGGGCTCTCATCAAGTGGAGCAGG
AGAAGGGCAGGGGCCTAAGAAACAGACCAGGTTGGGTCTTGAGGCAAAAAAAGAAGAAAATCTTGCTGATTGGTA
TTCTCAGGTCATCACAAAGTCAGAAATGATTGAATACCATGACATAAGTGGCTGTTATATTCTTCGTCCCTGGGC
CTATGCCATTTGGGAAGCCATCAAGGACTTTTTTGATGCTGAGATCAAGAAACTTGGTGTTGAAAACTGCTACTT
CCCCATGTTTGTGTCTCAAAGTGCATTAGAGAAAGAGAAGACTCATGTTGCTGACTTTGCCCCAGAGGTTGCTTG
GGTTACAAGATCTGGCAAAACCGAGCTGGCAGAACCAATTGCCATTCGTCCTACTAGTGAAACAGTAATGTATCC
TGCATATGCAAAATGGGTACAGTCACACAGAGACCTGCCCATCAAGCTCAATCAGTGGTGCAATGTGGTGCGTTG

FIGURE 599B

GGAATTCAAGCATCCTCAGCCTTTCCTACGTACTCGTGAATTTCTTTGGCAGGAAGGGCACAGTGCTTTTGCTAC
CATGGAAGAGGCAGCGGAAGAGGTCTTGCAGATACTTGACTTATATGCTCAGGTATATGAAGAACTCCTGGCAAT
TCCTGTTGTTAAAGGAAGAAAGACGGAAAAGGAAAAATTTGCAGGAGGAGACTATACAACTACAATAGAAGCATT
TATATCTGCTAGTGGAAGAGCTATCCAGGGAGGAACATCACATCATTTAGGGCAGAATTTTTCCAAAATGTTTGA
AATCGTTTTTGAAGATCCAAAGATACCAGGAGAGAAGCAATTTGCCTATCAAAACTCCTGGGGCCTGACAACTCG
AACTATTGGTGTTATGACCATGGTTCATGGGGACAACATGGGTTTAGTATTACCACCCCGTGTAGCATGTGTTCA
GGTGGTGATTATTCCTTGTGGCATTACCAATGCACTTTCTGAAGAAGACAAAGAAGCGCTGATTGCAAAATGCAA
TGATTATCGAAGGCGATTACTCAGTGTTAACATCCGCGTTAGAGCTGATTTACGAGATAATTATTCTCCAGGTTG
GAAATTCAATCACTGGGAGCTCAAGGGAGTTCCCATTAGACTTGAAGTTGGGCCACGTGATATGAAGAGCTGTCA
GTTTGTAGCCGTCAGACGAGATACTGGAGAAAAGCTGACAGTTGCTGAAAATGAGGCAGAGACTAAACTTCAAGC
TATTTTGGAAGACATCCAGGTCACCCTTTTCACAAGGGCTTCTGAAGACCTTAAGACTCATATGGTTGTGGCTAA
TACAATGGAAGACTTTCAGAAGATACTAGATTCTGGAAAGATTGTTCAGATTCCATTCTGTGGGGAAATTGACTG
TGAGGACTGGATCAAAAAGACCACTGCCAGGGATCAAGATCTTGAACCTGGTGCTCCATCCATGGGAGCTAAAAG
CCTTTGCATCCCCTTCAAACCACTCTGTGAACTGCAGCCTGGAGCCAAATGTGTCTGTGGCAAGAACCCTGCCAA
GTACTACACCTTATTTGGTCGCAGCTACTGAGGGATGAACGAAAGCCCCCTCTTCAACTCCTCTCACTTTTTAAA
GCATTGATATTAGTATCTTCTCAGATACAGACCGTTTTATGATTTTTTAAAAAGTAAAAGTTCTAAAATGAAGTC
ACACAGGACAATTATTCTTATGCCTAAGTTAACAGTGGATAAAAGACTTTTCTGTAAACAACTCCAGTAATAAAT
ATCATGAACTAATATGGTTTAAAAAAAAAAAAAAAAAAAAAGG

FIGURE 600

CCCAGGATGTAGAGCTGGCAGTGCCTGACGGCGCGTCTGACGCGGAGTTGGGTGGGGTAGAGAGTAGGGGGCGGT
AGTCGGGGGTGGTGGGAGAAGGAGGAGGCGGCAAATCACTTATAAATGGCGCGGAAGCAGGACCCGAAGCCTAAA
TTCCAGGAGGGTGAGCGAGTGCTGTGCTTTCATGGGCCTCTTCTTTATGAAGCAAAGTGTGTAAAGGTTGCCATA
AAGGACAAACAAGTGAAATACTTCATACATTACAGTGGTTGGAATAAAAATTGGGATGAGTGGGTTCCGGAGAGC
AGAGTACTCAAATACGTGGACACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCAATCAGGAGCAGTATGCA
GAGGGGAAGATGAGAGGGGCTGCCCCAGGAAAGAAGACATCTGGTCTGCAACAGAAAAATGTTGAAGTGAAAACG
AAAAAGAACAAACAGAAAACACCTGGAAATGGAGATGGTGGCAGTACCAGTGAGACCCCTCAGCCTCCTTGGAAG
AAAAGGGCCCGGGTAGATCCTACTGTTGAAAATGAGGAAACATTCATGAACAGAGTTGAAGTTAAAGTAAAGATT
CCTGAATAGCTAAAACCGTGGCTTGTTGATGACTGGGACTTAATTACCAGGCAAAAACAGCTCTTTTATCTTCCT
GCCAAGAAGAATGTGGATTCCATTCTTGAGGATTATGCAAATTACAAGAAATCTCGTGGAAACACAGATAATAAG
GAGTATGCGGTTAATGAAGTTGTGGCAGGGATAAAAGAATACTTCAACGTAATGTTGGGTACCCAGCTACTCTAT
AAATTTGAGAGACCACAGTATGCCGAAATTCTTGCAGATCATCCCGATGCACCCATGTCCCAGGTGTATGGAGCG
CCACATCTCCTGAGATTATTTGTACGAATTGGAGCAATGTTGGCCTATACACCTCTGGATGAGAAGAGCCTTGCT
TTATTACTCAATTATCTTCACGATTTCCTAAAGTACCTGGCAAAGAATTCTGCAACTTTGTTTAGTGCCAGCGAT
TATGAAGTGGCTCCTCCTGAGTACCATCGGAAAGCTGTGTGAGAGGCACTCTCACTCACTTATGTTTGGATCTCC
GTAAACACATTTTTGTTCTTAGTCTATCTCTTGTACAAACAATGTGCTTTGAAGATGTTAGTGTATAACAATTGA
TGTTTGTTTTCTGTTTGATTTTAAACAGAGAAAATAAAAGGGGTAATAGCTCCTTTTTTCTTTTCTTTTTTTTTT
TCATTTCAAAGTTGCTGCCAGTGTTTTCAATGATGGACAACAGAGGGATATGCTGTAGAGTGTTTTATTGCCTAG
TTGACAAAGCTGCTTTTGAATGCTGGTGGTTCTATTCCTTTGACACTATGCACTTTTATAATACATGTTAATGCT
ATATGACAAAATGCTCTGATTCCTAGTGCCAAAGGTTCAATTCAGTGTATATAACTGAACACACTCATCCATTTG
TGCTTTTTTTTTTTTTTTTATGGTGCTTAAAGTAAAGAGCCCATCCTTTGCAAGGCATCCATGTTGTTACTTAGG
CATTTTATCTTGGCTCAAATTGTTGAAGAATGGTGGCTTGTTTCATGGTTTTTGTATTTGTGTCTAATGCACGTT
TTAACATGATAGATGCAATGCACTGTGTAGCTAGTTTTCTGGAAAAGTCAATCTTTTAGGAATTGTTTTTCAGAT
CTTCAATAAATTTTTTCTTTAAATTTC

FIGURE 601

GAGGAGGCGGCAAATCACTTATAAATGGCGCGGAAGCAGGACCCGAAGCCTAAATTCCAGGAGGGTGAGCGAGTG
CTGTGCTTTCATGGGCCTCTTCTTTATGAAGCAAAGTGTGTAAAGGTTGCCATAAAGGACAAACAAGTGAAATAC
TTCATACATTACAGTGGTTGGAATAAAAATTGGGATGAGTGGGTTCCGGAGAGCAGAGTACTCAAATACGTGGAC
ACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCAATCAGGAGCAGTATGCAGAGGGGAAGATGAGAGGGGCT
GCCCCAGGAAAGAAGACATCTGGTCTGCAACAGAAAAATGTTGAAGTGAAAACGAAAAAGAACAAACAGAAAACA
CCTGGAAATGGAGATGGTGGCAGTACCAGTGAGACCCCTCAGCCTCCTTGGAAGAAAAGGGCCCGGGTAGATCCT
ACTGTTGAAAATGAGGAAACATTCATGAACAGAGTTGAAGTTAAAGTAAAGATTCCTGAATAGCTAAAACCGTGG
CTTGTTGATGACTGGGACTTAATTACCAGGCATTATGCAAATTACAAGAAATCTCGTGGAAACACAGATAATAAG
G

FIGURE 602

AATCACTTATAAATGGCGCGGAAGCAGGACCCGAAGCCTAAATTCCAGGAGGGTGAGCGAGTGCTGTGCTTTCAT
GGGCCTCTTCTTTATGAAGCAAAGTGTGTAAAGGTTGCCATAAAGGACAAACAAGTGAAATACTTCATACATTAC
AGTGGTTGGAATAAAAATTGGGATGAGTGGGTTCCGGAGAGCAGAGTACTCAAATACGTGGACACCAATTTGCAG
AAACAGCGAGAACTTCAAAAAGCCAATCAGGAGCAGTATGCAGAGGGGAAGATGAGAGGGGCTGCCCCAGGAAAG
AAGACATCTGGTCTGCAACAGAAAAATGTTGAAGTTACGAATTGGAGCAATGTTGGCCTATACACCTCTGGATGA
GAAGAGCCTTGCTTTATTACTCAATTATCTTCACGATTTCCTAAAGTACCTGGCAAAGAATTCTGCAACTTTGTT
TAGTGCCAGCGATTATGAAGTGGCTCCTCCTGAGTACCATCGGAAAGCTGTGTGAGAGGCACTCTCACTCACTTA
TGTTTGGATCTCCGTAAACACATTTTTGTTCTTAGTCTATCTCTTGTACAAACAATGTGCTTTGAAGATGTTAGT
GTATAACAATTGATGTTTGTTTTCTGTTTGATTTTAAACAGAGAAAATAAAAGGGGTAATAGCTCCTTTTTTCTT

FIGURE 603

TTTTGCGCTCGGACCTTCGCCAGAGGGGCCGGGACATC**ATG**ACGGTGGGAGCCAGGCTCCGAAGCAAGGCGGAGA
GCAGCCTCCTGCGCCGCGGCCCCGAGGGCGAGGGCGAACCGAGGGGGACGAGGAGGCGGCCGCCATCCTGGAGC
ACCTGGAGTACGCGGACGAGGCGGAGGCGGCGGCCGAGAGCGGGACGAGCGCGGCGGACGAGCGGGGCCCGGGGA
CCCGGGGCGCGCGGAGGGTGCACTTCGCCCTCCTGCCCGAGCGCTACGAGCCACTGGAGGAGCCGGCGCCGAGCG
AGCAGCCCAGGAAGAGGTACCGGAGGAAGCTGAAGAAGTACGGCAAGAATGTCGGGAAGGTCATCATCAAAGGAT
GCCGCTACGTGGTCATCGGCCTGCAAGGCTTCGCTGCAGCCTACTCCGCCCCGTTTGCGGTAGCCACCAGCGTGG
TATCCTTCGTGCGC**TAA**TGGGAGCTGCTGTGGCAGGTGCCCCCAGAGTGAACGGGAGCCCCTGCTGTGGGAACTT
TGTGAATCCTGGAGCATCTCAGACTTGAACACACAGCATATTTGGAAGAGAAAACATGCCTTTCTTTGTTGAATC
ACATTAGTATGATGAGTGAGTCATCCCTGCCCATCTGCTGAGCTTCTCACATCTCTCAGTCACACGTGGACCCAG
TGGTCAATCCTGCAGAGAATTCGGCGGAGGTTAGGTTTGGGAGTGGAGCTAGCGTGCTAAAGCCAGAGCCTTCAC
GTGAAGGTGGCAGGCACTGGGGCGGAAGCCAACACTCAACAGATGCAAGCAGTGTGGGTGTGCAGCAGAACAGTG
ATCTTGGGGGAGGAAGAGGATGTTACTAGAGTCAGATGATTTGCTGTATTCTCCTGAAAGGTCGTAGGCTGACAG
GCGCTCACATTCCTTGGCTGCCTCGGTTCTGAGGGCAGCTAAGGAGCTGTTTATTCCTCAAGTCATGCTCCCCGA
TCTCCTTCCTCTACCACTCTGTCACCAGGAGTTTAATTACAGGCTTGAGGAGAAGAAAGGAAGAAAAGATATCTT
GATGCTTTGAAAACTGTGTTGGCAGTGTGGCATGACTGTTTAAAGTAGATAAAACCTTGTCATTTTACCCCATCC
CTGCATGACTGTGAAGCTGGCGAGGAAGGAGGAAGAAGGGCAAGTTCAGATGCAGGCTGGGTGGCTGGGACAGGT
TGGCTAAGGGACTACTCTGGAGGGCTCTTCTGCCTGGCATTGCCCACTTCGGCCCAGCCACGTGTTTGCAGCGAC
CAGAGTCCCTGCAAAGGTGTGGCTGGCTGTGGTCAGGGTGCTACTAGCACCATCAGCGCACTCCCGCCATTGGCT
CAGCTCCTCTCTGCCAGTCCAACTAAGAGTGCTTTGTCCTGGGTGGGACATAGGGGCTGAGAGAGATGGGGGGAG
ACATAACACCCAGGAATGAAAATACAGATTTAGAGAAGGAACCAGTAAGTAGGAGACAGATGTGAAGGAAATGGA
AATGAGGCAAGAGGACATTGGAAGAGAGAAGTTTGCTGTCCAGGAGCCAGGTCTGGAGCATCAGTGTGAGGGAGT
TCAGGTAGGCTGGGCCTGTGCCTCTAGGTAGGGACAAGGGAGGCTGGGTAGCCAGGGCTGGTGCTTAAAACCCCT
GAGGCCATGAGCTCATTGGCTGCCTTTGTAGCATCCTGTCTTCTTCTGTGCTGCCTGGTTTGATCTCATCTCACC
TGGATTCAAAGGGTAAGGTGGGCATGGGTCTTGGGCCTGACACCCACCAAGGATGACCTGTGGACTGCCATCGGA
TGCTGAACAGGGAGATGAAAGGAGGTCCTCTTACCATACCCCTCTGCCAACCCCCCAGTAGGCCACTGTTCTGAC
TTTGTTTCCAGAATATCCAGAAATCCAAAGGGGCTGTTGCTGAACAGTCTGCAGGACCAGTGACAGCACCTACCT
GTTGTCCCAAGGCATACAAAGGAGGCCTCAACGCTCATGCTTCTCTAATCAAGCCCTACCAAGACAGACAGAAAG
ACAGACAGAAAAAAGGAAGGGGTAGAGGAGAAGGTTGAAGCTGTGGAGCTAGACTCTGCTTCACTTCCTGAAGCT
TCAACTTCATGTCGAAGATTCACTGGGACCCAATTCCTGCATTGTTAATATTTGTGAGGAAAAGTGAAACAAGTG
ATCTGGTTTTAGCCCAGATGATGAAAGTGGATATGGCACATTTTCACACACGTGAGATAATTACAGCTTGCCCCA
CAACACTGGGTGTTGGAGAAAGGGAGAGATAGTCATAAGTGGAAGAAAAAGCCAAGCATAGTGAGTGGGAAGGAG
AGTGAGAGCCTGTGCAGGCTGCTGACGAGCCCCAGGCAGCCCACAAGTTTCTCGTGGGGAGATGGAGGCAGAGCC
CAGGGTAGGGGACAGAGCTGCTGGGGCCTTTCCTTGCCTGGGAATCTGTCCCAGGAAGAGCTTCCCCACTCCCAT
CCCCCAAATTGGAAAAACCGTACATTCAAGCCTGTTTGGCCCTGAAATTCTTAAGAATCTGGTTAAGAATTAACT
CACTAATGTCAAAAGTCAAAACCTCCTAGGGGTTGTCCTGGGAGTCAGGTTCACGGGTACAGAAGATGAATCTCA
GATGTCACTCAACCTGAGCCGTCATTCTCTGTGGCAGGGCTGCCCTGGGTTTCTCTTACTCAATCCCTGGAGTGT
AAGCATTTGGATTGTGTCACAGATTACCTTTTTACCTTTTCTTTCTTTTTTTTTCTTTTTTTTCAATATCAGTGCC
CACACCTTACTGAGTATTGAGTTTTAGAGCTTTCGCTTGATGTGCTTGACCAAGAGACTTCTTTTGTATCCTTTT
CTTGTCCTATGATGTAAATAAAAGCCTCGATTTATGT

FIGURE 604

MTVGARLRSKAESSLLRRGPRGRGRTEGDEEAAAILEHLEYADEAEAAAESGTSAADERGPGTRGARRVHFALLP
ERYEPLEEPAPSEQPRKRYRRKLKKYGKNVGKVIIKGCRYVVIGLQGFAAAYSAPFAVATSVVSFVR

FIGURE 605

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACATGCCCACTGATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGCACCTAATAAATGTAAATGTGCTTAAATCTTTTGTCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTACCTCAC
GGCAGTCTCCGCAGATGAGCCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGTTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CGGCCTCTACAGTCCCAACATCTGCCTCACAGCAGATTCTTCAGGCCCAGCATCTGCCTCACTGTGGACCCCCCA
GACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTCTGCAGCCTCTCCAGGCCCAGCTCC
TCCTGCCTCCCAGTGGCCTCTTTCAGCCCAGCCCAGCTCATGCCTCCTGGCGGCCTTCCCAGGCCCTGCTTTTGA
CTTTTGGTGGCCTCTGCAGGCCTCGACAAGGCCCGGCCTCCTGCCTCCCGAA

FIGURE 606

GGCACGAGGGCTCTGTGGAGCTGCGCCTGCCAACTCATTGCTTTCTGCTGTGCTGTGATCCTGCAGTCAGTTGCC
GCTGTTGCTACTGCAATCATTTGCACCAAACTGAGCCAGAGAAGTTCCCTCTTTTAACATAAAGAGTCAAGAAAT
TGGAGC**ATG**GCTATGAGCAATGGAAACAATGATTTTGTGGTTCTGAGCAACAGCAGCATCGCAACCAGTGCTGCT
AACCCGAGTCCCCTCACCCCCTGTGATGGAGACCATGCAGCCCAGCAGCTCACACCCAAAGAAGCAACAAGAACA
AAAGTGAGTCCAAATGGATGCCTGCAACTTAATGGCACGGTCAAATCATCCTTTCTGCCTTTAGACAACCAAAGA
ATGCCTCAGATGTTACCCCAATGCTGCCATCCTTGCCCATACCATCACCCTTTGACTAGCCATAGCAGTCACCAA
GAGTGCCATCCCGAGGCTGGCCCTGCAGCACCCTCTGCTTTGGCCTCGTGTTGCATGCAGCCACACTCCGAGTAT
TCTGCATCTCTTTGTCCAAATCATTCACCTGTGTATCAGACTACGTGCTGTCTTCAGCCCTCTCCATCCTTCTGC
CTGCATCATCCGTGGCCTGACCATTTTCAGCATCAGCCTGTGCAACAGCACATAGCCAACATAAGACCATCCAGA
CCTTTCAAGTTGCCAAAAAGTTATGCAGCCCTGATAGCCGACTGGCCGGTGGTGGTCTTGGGCATGTGCACCATG
TTCATCGTAGTCTGTGCCTTGGTTGGAGTATTAGTGCCAGAGCTCCCTGACTTCTCTGATCCATTGCTGGGTTTT
GAACCAAGAGGAACAGCAATAGGCCAGAGATTGGTCACATGGAATAATATGGTGAAAAATACAGGATACAAAGCA
ACATTAGCAAATTATCCCTTTAAATATGCAGATGAACAAGCCAAAAGCCATCGGGATGATAGATGGTCAGATGAT
CATTATGAAAGAGAGAAAAGAGAAGTTGACTGGAACTTCCACAAGGACAGCTTTTTCTGCGACGTTCCAAGTGAC
CGATATTCCAGAGTGGTATTTACTTCATCTGGAGGGGAGACATTATGGAATTTACCTGCAATTAAATCAATGTGC
AATGTAGATAATTCCAGGATCAGATCTCATCCCCAGTTTGGTGATCTCTGCCAGAGGACCACTGCTGCCTCCTGC
TGCCCCAGCTGGACACTGGGAAACTACATCGCCATTCTGAACAATAGATCGTCCTGTCAGAAAATAGTTGAGCGA
GACGTTTCTCATACCTTGAAGCTGCTTCGGACTTGTGCCAAACACTACCAAAATGGCACTCTGGGGCCAGACTGC
TGGGACATGGCAGCCAGAAGAAAGGACCAGCTCAAGTGCACCAATGTGCCACGCAAATGTACCAAGTACAATGCT
GTGTACCAGATCCTCCATTACTTGGTGGACAAAGACTTTATGACCCCAAAGACGGCTGACTATGCCACGCCAGCT
TTAAAATACAGCATGCTCTTCTCTCCCACAGAGAAAGGGGAGAGCATGATGAACATTTACTTGGACAACTTTGAA
AACTGGAACTCTTCTGACGGCGTGACTACCATCACCGGGATTGAGTTTGGTATCAAACACAGTTTGTTTCAGGAT
TATCTTCTAATGGATACTGTGTATCCTGCCATAGCCATTGTGATTGTCCTTTTAGTTATGTGTGTCTACACCAAG
TCCATGTTTATCACTCTGATGACAATGTTTGCAATAATCAGTTCTTTGATTGTTTCC**TAA**AAAAAAAAAAAAAAA
A

FIGURE 607

MAMSNGNNDFVVLSNSSIATSAANPSPLTPCDGDHAAQQLTPKEATRTKVSPNGCLQLNGTVKSSFLPLDNQRMP
QMLPQCCHPCPYHHPLTSHSSHQECHPEAGPAAPSALASCCMQPHSEYSASLCPNHSPVYQTTCCLQPSPSFCLH
HPWPDHFQHQPVQQHIANIRPSRPFKLPKSYAALIADWPVVVLGMCTMFIVVCALVGVLVPELPDFSDPLLGFEP
RGTAIGQRLVTWNNMVKNTGYKATLANYPFKYADEQAKSHRDDRWSDDHYEREKREVDWNFHKDSFFCDVPSDRY
SRVVFTSSGGETLWNLPAIKSMCNVDNSRIRSHPQFGDLCQRTTAASCCPSWTLGNYIAILNNRSSCQKIVERDV
SHTLKLLRTCAKHYQNGTLGPDCWDMAARRKDQLKCTNVPRKCTKYNAVYQILHYLVDKDFMTPKTADYATPALK
YSMLFSPTEKGESMMNIYLDNFENWNSSDGVTTITGIEFGIKHSLFQDYLLMDTVYPAIAIVIVLLVMCVYTKSM
FITLMTMFAIISSLIVS

FIGURE 608

GCTTCCGCCTCGGCTCCTCTTCCTGCCGGCATCCGGGATCCCTACGTCCCGCGTCCCCCGAGCGCTCGGAGCCTA
CGCGCCCAGCGCTACCGAAACCCAGAGTCCTGCGCCCTGGAGTCCCCGCGCCCCGGAGCCCGAGCACCCGGGAGT
CCCGAGCCTCGCGCCCCGGAGTGCCCGAGCCTGCGCCGCCGCACCCGGATACCCCGGGTCCCCGCGAGCTGCCGA
GGCCGCCCGCCGCCGCCCCGCGGACAGTACCGCCTTCCTCCCCTCTGTCCGCGCCATGGCCGCCCCCGACCTGTC
CACCAACCTCCAGGAGGAGGCCACCTGCGCCATCTGCCTCGACTACTTCACGGATCCGGTGATGACCGACTGCGG
CCACAACTTCTGCCGCGAGTGCATCCGGCGCTGCTGGGGCCAGCCCGAGGCCCGTACGCGTGCCCCGAGTGCCGC
GAGCTGTCCCCGCAGAGGAACCTGCGGCCCAACCGCCCGCTTGCTAAGATGGCCGAGATGGCGCGGCGCCTGCAC
CCGCCGTCGCCGGTCCCGCAGGCGTGTGCCCGCGCACCGCGAGCCACTGGCCGCCTTCTGTGGCGACGAGCTGCG
CCTCCTGTGTGCGGCCTGCGAGCGCTCTGGGGAGCACTGGGCGCACCGCGTTGGCCGCTGCAGGACGCGGCCGAA
GACCTCAAGGCGAAGCTGGAGAAGTCACTGGAGCATCTCCGGAAGCAGATGCAGGATGCGTTGCTGTTCCAAGCC
CAGGCGGATGAGACCTGCGTCTTGTGGCAGAAGATGGTGGAGAGCAGCGGCAGAACGTGCTGCGTGAGTTCGAGC
GTCTTCGCCGTTTGCTGGCAGAGGGAGGGACAGCAGCTGCTGCAGAGGCTGGAGAGGAGGAGCTGAAGGTGCTGC
CCCGGCTGCGGGAGGCGCAGCCCACCTAGGCCAGCAGAGCGCCCACCTAGCTGAGCTCATCGCCGAGCTCGAGAG
GCCGCTGCCAGCTGCCTGCGCTGGGGCTGCTGCAGGACATCAAGGACGCCCTGCGCAGGGTCCAGGATGTGAAGC
TGCAGCCCCCAGAAGTTGTGCCTATGGAGCTGAGGACCGTGTGCAGGGTCCCGGGACTGGTAGAGACACTGCGGA
GGTTTCGAGGGGACGTGACCTTGGACCCGGACACCGCCAACCCTGAGCTGATCCTGTCTGAAGACAGGCGGAGCG
TGCAGCGGGGGGACCTACGGCAGGCCCTGCCGGACAGCCCAGAGCGCTTTGACCCCGGCCCCTGCGTGCTGGGCC
AGGAGCGCTTCACCTCAGGCCGCCACTACTGGGAGGTGGAGGTTGGGGACCGCACCAGCTGGGCCCTGGGGGTGT
GCAGGGAGAACGTGAACAGGAAGGAGAAGGGCGAGCTGTCCGCGGGCAACGGCTTCTGGATCCTGGTCTTCCTGG
GGAGCTATTACAATTCCTCGGAACGGGCCTTGGCTCCACTCCGGGACCCACCCAGGCGCGTGGGGATCTTTCTGG
ACTACGAGGCTGGACATCTCTCTTTCTACAGTGCCACCGATGGGTCACTGCTATTCATCTTTCCCGAGATCCCCT
TCTCGGGGACGCTGCGGCCCCTCTTCTCACCCCTGTCCAGCAGCCCGACCCCGATGACTATCTGCCGGCCGAAAG
GTGGGTCCGGGGACACCCTGGCTCCCCAGTGACTCGGGCCCTCCTGGAGGAGTCCTGTTGCCTCTCCTGCCCCTC
CAGGCCACTGAGTGTTTTGGCCACTTGGAGGACCTGGGAGGAGGGAGTGTGTCCTTTGAGCAAGAGGAGGAACTC
CTGGTGCCTTTCTGAGCCTGCGTGGGAGAACCCCAATTCTAGCACTCCAGGAAACTGTGGGAGAGTGTGGGGCAG
GCTCCGTCCTCCCTGGGAGACCCCTCCAGCCACCGGGTGCCACTTAATGCCAACAGCCCTTACCAAAGCTGGGAG
CCCCATTGCCCCGGCAGCTCTGGCCTGTGGTTCCAGAAGCTGAGAAAACTCCACTGGGGCTTGCAGAATCCAGGG
TTCACCTAAGCTGCACAGTTCCTGCAGCTTTGTCAGCCCCCTGAAAGTCTTGTGTACCCCACCTCTGAAGATGCT
GGGGAAGGCAGCTGGGATGGGAGCCAGCCCCATGCCTGTCTGTGACCCCACAGTGGGTGAGAGCCCGTCACAGTC
CTGGGTGTGGCTGCTCTGGAAGAATTAGGAGGCAGCCATAATAAGAGTCTTCAGAGAGATGATGGGAGGGGCCAG
TGAGGACAGGAACAGAGAGTAGATGTCCTATAATAAAGGGGCTTCTGGGAGGTGCCTGGGCACAGATGTCTGTTC
AGCAGGTGTGTGGGCCTAGAGGAGAGAGCAGAGCCCAGAAATGTCTTTTGCAGGCCCACGTTCTGACTTGAAGCT
TTCGTGGGCATGTTGCCATTGGGTTTTGCCCTTGCAAAGGCTTCCTAGGTCTCCAGTGGCCCCTCAGGACCCAGG
GTCCCAGCTGCTGCTTGGGGATGTGCACTGCTGCGCCGGCCTTGCAGTCTCTCTACCCTGGGGAGGAACAGTGGC
TTCTCAGAGCCTGGGGCATACAGAAGAAGGCAGGAGTTGATTTTTGTGTTGGGTTTGGGGTTTCTTTGTCCTCAA
GGTACTGTTCTGTTTCTCTTTACCCCTCTGCTTTATTTATTGTAAGCATTCCCACGTTAAATAAACTTTGGCTGT
TGTCTAC

FIGURE 609

MELRTVCRVPGLVETLRRFRGDVTLDPDTANPELILSEDRRSVQRGDLRQALPDSPERFDPGPCVLGQERFTSGR
HYWEVEVGDAPAGPWGCAGRT

FIGURE 610

CCGCAGGCAGTAGAGTGAAGCGCGCAGCTGCCAGGACTTGCGCGGTGACGTGCGCCGCTGCCAGGACCTTGCAGG
TGGAGAGCATAGTTGCCAAAATCAAGGCGGAGGAGCGCACCGCCGCTAGGATCCAGGCGGAGAAGCCCACCGCGG
CCAGGACCTAAGG**ATG**CAGTACACTGCTGCCAGGATCTTGTCTGTGGAGCGCAGCGCGGCCAGGACCTCCGGCTG
CAGCACACCGCTGCCAGGATCTTATCGGCAGAGCGCTCCGCGGTCCGGACCCCGCCCCGTGCGCGTCCCCGACCC
CGCCCCGTGCGCGTCCCCGGCGTTGGCGTCTTCGTCCTGTTGCTGGTCTCCGTCCGGTCGCCGGCCGTCTAGGTC
TCCGGCCCTCCCCAGCCGCTCCTGCGCCCTTGCCGGCCCCGCCGCCCGCAGCCCTGGCGCTCCCTGCGGGCCCCG
CCGAGGCCGCCTGCGCCCTGTGCCAGCGCGCGCCCCGGGAACCGGTGCGCGCCGACTGCGGCCACCGCTTCTGTC
GGGCGTGCGTGGTGCGCTTCTGGGCCGAGGAGGACGGGCCCTTCCCGTGCCCCGAGTGCGCCGACGACTGCTGGC
AGCGCGCCGTGGAGCCCGGCAGGCCCCCGCTCAGCCGCCGCCTTCTGGCGCTCGAGGAGGCGGCCGCGGCGCCCG
CGCGCGACGGCCCGGCCAGCGAGGCCGCGCTGCAGCTGCTGTGCCGCGCCGACGCCGGCCCGCTCTGCGCCGCCT
GCCGTATGGCTGCGGGCCCCGAGCCGCCCGAGTGGGAACCGCGCTGGAGGAAGGCGCTGCGCGGCAAGGAGAACA
AGGGGTCTGTGGAAATCATGAGAAAGGACTTGAA**TGA**CGCCCGGGACCTGCATGGCCAGGCAGAGTCAGCAGCTG
CAGTGTGGAAGGGACACGTGATGGACCGTAGGAAGAAGGCACTGACCGACTACAAGAAGCTGCGGGCCTTCTTTG
TGGAGGAGGAGGAGCATTTCCTGCAGGAGGCTGAGAAGGAGGAGGGGCTCCCTGAGGACGAGCTGGCTGACCCCA
CTGAGCGGTTCAGGTCACTGCTGCAGGCGGTCTCGGAGCTGGAGAAGAAGCATCGCAACCTGGGCCTCAGCATGC
TGCTGCAGTGATGGCGCCAACCCGTGGCAGTCCCAGAGCTGGAGGCAGGAGGATGGATCCTCATCTCCATGGGAA
GTGTCAGCGTGTGGCTGCCAGGGAAGCGTGGCAGGCGCCTGGCCTTGGGTCCATCTACATAGTTGCGTGTTTCAA
CAATGTCCATTTATCCTTCACCCCGAGGCGTGTTTTGGGGGCTGCAAACACCTCCCTGTGCTCCACCTGCCTCCG
CAGAAGGAAGCCTCTTTCTCTGTTTCCCTGGGTGAGGGGGCTGGCAGGTGGCTAACCCCATTTAGCATCTCCAGG
CCCTGCCATCGTGTCTCATCTTGCTGTTATCTCTAGCTCTTTCCCTCCTCCCATTTCCTTTAGTAGTTGAATTTT
GCAAAGCTTGTAGCAGTAGCTCAGTTGCCTGCAGCATCCTTGTGTGTAGATAAATTAGTCGACAGAAACTCAGCA
CTGGGGACAGGATTGCAAAGTCGGGGACATAGATGCAGACAGTTGTTGAGATTTGGGGATAGCCGGGCTTGTGAG
CGGTGCCCATTTCCAGATGAAGCCTTTCAGCCCTTCTGAGTCCCCGGCCCTTGGTGCGATGTCTGTGAGTTTGAC
CTGCCCAGCGTGTGGGCTGGCTCAATGCTGAATAAAGTGGGTTTGTGTCAGCTCGTTTGCTTCGTCTCCGTGTGT
CCACCTGGCCTCTTCCCCCTGCCCTGGCCACCCTCCAGTGTCAAAGGAAACTTCCTCGTGACACGTGCTAAAGCA
TGGTGAGGAGGACTTTGATTGGGACCATTGAGATGGGTGTGGGACCCTTTCCTTGGGGCCTGGGGGGAGATGGGG
CTCCACCCCGACGTAGCAGGGCAGGGGTTGGAGGAGCGAGGAGCAGTATAGGGTCCATGGGTGGGAATGACTGTG
AGGAGACATCAGGGCTGAGGGGGCTCTGGCTAAACCCACCTCACAGAGTCCTTGCTGCAGGCAGGCAGGGCGATC
AGA

FIGURE 611

MQYTAARILSVERSAARTSGCSTPLPGSYRQSAPRSGPRPVRVPDPAPCASPALASSSCCWSPSGRRPSRSPALP
SRSCALAGPAARSPGAPCGPRRGRLRPVPARAPGTGARRLRPPLLSGVRGALLGRGGRALPVPRVRRRLLAARRG
ARQAPAQPPPSGARGGGRGARARRPGQRGRAAAAVPRRRRPALRRLPYGCGPRAARVGTALEEGAARQGEQGVCG
NHEKGLE

FIGURE 612

GGCACGAGGCGCTGGCCGGGCTGGCTGCGGCCGCCCTGGGCCGGGCCCCACCGGACGGCTTGCTCTGCTCTTTAC
CTGGGGTTGCTGTCGAGGACCCTGTGCAAGACTCGGCCGGTTTTTCTTTCTCCCTGATGGACAGACCCAAACATA
GCCGCGCAGCATCGTGAAGGGCTGGGGCCTTCACTCCTCTGTGGCTCTGGAAGAGCCCGATTTCCTCAGGAGGC**A**
TGTCGGGCCCCAGGCCTGTGGTGCTGAGCGGGCCTTCGGGAGCTGGGAAGAGCACCCTGCTGAAGAGGCTGCTCC
AGGAGCACAGCGGCATCTTTGGCTTCAGCGTGTCCCATACCACGAGGAACCCGAGGCCCGGCGAGGAGAACGGCA
AAGATTACTACTTTGTAACCAGGGAGGTGATGCAGCGTGACATAGCAGCCGGCGACTTCATCGAGCATGCCGAGT
TCTCGGGGAACCTGTATGGCACGAGCAAGGTGGCGGTGCAGGCCGTGCAGGCCATGAACCGCATCTGTGTGCTGG
ACGTGGACCTGCAGGGTGTGCGGAACATCAAGGCCACCGATCTGCGGCCCATCTACATCTCTGTGCAGCCGCCTT
CACTGCACGTGCTGGAGCAGCGGCTGCGGCAGCGCAACACTGAAACCGAGGAGAGCCTGGTGAAGCGGCTGGCTG
CTGCCCAGGCCGACATGGAGAGCAGCAAGGAGCCCGGCCTGTTTGATGTGGTCATCATTAACGACAGCCTGGACC
AGGCCTACGCAGAGCTGAAGGAGGCGCTCTCTGAGGAAATCAAGAAAGCTCAAAGGACCGGCGCC**TGA**GGCTTGC
TGTCTGTTCTCGGCACCCCGGGCCCATACAGGACCAGGGCAGCAGCATTGAGCCACCCCCTTGGCAGGCGATACG
GCAGCTCTGTGCCCTTGGCCAGCATGTGGAGTGGAGGAGATGCTGCCCCTGTGGTTGGAACATCCTGGGGTGACC
CCCGACCCAGCCTCGCTGGGCTGTCCCCTGTCCCTATCTCTCACTCTGGACCCAGGGCTGACATCCTAATAAAAT
AACTGTTGGATTAGAAAAAAAAAAAAAAAAAA

FIGURE 613

MSGPRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQRDIAAGDFIEHAE
FSGNLYGTSKVAVQAVQAMNRICVLDVDLQGVRNIKATDLRPIYISVQPPSLHVLEQRLRQRNTETEESLVKRLA
AAQADMESSKEPGLFDVVIINDSLDQAYAELKEALSEEIKKAQRTGA

FIGURE 614

GGCACGAGGTCGGGCCTGGGTCCGACGGTAGTGGGTAGCGGGTCTCGGGTTGCGGGTTGCAGGTTGCAAGCCGCA
GGCCCCAGGCAACTGCCTTCCCGGCGCC**ATG**TTCGGCTCCAGTCGTGGAGGCGTGCGCGGCGGGCAGGACCAGTT
CAACTGGGAGGACGTGAAGACTGACAAGCAGCGGGAGAACTACCTGGGCAACTCGCTGATGGCGCCGGTAGGCCG
CTGGCAGAAGGGCCGCGACCTCACCTGGTACGCCAAGGGCCGGGCGCCATGCGCGGGCCCGAGCCGCGAGGAGGA
ACTGGCAGCCGTGCGGGAGGCGGAGCGCGAGGCGCTGCTGGCCGCCCTTGGCTACAAGAACGTGAAGAAGCAGCC
CACGGGCCTGAGCAAGGAGGACTTCGCGGAGGTCTGCAAGCGGGAAGGAGGCGACCCCGAGGAGAAGGGCGTGGA
CCGGCTGCTGGGGCTGGGGAGCGCAAGTGGCTCCGTGGGCCGCGTGGCGATGTCCCGAGAGGACAAGGAGGCCGC
CAAACTGGGGCTGTCTGTGTTCACGCATCACCGCGTAGAGAGCGGCGGGCCCGGGACCTCGGCAGCCTCGGCCAG
GAGGAAGCCGCGGGCGGAGGATCAGACGGAAAGCAGTTGTGAGAGCCACAGGAAAAGCAAGAAGGAGAAGAAGAA
AAAGAAAAAGAGGAAACACAAGAAAGAGAAGAAGAAGAAAGACAAAGAGCACAGGCGGCCAGCTGAGGCCACCTC
CTCTCCCACATCTCCTGAGAGGCCCAGGCACCACCACCATGACTCCGACTCCAACTCCCCCTGCTGTAAGAGGAG
GAAGCGGGGACACAGTGGGGACAGGAGGAGCCCGTCTCGCAGGTGGCATGACAGAGGCTCTGAGGCC**TGA**TGGCT
GGACCCTGCTCACTGCTGTTGTGGACCCTGAACCCTCCCTTCACCTTGCTTGCCTCCTGCCTCGGAAGCTCCTT
GGGTGTGGGTGAAGCCCGAGGCTGCTCCTGTGGAAGTGGCTCTGGGCACCAGCCTGTGGGGCTAAAGACTTGACA
GCTAGCTCTGGAGCAGCCGGCTTCCTGGAAAACCTCCAGGTTTCGCATACCAGGGATGGCCCCTGGCTTGGCCTG
CGAAGGTGAACCTGCCCAGATTTATCAGTAGAGGCTGGACTCCCTCTGTGTCCTGCCCATGGTTGCAGCAGCCAT
GGGCCTATGAGCGGTCTAACTGTGGCCAAGTATGGTGACCTCTATTTTTCTTTATATTGACTCTTTGTATTTCAA
TAAATATATTTTAAAAGGAAGGTAAAAAAAAAAAAAAAAAA

FIGURE 615

MFGSSRGGVRGGQDQFNWEDVKTDKQRENYLGNSLMAPVGRWQKGRDLTWYAKGRAPCAGPSREEELAAVREAER
EALLAALGYKNVKKQPTGLSKEDFAEVCKREGGDPEEKGVDRLLGLGSASGSVGRVAMSREDKEAAKLGLSVFTH
HRVESGGPGTSAASARRKPRAEDQTESSCESHRKSKKEKKKKKKRKHKKEKKKKDKEHRRPAEATSSPTSPERPR
HHHHDSDSNSPCCKRRKRGHSGDRRSPSRRWHDRGSEA

FIGURE 616

AGGAAGCCCTGCTTGATGAGCATGAGGCTCCACGGGGGCAGTGGCTGTGACGGTGAGTGCCACACAGAGCTGCCC
ACACTGGTGGAGGGAAGGCAGGGAGATACCAGGACCATCCGGAAGGGGCTGAGTGTCATTTGACAGGTGCCATGT
GAGCAGAGATGTGAAGGAGTGGCCCGGGACAATCAGGGCAGAATCCCTGAGGTGTCCCTGGCCAGTGTCCTTCCA
CCTGTCCACAAGCATGGGGAACATCTTCGCCAACCTCTTCAAGGGCCTTTTTGGCAAAAAAGAAATGCGCATCCT
CATGGTGGGCCTGGATGCTGCAGGGAAGACCACGATCCTCTACAAGCTTAAGCTGGGTGAGATCGTGACCACCAT
TCCCACCATAGGCTTCAACGTGGAAACCGTGGAGTACAAGAACATCAGCTTCACTGTGTGGGACGTGGGTGGCCA
GGACAAGATCCGGCCCCTGTGGCGCCACTACTTCCAGAACACACAAGGCCTGATCTTCGTGGTGGACAGCAATGA
CAGAGAGCGTGTGAACGAGGCCCGTGAGGAGCTCATGAGGATGCTGGCCGAGGACGAGCTCCGGGATGCTGTCCT
CCTGGTGTTCGCCAACAAGCAGGACCTCCCCAACGCCATGAATGCGGCCGAGATCACAGACAAGCTGGGGCTGCA
CTCACTACGCCACAGGAACTGGTACATTCAGGCCACCTGCGCCACCAGCGGCGACGGGCTCTATGAAGGACTGGA
CTGGCTGTCCAATCAGCTCCGGAACCAGAAGTGAACGCGACCCCCCTCCCTCTCACTCCTCTTGCCCTCTGCTTT
ACTCTCATGTGGCAAACGTGCGGCTCGTGGTGTGAGTGCCAGAAGCTGCCTCCGTGGTTTGGTCACCGTGTGCAT
CGCACCGTGCTGTAAATGTGGCAGACGCAGCCTGCGGCCAGGCTTTTTATTTAATGTAAATAGTTTTTGTTTCCA
ATGAGGCAGTTTCTGGTACTCCTATGCAATATTACTCAGCTTTTTTTATTGTAAAAAGAAAAATCAACTCACTGT
TCAGTGCTGAGAGGGGATGTAGGCCCATGGGCACCTGGCCTCCAGGAGTCGCTGTGTTGGGAGAGCCGGCCACGC
CCTTGGCTTTAGAGCTGTGTTGAAATCCATTTTGGTGGTTGGTTTTTAACCCAAACTCAGTGCATTTTTTAAAAT
AGTTAAGAATCCAAGTCGAGAACACTTGAACACACAGAAGGGAGACCCCGCCTAGCATAGATTTGCAGTTACGGC
CTGGATGCCAGTCGCCAGCCCAGCTGTTCCCCTCGGGAACATGAGGTGGTGGTGGCGCAGCAGACTGCGATCAAT
TCTGCATGGTCACAGTAGAGATCCCCGCAACTCGCTTGTCCTTGGGTCACCCTGCATTCCATAGCCATGTGCTTG
TCCCTGTGCTCCCACGGTTCCCAGGGGCCAGGCTGGGAGCCCACAGCCACCCCACTATGCCGCAGGCCGCCCTAC
CCACCTTCAGGCAGCCTATGGGACGCAGGGCCCCATCTGTCCCTCGGTCGCCGTGTGGCCAGAGTGGGTCCGTCG
TCCCCAACACTCGTGCTCGCTCAGACACTTTGGCAGGATGTCTGGGGCCTCACCAGCAGGAGCGCGTGCAAGCCG
GGCAGGCGGTCCACCTAGACCCACAGCCCCTCGGGAGCACCCCACCTCTGTGTGTGATGTAGCTTTCTCTCCCTC
AGCCTGCAAGGGTCCGATTTGCCATCGAAAAAGACAACCTCTACTTTTTTCTTTTGTATTTTGATAAACACTGAA
GCTGGAGCTGTTAAATTTATCTTGGGGAAACCTCAGAACTGGTCTATTTGGTGTCGTGGAACCTCTTACTGCTTT
CAATACACGATTAGTAATCAACTGTTTTGTATACTTGTTTTCAGTTTTCATTTCGACAAACAAGCACTGTAATTA
TAGCTATTAGAATAAAATCTCTTAACTATT

FIGURE 617

MGNIFANLFKGLFGKKEMRILMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIR
PLWRHYFQNTQGLIFVVDSNDRERVNEAREELMRMLAEDELRDAVLLVFANKQDLPNAMNAAEITDKLGLHSLRH
RNWYIQATCATSGDGLYEGLDWLSNQLRNQK

FIGURE 618A

GTGGGACCATCCAGTTGCAGGAAAACAAGCTTAACACGCCCACTGATTCTACATTATGCTCCTACCTCCCAGCAG
CCTCTCCAGGCCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCC
CATACCCTACCTCACGGCAGTCTCCGCAGATGAGCCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCG
TTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCT
CACCAGGCCCAGCTCATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCACCTCCAGGCCCA
GCCTCTGCCTCCCGTCGGCCTCTACAATCCCAACATCTGCCTCACAGCAGATTCTTCAGGCCCAGCATCTGCCTC
ACTGTGGACCCCCCAAGCCAAGCTCCCAACCTTTCAGCAGCTTCTACACACCCAACTCCTGCCACCCAGTGGCCT
CTTTAGGCCAAGCTCATGCTTCACAAGGGCCTTTCCAGGCTCAACTTTTGTCTCATGGCAACCTTTCCTGGCCAG
ATTCCTGCCTGTCTCCCAGCAGCCTAGACAGGCCCAGGTCTTGCCTCACACTGGCCTCTCTACATCCAGCTCATG
CCTCACGGTGGCCTCTCCAGGCCCAACTCCTGTCCCAGGACGTCATCTCCGGGCCCAAAACTTACTCAAGTCAGA
CTCTCTAGTCCCAACTGCTGCCTCCTGGTGGCCTATGAAGGCCCAAAATCTCCTCAAGTGGACCTCTCCAGGCCC
AGCTCCTGCCTCCTGTCAGCGTCTACAGGCCCAACCTCTGCCTCATGGGGGCTTCTCCAGGCCCACCTCTTCCTC
TTGGCTGGGTCTACAGGCACAACTGCTGCCTCACAACAGCCTTTTTTGGCCCAGTTCCTGTCCAGCTCATGGCGG
CCAATGTAGGCCCAAAACTTCCTCAAGTCAAACTCTCCAGGCCCACCTTCTGCTTCCCGGTGGCATGAACAGGCC
CAGCTTTGACTTGAGAACAGCCTCTGCAGGCCCTGCTCTTGCCTCCCAGGGGCTTTTTCCAGACCCAGCTCCTGC
CTCATGGCAGCTGCCCCAGGCCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTCCTCCCTCACAG
TGGCCCATTTAGGCCCAACTCATGACTGTCGGGCCATTTCCAGGCCTAGTGCCTGCCTCGTGGCTGACTCTTGAA
GCCCAAAACTTCCTCAAATCAGCCTTTTGCCCAACTTCTGTCTACTGTCGGACTCTACAGGCCAGCCTCTGCCTC
ACAGTGGACCCTCCAGACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCCGCAGCCTC
TACAGGCCCAGCTCCTGCCTTGCAGTGGCCTCTTTAGGCCAAGCTCATGCCCCATGGCGACTTTTCCAGGCACAG
CTTTTGCCTTTTGCAGCCTGTCGAGGCCCAGAATGTCCTTAACTCGGCATCTCCAGGATGAGCTCATCCTCCCAG
TGCGTCTACAGGCCCGTCTCCTGCCTCACAACAACCTCCTTTGGCCCAACTCCTGCTGAGCTGCTGGCAGCCTCT
GTAGGCCACAGAATTCTTAAGGTAAAGCTTTCCAGGCCCACCTTTGGCCTCCCGGCAGGCTCAGCAATCAAACTA
TTCCCTCACTGCGGCCACCGAAAGCCAAGTTTCTCCCTGCCTCACGGCATCCTCCGAAAACTGAGCATTTGCCTC
ACGGTGGCCTCCCCAGGCCATGAATCTGCCTGCCTCCCAGGCAGCTGCTGCCTCACAATGGTCTCTTTAGGCCCA
GCTCATGCTAAAAGATGGACTCTCCAGGCACAGCTCTTGCCTCCTGGCAGCCTCTGCAGGCCCAAATTCTCCAAA
AGTTGGCCTCTCCTAACTCAGCTCCTGCCTCATGTCTGCCTACACAGGCCCAGACTCTTACCACACAGTAGACCC
TCCAGGCCCACCACTTGCCTGATCATAGCCTCCTAAGGCCAAGCTCCTGCCTTTCGGCAGCCTCTACAGGCCAAG
CTCCTGCCTCGCAATTGCCTCTGTAGGCCAAGATCATGCCGTGAAGTGGCCTTCCCTAGCCTAACTTTTGCTTTT
TGACGCATACTCCAGTCCCAAAACTTCCTCCAGTCAGCCGGTCCAGGCCAAGCTCTTCCTCCCAAAGGCTTCTGC
AGGCCAAAATCATCCTGAAGTCACCCTCTGCAGGCGCAGCTCCTGCCTCCAAGTGCTGTGTAGGCCAAGCTAATG
CCTCACAGCACACTTTCCAGGCTGAGCATTTCCTTTTGTGCATCCTCTCCAAGCCCTGAACTTACTCCAGTTGGC
CTCTCCAGACCAAGCTCTCCCTCCCAGTGGCCTCTACAGGCCAAAATTGTCCTCAGGTCAGCCTCTCCAGGGCCA
ACTCCTAGCTACCGGTGGCTTCTGCAGGCCAAAATCGACCTCAAGTCAGCCTCTTCACACCCAGCTCTTGCCTCT
GAGTGGCCTCTCCAGGAGCAAAACTTTCTCAAGTCGGCCTCTCCAGGCCCAGCCTCCTGCTTCCCGAGGGCATGT
ACAGGCCCAGCCTCTGCCTCACAGCAGACTCTTCACACCCAGCTCTTCCCTGTCTGCGGCCTCTCCAGTCCAAAG
CTGCTCCTGCCTTTTGGCAGCTTGTACAGGCCCAGCTCCTCCCTCACGGTGGCCTCTTTCGGCCCAACTCATGCC
TCTTGCAACGTGCCCAAGTGTCAGCTCCTGCCTCACACTGGCCTGTTGAGGCCCAGCTCATGCCTCTCGTGGCCT
CAACGGGCCCATCCCCTGCCTGTCGGCGGCCTCTACAGGCCCGGCCTCTACCTCACAGTGGGCTCTCCAGGCCCA
CCTCTTCCTCACCGTGGCCTCCTGGGGCAATGCTCCTCCCTCTCGGGAGCCTCTGTGGGCCCAGCTCCTGCCTCC
CAGTGGCCTCTGCTGGCCAAGCCCGTGCCTCAGGGCAGCCTTTCCAGGCCTAGCGTTTGCTGCTTTGCATCCTCT
CCAGGCCCTGGACTTCCTCCAGTCGGCCTCTCCAGGCCCAGCTCTTCCTCTCGGCGGCCTCTGCAGGCCCAGACT
GTCGTCAAGTCGGCCTGTCCAGGGCCAGCTCCTGCCTCCCGGCGGCCTCTGCAGGCCCAAGTCGTCCTCAAGTTG
GCCTCCCCAGGCCCAGCAACGGCCTCTCGGCGGCCTTTCCGGGTGCAAAAGTTCCTCGAGTCAGCCTCTCCAGGC
CCAGCTCCTCCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAGGCCCT
GCTTTTGACTTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCAGGCCTCCTGCCTCCCAAAGGCCTGCACAGGCCC
AGCCTCTGCCTCACAGCAGACTCTCCACGCCCAGCTAGCTCTCGCCTCACTGCGGCTTCCCGAGTCCAAAGCTCC
TGCCTCTCAGCCGCTTCGGCAGGCCCAGCTCCCGCCTGCCAGTGGCCTCTTCAGGCCCATGGGGCTCATTCCTCA

FIGURE 618B

CAACGGCCTTTCCAGGCCCAGTTTTTCCCTTCCGGCGGCCTCTTGGCCTCTAATTTGTTTATCTTTTGGGTATAA
ATCCCAAAATATTGAATTTTGGAATATTTCCACCATT

FIGURE 619

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCACTGATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGTAAATGTGCTTAAATCTTTTGGCCCAGCTCCTACCTCCCAGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTACCTCAC
GGCAGTCTCCGCAGATGAGCCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCACCTCCAGGCCCAGCCTCTGCCTCCCGT
CGGCCTCTACAATCCCAACATCTGCCTCACAGCAGATTCTTCAGGCCCAGCATCTGCCTCACTGTGGACCCCCCA
GACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCCGCAGCCTCTCCAGGCCCAGCTCC
TCCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGGCTCTCGGCGGCCTTCCCAGGCCCCGCTTTTGA
CTTTTGGCGGCCTCTTCAGGCC

FIGURE 620

TTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAGAGGGAACATGCTGAGAAACTG**ATG**AAGCTG
CAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTG
AATGCGATGGAGTGTGCATTACATTTGGAAAAAAGTGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCACT
GACAAAAATGACCCCCATTTGTGTGACTTCATTGAGACACATTACCTGAATAAGCAGGTGAAAGCCATCAAAGAA
TTGGGTGAGCACGTGACCAACTTGTGCAAGATGGGAGCGCCCGAATCTGGCTCGGCGGAATACCTCTTAGACAAG
CACACCCTGGGGGACAGTGATAATGAAAGC**TAA**GCCTCAGGCTAATTTCCACATAGCCGTGGGAGTGACTTCCCT
GGTCACCAAG

FIGURE 621

MKLQNQRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKSVNQSLLELHKLATDKNDPHLCDFIETHYLNKQVKA
IKELGEHVTNLCKMGAPESGSAEYLLDKHTLGDSDNES

FIGURE 622

ATGGCCGGCACAAAGATGGGGCGGGAGGACAGCGTGCTGGATACGGCGTGGGGCGGGTCCGCGGCCCGGGAGACC
CATGCTGGGGCGGCCCTGTCACTCGTCTCGCTGCCAAGCACAGGGCTGAGGTGCGGAGGGACCACTGAGAGGACT
TCGCTGCGTGTCAGCTCAGCTCTGGACGGCGTGGAGGAGCCCTGGAAACTTTATTTACAAAAACTGACAGCAGCT
GCCCTTAGTTTGGCAGCTGGAAAATGGGAAAGAGAAAGTAAGAGGAAGGGTGGCAAAGGAGGGAGCCCATGTGGA
CAGCAGGAACGGGTACACGATAGCACAAGAATCAAAACAAAGGCTCTCTGGTCGGAGTTTAGAAAGGCTGAAGGG
GATACTAAAGGAGGAGATAAAGCCCAGGTGAAGGACGAACCACAGAATAGATCCGCGAGGTTGTCTGCTAAACCT
GCTCCTCCAAAACCAGAGCCCAAGCCTAAAAAGGCCCCTGCAGAGACAGTACCCAAAGGGAAAAAGGGAAAAGCT
GTTGCTGGCAAGGAGGGGAATAACCCTGCAGAAAATGGAGATGCCAAAACAGACCAGGCACAGAAAGCTGAAGGT
GCTGGAGATGCCAAGGCAAATCTGCTGCCACGGTGTGGCAGCAAAGAAATGAAAGGAAGTGTCTGGCAGCGCAGG
GGAGAAATTGTGTTTCCTCCTTCTCCAAAGGTTCACCTTTTCTATTTCACCTTCATCATTCATAAGAAGGTGAAA
GGATGCCAGGAGCAAGGCGGATCTACGGGACTTTTGAAAAGAAATGTACTGACCTTTGGCTGTAAAAACTGTGTC
ATGAGAACAGAAAGCCCTGAGAGAAGAAGACAGCCATTCATGGGATCTATGGCGCACTCTGTGCTAGGGCAGAAT
GCCAGGGAAGAGCTGCCTGTCTTCAGCGCCCTTGCTGGGAACCACACGCCAGAACCCGACCCTGCCATGCTTTGT
GCTTCAGGCAGCAGGACCCCACCCCTAACAGAGTCTCAAGTCAGACAC**TAA**

FIGURE 623

MAGTKMGREDSVLDTAWGGSAARETHAGAALSLVSLPSTGLRCGGTTERTSLRVSSALDGVEEPWKLYLQKLTAA
ALSLAAGKWERESKRKGGKGGSPCGQQERVHDSTRIKTKALWSEFRKAEGDTKGGDKAQVKDEPQNRSARLSAKP
APPKPEPKPKKAPAETVPKGKKGKAVAGKEGNNPAENGDAKTDQAQKAEGAGDAKANLLPRCGSKEMKGSVWQRR
GEIVFPPSPKVHLFYFTFIIHKKVKGCQEQGGSTGLLKRNVLTFGCKNCVMRTESPERRRQPFMGSMAHSVLGQN
AREELPVFSALAGNHTPEPDPAMLCASGSRTPPLTESQVRH

FIGURE 624

AAGAAGCTGCCGTTGTTCTGGGTACTACAGCAGAAGGGT<u>ATG</u>CGGAAGCGAGCACCCCAGTCTGAGATGGCTCCT
GCCGGTGTGAGCCTGAGGGCCACCATCCTCTGCCTCCTGGCCTGGGCTGGCCTGGCTGCAGGTGACCGGGTGTAC
ATACACCCCTTCCACCTCGTCATCCACAATGAGAGTACCTGTGAGCAGCTGGCAAAGGCCAATGCCGGGAAGCCC
AAAGACCCCACCTTCATACCTGCTCCAATTCAGGCCAAGACATCCCCTGTGGATGAAAAGGCCCTACAGGACCAG
CTGGTGCTAGTCGCTGCAAAACTTGACACCGAAGACAAGTTGAGGGCCGCAATGGTCGGGATGCTGGCCAACTTC
TTGGGCTTCCGTATATATGGCATGCACAGTGAGCTATGGGGCGTGGTCCATGGGGCCACCGTCCTCTCCCCAACG
GCTGTCTTTGGCACCCTGGCCTCTCTCTATCTGGGAGCCTTGGACCACACAGCTGACAGGCTACAGGCAATCCTG
GGTGTTCCTTGGAAGGACAAGAACTGCACCTCCCGGCTGGATGCGCACAAGGTCCTGTCTGCCCTGCAGGCTGTA
CAGGGCCTGCTAGTGGCCCAGGGCAGGGCTGATAGCCAGGCCCAGCTGCTGCTGTCCACGGTGGTGGGCGTGTTC
ACAGCCCCAGGCCTGCACCTGAAGCAGCCGTTTGTGCAGGGCCTGGCTCTCTATACCCCTGTGGTCCTCCCACGC
TCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAAGATTGACAGGTTCATGCAGGCTGTGACAGGATGGAAG
ACTGGCTGCTCCCTGATGGGAGCCAGTGTGGACAGCACCCTGGCTTTCAACACCTACGTCCACTTCCAAGGGAAG
ATGAAGGGCTTCTCCCTGCTGGCCGAGCCCCAGGAGTTCTGGGTGGACAACAGCACCTCAGTGTCTGTTCCCATG
CTCTCTGGCATGGGCACCTTCCAGCACTGGAGTGACATCCAGGACAACTTCTCGGTGACTCAAGTGCCCTTCACT
GAGAGCGCCTGCCTGCTGCTGATCCAGCCTCACTATGCCTCTGACCTGGACAAGGTGGAGGGTCTCACTTTCCAG
CAAAACTCCCTCAACTGGATGAAGAAACTGTCTCCCCGGACCATCCACCTGACCATGCCCCAACTGGTGCTGCAA
GGATCTTATGACCTGCAGGACCTGCTCGCCCAGGCTGAGCTGCCCGCCATTCTGCACACCGAGCTGAACCTGCAA
AAATTGAGCAATGACCGCATCAGGGTGGGGGAGGTGCTGAACAGCATTTTTTTTGAGCTTGAAGCGGATGAGAGA
GAGCCCACAGAGTCTACCCAACAGCTTAACAAGCCTGAGGTCTTGGAGGTGACCCTGAACCGCCCATTCCTGTTT
GCTGTGTATGATCAAAGCGCCACTGCCCTGCACTTCCTGGGCCGCGTGGCCAACCCGCTGAGCACAGCA<u>TGA</u>GGC
CAGGGCCCCAGAACACAGTGCCTGGCAAGGCCTCTGCCCCTGGCCTTTGAGGCAAAGGCCAGCAGCAGATAACAA
CCCCGGACAAATCAGCGATGTGTCACCCCCAGTCTCCCACCTTTTCTTCTAATGAGTCGACTTTGAGCTGGAAAG
CAGCCGTTTCTCCTTGGTCTAAGTGTGCTGCATGGAGTGAGCAGTAGAAGCCTGCAGCGGCACAAATGCACCTCC
CAGTTTGCTGGGTTTATTTAGAGAATGGGGGTGGGGAGGCAAGAACCAGTGTTTAGCGCGGGACTACTGTTCCA
AAAAGAATTCCAACCGACCAGCTTGTTTGTGAAACAAAAAAGTGTTCCCTTTTCAAGTTGAGAACAAAAATTGGG
TTTTAAAATTAAAGTATACATTTTTGCATTGCCTTCGGTTTGTATTTAGTGTCTTGAATGTAAGAACATGACCTC
CGTGTAGTGTCTGTAATACCTTAGTTTTTCCACAGATGCTTGTGATTTTTGAACAATACGTGAAAGATGCAAGC
ACCTGAATTTCTGTTTGAATGCGGAACAATAGCTGGTTATTTCTCCCTTGTGTTAGTAATAAACGTCTTGCCAC

FIGURE 625

MRKRAPQSEMAPAGVSLRATILCLLAWAGLAAGDRVYIHPFHLVIHNESTCEQLAKANAGKPKDPTFIPAPIQAK
TSPVDEKALQDQLVLVAAKLDTEDKLRAAMVGMLANFLGFRIYGMHSELWGVVHGATVLSPTAVFGTLASLYLGA
LDHTADRLQAILGVPWKDKNCTSRLDAHKVLSALQAVQGLLVAQGRADSQAQLLLSTVVGVFTAPGLHLKQPFVQ
GLALYTPVVLPRSLDFTELDVAAEKIDRFMQAVTGWKTGCSLMGASVDSTLAFNTYVHFQGKMKGFSLLAEPQEF
WVDNSTSVSVPMLSGMGTFQHWSDIQDNFSVTQVPFTESACLLLIQPHYASDLDKVEGLTFQQNSLNWMKKLSPR
TIHLTMPQLVLQGSYDLQDLLAQAELPAILHTELNLQKLSNDRIRVGEVLNSIFFELEADEREPTESTQQLNKPE
VLEVTLNRPFLFAVYDQSATALHFLGRVANPLSTA

FIGURE 626

GAATTCGGCACGAGCCGGGATCCTGTGTAGCGGCTGCAGAGGGTGCCGCCGCCCTAGGCGAAGTAGGGCCGTCCT
GAGCGAAAGAACCGCCCCCAGCAGGAGCACCACCACGGCTTAGCAAAGAATCCCAGACCCCGCCCGGGAAGGCAG
CCGCACC**ATG**GAGTCTTCCAGTTCATCTAACTCTTATTTCTCCGTTGGCCCAACCAGTCCCAGCGCTGTCGTGCT
CCTCTACTCGAAGGAGCTCAAAAAGTGGGATGAGTTTGAAGATATTTTAGAAGAGAGGAGGCATGTCAGTGACTT
GAAATTTGCAATGAAATGCTACACACCTCTTGTCTATAAGGGAATTACTCCATGTAAACCAATTGATATTAAATG
TAGTGTTCTCAATTCTGAGGAGATTCATTATGTCATTAAACAGCTTTCCAAGGAATCCCTTCAATCTGTGGATGT
CCTCCGAGAGGAAGTGAGTGAGATCTTAGATGAAATGAGTCACAAACTGCGTCTTGGAGCCATTCGGTTTTGTGC
CTTCACCCTGAGCAAAGTATTTAAACAAATTTTCTCGAAGGTGTGTGTAAATGAAGAAGGTATTCAGAAACTACA
AAGAGCCATCCAGGAGCATCCTGTTGTTCTGCTGCCTAGTCATCGAAGTTACATTGACTTCCTCATGTTGTCTTT
TCTTCTATACAATTATGATTTGCCTGTGCCAGTTATAGCAGCAGGAATGGACTTCCTGGGAATGAAAATGGTTGG
TGAGCTGCTACGAATGTCGGGTGCCTTTTTCATGCGGCGTACCTTTGGTGGCAATAAACTCTACTGGGCTGTATT
CTCTGAATATGTAAAAACTATGTTACGGAATGGTTATGCTCCTGTTGAATTTTTCCTCGAAGGGACAAGAAGCCG
CTCTGCCAAGACATTGACTCCTAAATTTGGTCTTCTGAATATTGTGATGGAGCCATTTTTTAAAAGAGAAGTTTT
TGATACCTACCTTGTCCCAATTAGTATCAGTTATGATAAGATCTTGGAAGAAACTCTTTATGTGTATGAGCTTCT
AGGGGTTCCTAAACCAAAAGAGTCTACAACTGGGTTGCTGAAAGCCAGAAAGATTCTCTCTGAAAATTTTGGAAG
CATCCATGTGTACTTTGGAGATCCTGTGTCACTTCGATCTTTGGCAGCTGGGAGGATGAGTCGGAGCTCATATAA
CTTGGTTCCAAGATACATTCCTCAGAAACAGTCTGAGGACATGCATGCCTTTGTCACTGAAGTTGCCTACAAAAT
GGAGCTTCTGCAAATTGAAAACATGGTTTTGAGCCCCTGGACCCTAATAGTTGCTGTTCTGCTTCAGAACCGGCC
ATCCATGGACTTTGATGCTCTGGTGGAAAAGACTTTATGGCTAAAAGGCTTAACCCAGGCATTTGGAGGGTTTCT
CATTTGGCCTGATAATAAACCTGCTGAAGAAGTTGTCCCGGCCAGCATTCTTCTGCATTCCAACATTGCCAGCCT
TGTCAAAGACCAGGTGATTCTGAAAGTGGACTCCGGAGACTCGGAAGTGGTCGATGGGCTTATGCTCCAGCACAT
CACTCTCCTCATGTGCTCAGCTTATAGGAACCAGCTGCTCAACATTTTTGTGCGCCCATCCTTAGTAGCAGTAGC
ATTGCAGATGACACCAGGGTTCAGGAAAGAGGATGTCTACAGTTGCTTTCGCTTCCTACGTGATGTTTTTGCAGA
TGAGTTCATCTTCCTTCCAGGAAACACACTAAAGGACTTTGAAGAAGGCTGTTACCTGCTTTGTAAAAGTGAAGC
CATACAAGTGACTACGAAAGACATCCTAGTTACAGAGAAAGGAAATACTGTGTTAGAATTTTTAGTAGGACTCTT
TAAACCTTTTGTGGAAAGCTATCAGATAATTTGCAAGTACCTTTTGAGTGAAGAAGAGGACCACTTCAGTGAGGA
ACAGTACTTGGCTGCAGTCAGAAAATTCACAAGTCAGCTTCTCGATCAAGGTACCTCTCAATGTTATGATGTATT
ATCTTCTGATGTGCAGAAAAACGCCTTAGCAGCCTGTGTGAGGCTCGGAGTAGTGGAGAAGAAGAAGATAAATAA
TAACTGTATATTTAATGTGAATGAACCTGCCACAACCAAATTAGAAGAAATGCTTGGTTGTAAGACACCAATAGG
AAAACCAGCCACTGCAAAACTT**TAA**TAATCAACAAATAGTTATGGAAAATTCGGTCACGTAATTACTCTCATCGA
AGGACTCATTACAACAAACAGGGAAGTAAAGGAAGAGACACATCCTCTCATACTCCCTGAGACTCTGAGAACAGT
GGACGCAGAGGGAAGAGATGATCATTGGAAGCAATCAGTTTACTCTTCCCCACCACAGTGGTTAAAAGGCGTTTG
TATCTGACACTATGTGTGTGTTTTAAAATAAACTTTTGGAAACATGAAAAAAAAAAAAAAAAAAACTCGAG

FIGURE 627

MESSSSSNSYFSVGPTSPSAVVLLYSKELKKWDEFEDILEERRHVSDLKFAMKCYTPLVYKGITPCKPIDIKCSV
LNSEEIHYVIKQLSKESLQSVDVLREEVSEILDEMSHKLRLGAIRFCAFTLSKVFKQIFSKVCVNEEGIQKLQRA
IQEHPVVLLPSHRSYIDFLMLSFLLYNYDLPVPVIAAGMDFLGMKMVGELLRMSGAFFMRRTFGGNKLYWAVFSE
YVKTMLRNGYAPVEFFLEGTRSRSAKTLTPKFGLLNIVMEPFFKREVFDTYLVPISISYDKILEETLYVYELLGV
PKPKESTTGLLKARKILSENFGSIHVYFGDPVSLRSLAAGRMSRSSYNLVPRYIPQKQSEDMHAFVTEVAYKMEL
LQIENMVLSPWTLIVAVLLQNRPSMDFDALVEKTLWLKGLTQAFGGFLIWPDNKPAEEVVPASILLHSNIASLVK
DQVILKVDSGDSEVVDGLMLQHITLLMCSAYRNQLLNIFVRPSLVAVALQMTPGFRKEDVYSCFRFLRDVFADEF
IFLPGNTLKDFEEGCYLLCKSEAIQVTTKDILVTEKGNTVLEFLVGLFKPFVESYQIICKYLLSEEEDHFSEEQY
LAAVRKFTSQLLDQGTSQCYDVLSSDVQKNALAACVRLGVVEKKKINNNCIFNVNEPATTKLEEMLGCKTPIGKP
ATAKL

FIGURE 628

CTCTTCCTAAGCCGGCGCTCGGCAAGTTCTCCCAGGAGAAGGCC**ATG**TTCAGTACGAGCGCCAAGATCGTGAAGC
CTAATGGCGAGAAGCCGGACGAGTTCGAGTCCCGCATCTCCCAGGCTCTTCTGGAGCTGGAGATGAACTTGGACC
TCAAGGCTCAGCTCAGGGAGCTGAATATTATGGCAGCCAAGGAAATTGAGGTTGGTGGTGGTCAGAAAGCTATCA
TAATCTTTGTTCCCGTTCCTCAACTGAAATCTTTCCAGAAAATCCAAGTCCGGCTAGTATGTGAATTGGAGAAAA
AGTTCAGTGGGAAGCATGTTGTCTTTATCGCTTAAAGGAGAATCCTGCCTAAGCCAACTTGGAAAAGCTGTACAA
AATATAAGCAAAAGCATCCCAGGAGCCATACTCTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCA
CAAGCAAAATTGTGGGCAAGAGAATCCGCGTGAAACTAGATGGCAGCCGGCTCATGAAGGTTCATTTGGACAAAG
CACAGCAGAACAATGTGGAACACAAGGTTGAAACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTA
ATTTTGAATTCCCAGAGTTTCAATTG**TAA**ACAAAAATGACTAAATAAAAAATATATATTCACAGT

FIGURE 629

MFSTSAKIVKPNGEKPDEFESRISQALLELEMNLDLKAQLRELNIMAAKEIEVGGGQKAIIIFVPVPQLKSFQKI
QVRLVCELEKKFSGKHVVFIAKRRILPKPTWKSCTKYKQKHPRSHTLTAVHDAILEDLVFTSKIVGKRIRVKLDG
SRLMKVHLDKAQQNNVEHKVETFSGVYKKLMGKDVNFEFPEFQL

FIGURE 630

GTCGCGACCCTGGTCCGGACCTGACCTGAATTGCGACCCCAACCTGGACTGCTCCCCTGACCGCAACCCCTACCC
CCGCCCACCAGT**ATG**GCCCGGCACGTGTTCCTAACGGGGCCCCCAGGAGTTGGAAAAACAACATTGATCCATAAA
GCCAGTGAGGTTTTAAAATCCTCTGGTGTGCCTGTTGATGGATTTTATACCGAAGAAGTCAGACAGGGAGGGAGA
AGAATAGGATTCGATGTCGTCACGTTGTCCGGCACCCGGGGGCCTTTATCGAGAGTTGGGTTAGAGCCTCCACCT
GGAAAACGTGAATGCCGAGTTGGGCAGTATGTGGTCGACCTGACTTCTTTTGAGCAGTTGGCACTACCCGTCTTG
AGGAATGCCGACTGCAGCAGTGGCCCAGGGCAAAGAGTGTGCGTCATCGATGAGATTGGGAAGATGGAGCTCTTC
AGTCAGCTTTTCATTCAAGCTGTTCGTCAGACGCTGTCTACCCCAGGGACTATAATCCTTGGCACAATCCCAGTT
CCTAAAGGAAAGCCACTGGCTCTTGTAGAAGAAATCAGAAACAGAAAGGATGTGAAGGTGTTTAATGTCACCAAG
GAAAACAGAAACCACCTTCTGCCAGATATCGTGACGTGCGTGCAGAGCAGCAGGAAG**TGA**AGACACGTGCATTCC
TGCCTTCCGTGAAGGAGTGCCCAGTTCAAGAGGAGCCTGATGGAGCCCTGCCTGTCGAGGCTGTATGCCTATGGG
GTTATGGAACCTTGTGGGCTTTTCTAGAGAAAACTCAACAGCTGTTTCCCATAAAATGTTTAAAAGATCAAATTA
GCCTTAATGCTGGATTGTCTGTACAAGATTAACTATCCATTGTGGCTTATCTATGCTTAAAGATTTCTTGTTTAT
TTAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 631

MARHVFLTGPPGVGKTTLIHKASEVLKSSGVPVDGFYTEEVRQGGRRIGFDVVTLSGTRGPLSRVGLEPPPGKRE
CRVGQYVVDLTSFEQLALPVLRNADCSSGPGQRVCVIDEIGKMELFSQLFIQAVRQTLSTPGTIILGTIPVPKGK
PLALVEEIRNRKDVKVFNVTKENRNHLLPDIVTCVQSSRK

FIGURE 632

GCAAG**ATG**GCAGAAGTAGAGCAGAAGAAGAAGCGGACCTTCCGCAAGTTCACCTACCGCGGCGTGGACCTGGACC
AGCTGCTGGACATGTCCTACGAACAGCTGATGCAGCTGTACAGTGCGCGCCAGCGGCGGCGGCTGAACCGGGGCC
TGCGGCGGAAGCGGCACTACCTGCTGAAGCGCCTGCGCAAGGCCAAGAAGGAGGCGCCGCCCATGGAGAAGCCGG
AAGTGGTGAAGACGCACCTGAGGGACGTGATCATCCTGCCCGAGGTGGTGGGCAGCATGGTGGGCGTCCACAACG
GCAAGACCTTCACCTACAAGCCCGTAAAGCAATGCCGGTCCGGCATCGGCGCCACCCACTCCTTCTGCTTCATCC
CTCTCAAG**TAG**TGGCTCAGCTAATAAAGGCGCACATG

FIGURE 633

MAEVEQKKKRTFRKFTYRGVDLDQLLDMSYEQLMQLYSARQRRRLNRGLRRKRHYLLKRLRKAKKEAPPMEKPEV
VKTHLRDVIILPEVVGSMVGVHNGKTFTYKPVKQCRSGIGATHSFCFIPLK

FIGURE 634

ACC**ATG**TCTATTCTCAAGATCCATGCCAGGGAGCTCTTTGACTCTCGTGGGAATCCCACTGTTGAGGTTGATCTC
TTCACCTCAGAAGGTCTCTTCAGAGCTGCTGTGCCCAGTGGTGCTTCAACTGGTATCTATGAGGTCCTAGAGCTC
CAGGACAATGATAAGACTCGCTATATGGGGAAGGGTGTCTCAAAGCCTGTTGAGCCCATCAATAAAACTATTGCA
CCTGTCCTGGTTAGCAAGAAACTGAACGTCACAGAACTTCTACAGAAGCCAAGCTCCCTGGAGCCCTGTTGGCAG
CTC**TAG**CCTTGCAGTCATGTAATTGGCCCAAATCACCGGAGCCACGTGACCCTCCAGTGTCATCTCCGGGGTGGC
CACAGGCAAGATCCCCAGTGATTTTGTGCTCAAAATAAAAAGCCTCATTGACCCATGAG

FIGURE 635

MSILKIHARELFDSRGNPTVEVDLFTSEGLFRAAVPSGASTGIYEVLELQDNDKTRYMGKGVSKPVEPINKTIAP
VLVSKKLNVTELLQKPSSLEPCWQL

FIGURE 636

CCCAGAAATTCTACCCAAGCTCCCTCAGCACC**ATG**TACCGAGCACTTCGGCTCCTCGCGCGCTCGCGTCCCCTCG
TGCGGGCTCCAGCCGCAGCCTTAGCTTCGGCTCCCGGCTTGGGTGGCGCGGCCGTGCCCTCGTTTTGGCCTCCGA
ACGCGGCTCGAATGGCAAGCCAAAATTCCTTCCGGATAGAATATGATACCTTTGGTGAACTAAAGGTGCCAAATG
ATAAGTATTATGGCGCCCAGACCGTGAGATCTACGATGAACTTTAAGATTGGAGGTGTGACAGAACGCATGCCAA
CCCCAGTTATTAAAGCTTTTGGCATCTTGAAGCGAGCGGCCGCTGAAGTAAACCAGGATTATGGTCTTGATCCAA
AGATTGCTAATGCAATAATGAAGGCAGCAGATGAGGTAGCTGAAGGTAAATTAAATGATCATTTTCCTCTCGTGG
TATGGCAGACTGGATCAGGAACTCAGACAAATATGAATGTAAATGAAGTCATTAGCAATAGAGCAATTGAAATGT
TAGGAGGTGAACTTGGCAGCAAGATACCTGTGCATCCCAACGATCATGTTAATAAAAGCCAGAGCTCAAATGATA
CTTTTCCCACAGCAATGCACATTGCTGCTGCAATAGAAGTTCATGAAGTACTGTTACCAGGACTACAGAAGTTAC
ATGATGCTCTTGATGCAAAATCCAAAGAGTTTGCACAGATCATCAAGATTGGACGTACTCATACTCAGGATGCTG
TTCCACTTACTCTTGGGCAGGAATTTAGTGGTTATGTTCAACAAGTAAAATATGCAATGACAAGAATAAAAGCTG
CCATGCCAAGAATCTATGAGCTCGCAGCTGGAGGCACTGCTGTTGGTACAGGTTTAAATACTAGAATTGGCTTTG
CAGAAAAGGTTGCTGCAAAAGTGGCTGCACTTACAGGCTTGCCTTTTGTCACTGCTCCGAATAAATTTGAAGCTC
TGGCTGCTCATGACGCTCTGGTTGAGCTCAGTGGAGCCATGAACACTACTGCCTGCAGTCTGATGAAGATAGCAA
ATGATATTCGATTTTTGGGTTCTGGTCCTCGGTCAGGTCTGGGAGAATTGATCTTGCCTGAAAATGAACCAGGAA
GCAGTATCATGCCAGGCAAGGTGAACCCTACTCAGTGTGAAGCAATGACCATGGTTGCAGCCCAAGTCATGGGGA
ACCATGTTGCTGTCACTGTCGGAGGCAGCAATGGACATTTTGAGTTGAATGTTTTCAAGCCAATGATGATTAAAA
ATGTGTTACACTCAGCCAGGCTGCTGGGGGATGCTTCAGTTTCCTTTACAGAAAACTGCGTGGTGGGAATCCAGG
CCAATACAGAAAGGATCAACAAGCTGATGAATGAGTCTCTAATGTTGGTGACAGCTCTCAATCCTCATATAGGGT
ATGACAAGGCAGCAAAGATTGCTAAGACAGCACACAAAAATGGATCAACCTTAAAGGAAACTGCTATCGAACTTG
GCTATCTCACAGCAGAGCAGTTTGACGAATGGGTAAAACCTAAGGACATGCTGGGTCCAAAG**TGA**TTTACATAAA
TTTATAATGAAAATAAACATGTATAAAATTTAAAAAAACAGACTCCCATTTCTTAAAAACGGATAAGTTTGAAAG
GAAACTGCTATTGAACTTAAGCATCTCTAGCAGAGCAATTTGATCAGTATATAAAACCCTAGGATGTGCTAGGTC
TAAGATGGATTAAACAAGTATAAAATAAAATACATTTATAAAATAAAAAGGAAAACAGACTTAAAA

FIGURE 637

MYRALRLLARSRPLVRAPAAALASAPGLGGAAVPSFWPPNAARMASQNSFRIEYDTFGELKVPNDKYYGAQTVRS
TMNFKIGGVTERMPTPVIKAFGILKRAAAEVNQDYGLDPKIANAIMKAADEVAEGKLNDHFPLVVWQTGSGTQTN
MNVNEVISNRAIEMLGGELGSKIPVHPNDHVNKSQSSNDTFPTAMHIAAAIEVHEVLLPGLQKLHDALDAKSKEF
AQIIKIGRTHTQDAVPLTLGQEFSGYVQQVKYAMTRIKAAMPRIYELAAGGTAVGTGLNTRIGFAEKVAAKVAAL
TGLPFVTAPNKFEALAAHDALVELSGAMNTTACSLMKIANDIRFLGSGPRSGLGELILPENEPGSSIMPGKVNPT
QCEAMTMVAAQVMGNHVAVTVGGSNGHFELNVFKPMMIKNVLHSARLLGDASVSFTENCVVGIQANTERINKLMN
ESLMLVTALNPHIGYDKAAKIAKTAHKNGSTLKETAIELGYLTAEQFDEWVKPKDMLGPK

FIGURE 638

GGGXTCGGCCCCTCCCCCTCTTCTGCGCTCTCTTCGGGATACACGTGGGCTTCGGGCCTGGGCCGCGCAGTTTTT
CTTTGGCTTTCTCGAATCATCGAGGAGACTGGCAAAATTAGTAATGTCTTTAGACTGCGTCACTAGCGCCAATCG
AATTCGTAGTTGATTGTTCTTTGAATTCACATTTGAGTCCTCGGTTAAAACCTCAGTTAAAAAGCAGGATAAAGT
CGAGCTGCTTTGGTTCTCGGAACGGAAAAGCGTTTTTTTGTTGTTTAGAGGCTTGGCCTTTATGGGGCTCGTGTG
TGTTTTAGGGGACGGCAAAACAGAACAGAAAGGCGGAGATAAAAAGAGGGGTGTTAAAAGACCACGAGAAGATCA
TGGCCGTGGATATTTTGAGTACATTGAAGAGAACAAGTATAGCAGAGCCAAATCTCCTCAGCCACCTGTTGAAGA
AGAAGATGAACACTTCGATGACACAGTGGTTTGTCTTGATACTTATAATTGTGATCTACATTTTAAAATATCAAG
AGATCGTCTCAGTGCTTCTTCCCTTACAATGGAGAGTTTTGCTTTTCTTTGGGCTGGAGGAAGAGCATCCTATGG
TGTGTCAAAAGGCAAAGTGTGTTTTGAGATGAAGGTTACAGAGAAGATCCCAGTAAGGCATTTATATACAAAAGA
TATTGACATACATGAAGTTCGTATTGGCTGGTCACTAACTACAAGTGGAATGTTACTTGGTGAAGAAGAATTTTC
TTATGGGTATTCTCTAAAAGGAATAAAAACATGCAACTGTGAGACTGAAGATTATGGAGAAAAGTTTGATGAAAA
TGATGTGATTACATGTTTTGCTAACTTTGAAAGTGATGAAGTAGAACTCTCGTATGCTAAGAATGGACAAGATCT
TGGCGTTGCCTTCAAAATCAGTAAGGAAGTTCTTGCTGGACGGCCACTGTTCCCGCATGTTCTCTGCCACAACTG
TGCAGTTGAATTTAATTTTGGTCAGAAGGAAAAGCCATATTTTCCAATACCTGAAGAGTATACTTTCATCCAGAA
CGTCCCCTTAGAGGATCGAGTTAGAGGACCAAAGGGGCCTGAAGAGAAGAAAGATTGTGAAGTTGTGATGATGAT
TGGCTTGCCAGGAGCTGGAAAAACTACCTGGGTTACTAAACATGCAGCAGAAAATCCAGGGAAATATAACATTCT
TGGCACAAATACTATTATGGATAAGATGATGGTGGCAGGTTTTAAGAAGCAAATGGCAGATACTGGAAAACTGAA
CACACTGTTGCAGAGAGCCCCCCAGTGTCTTGGGAAATTTATTGAGATTGCTGCCCGAAAGAAGCGAAATTTTAT
TCTGGATCAGACAAATGTGTCTGCTGCTGCCCAGAGGAGAAAAATGTGCCTGTTTGCAGGCTTCCAGCGAAAAGC
TGTTGTAGTTTGCCCAAAAGATGAAGACTATAAGCAAAGAACACAGAAGAAAGCAGAAGTAGAGGGGAAAGACCT
ACCAGAACATGCGGTCCTCAAAATGAAAGGAAACTTTACCCTCCCAGAGGTAGCTGAGTGCTTTGATGAAATAAC
CTATGTTGAACTTCAGAAGGAAGAAGCCCAAAAACTCTTGGAGCAATATAAGGAAGAAAGCAAAAAGGCTCTTCC
ACCAGAAAAGAAACAGAACACTGGCTCAAAGAAAAGCAATAAAAATAAGAGTGGCAAGAACCAGTTTAACAGAGG
TGGTGGCCATAGAGGACGTGGAGGATTCAATATGCGTGGTGGAAATTTCAGAGGAGGAGCCCCTGGGAATCGTGG
CGGATATAATAGGAGGGGCAACATGCCACAGAGAGGTGGTGGCGGTGGAGGAAGTGGTGGAATCGGCTATCCATA
CCCTCGTGCCCCTGTTTTTCCTGGCCGTGGTAGTTACTCAAACAGAGGGAACTACAACAGAGGTGGAATGCCCAA
CAGAGGGAACTACAACCAGAACTTCAGAGGACGAGGAAACAATCGTGGCTACAAAAATCAATCTCAGGGCTACAA
CCAGTGGCAGCAGGGTCAATTCTGGGGTCAGAAGCCATGGAGTCAGCATTATCACCAAGGATATTATTGAATACC
CAAATAAAACGAACTGATACATATTTCTCCAAAACCTTCACAAGAAGTCGACTGTTTTCTTTAGTAGGCTAACTT
TTTAAACATTCCACAAGAGGAAGTGCCTGCGGGTTCCTTTTTTAGAAGCTTTGTGGGTTGATTTTTTTTCTTTTC
TTTTTTGTACATTTTTAATTGCAGTTTAAAAGTGAATCGTAAGAGAACCTCAGCATTGTGCACGATAAGAGAATG
TGTCAGTATTTCAGGGTTCTACATTTTATCTGTAAAATGTGACTTTTTTTTTTTTTTATCACAACAGAAGTAAAA
TGTTGCTTTGTACCTGGTGTCTTTTATTAAGAATTTACTCCCCCCATTTCTCACAGAGAATAACAGTCGGGAGTC
ATTGTCACAATATAATAGAAATGTTAGCAACCAGATTCATGTAAGGACTAAGTGGTCCTCATGAATTGCATTAAG
ACTCTGTACTGCTCATATTACACTCCATCCTCTCTGTAGTTTGCTGGGTAGTGGAGGGGGTAAGCTAAATCATAG
TTTCTGACAATAACTGGGAAGGTTTTTCTTAAAATAACAATGGAATTGGTATAATTGGGATTGAAAACTAAAAC
TTGGAACTAAGATAGAGAAGATGGAGTGTATGTAGAAGGGCTGTTAAAAATGTAAAACTTGGTTGCATTATTTGT
GGAGGCTCAAACTTGTGAAGGTTAATACCATAATTTTTCCATTTGTTCTGCATTTTGATTCTGAAAAGAAAGCTG
GCTTTGCCCATTTCTTATTAAAAAAACTTGTTGTAAATCCAGTTGTCTAATGGGATCTATATGAAGTTAGCCATG
TCTGTATGCCCTTCTCCCACAAAATACTGTATAACTAGTGTGCTTGTAGTAGTTAACTCCACCATCTTTGTAAGC
TAATGAAATTGTGAGTCACCCATTTATATCTTAATTTTTAATCATGTCAGTTCTTGAATGGGTATCTCCTTAGCC
TGCTGATTTCTTTTTCTTTCTAAAGAAAGTGGGTGGAGAAATTAATTTAGACGTTTGTTTGCAATAAAAAGAATT
CATTTT

FIGURE 639

GGCGTTGCCGGCCGTGGGTGCTCTGGCCACAGTGAGTTAGGGGCGTCGGAGCGGGTTTCTCCAACCGCAATCGGC
TCCGCTCAAGGGGAGGAGGAGAGTCCCTTCTCGGAAGGCCTAAGGAAACGTGTCGTCTGGAATGGGCTTGGGGGC
CACGCCTGCACATCTCCGCGAGACAGAGGGATAAAGTGAAGATGGTGCTGTTATTGTTACCTCGAGTGCCACATG
CGACCTCTGAGATATGTACACAGTCATTCTTACTATCGCACTCAGCCATTCTTACTACGCTAAAGAAGAAATAAT
TATTCGAGGATATTTGCCTGGCCCAGAAGAAACTTATGTAAATTTCATGAACTATTATATCCGTTTTCCTCGGAG
TGAGAGAAAACTCTTTTTAGATATCATCTGAGAGAACTAGTGAATCCCAGTCACTGAGTGGAGTTGAGAGTCTAA
GAACCTCTGAAATTTGAGAACTGCTGGACCAGAGCCTTTAGAGCTCTGATAAGGTGTCAACAGGGTAGTTAATTT
GGCACC**ATG**GGGATACAGGGATTGCTACAATTTATCAAAGAAGCTTCAGAACCCATCCATGTGAGGAAGTATAAA
GGGCAGGTAGTAGCTGTGGATACATATTGCTGGCTTCACAAAGGAGCTATTGCTTGTGCTGAAAAACTAGCCAAA
GGTGAACCTACTGATAGGTATGTAGGATTTTGTATGAAATTTGTAAATATGTTACTATCTCATGGGATCAAGCCT
ATTCTCGTATTTGATGGATGTACTTTACCTTCTAAAAAGGAAGTAGAGAGATCTAGAAGAGAAAGACGACAAGCC
AATCTTCTTAAGGGAAAGCAACTTCTTCGTGAGGGGAAAGTCTCGGAAGCTCGAGAGTGTTTCACCCGGTCTATC
AATATCACACATGCCATGGCCCACAAAGTAATTAAAGCTGCCCGGTCTCAGGGGGTAGATTGCCTCGTGGCTCCC
TATGAAGCTGATGCGCAGTTGGCCTATCTTAACAAAGCGGGAATTGTGCAAGCCATAATTACAGAGGACTCGGAT
CTCCTAGCTTTTGGCTGTAAAAAGGTAATTTTAAAGATGGACCAGTTTGGAAATGGACTTGAAATTGATCAAGCT
CGGCTAGGAATGTGCAGACAGCTTGGGGATGTATTCACGGAAGAGAAGTTTCGTTACATGTGTATTCTTTCAGGT
TGTGACTACCTGTCATCACTGCGTGGGATTGGATTAGCAAAGGCATGCAAAGTCCTAAGACTAGCCAATAATCCA
GATATAGTAAAGGTTATCAAGAAAATTGGACATTATCTCAAGATGAATATCACGGTACCAGAGGATTACATCAAC
GGGTTTATTCGGGCCAACAATACCTTCCTCTATCAGCTAGTTTTTGATCCCATCAAAAGGAAACTTATTCCTCTG
AACGCCTATGAAGATGATGTTGATCCTGAAACACTAAGCTACGCTGGGCAATATGTTGATGATTCCATAGCTCTT
CAAATAGCACTTGGAAATAAAGATATAAATACTTTTGAACAGATCGATGACTACAATCCAGACACTGCTATGCCT
GCCCATTCAAGAAGTCATAGTTGGGATGACAAAACATGTCAAAAGTCAGCTAATGTTAGCAGCATTTGGCATAGG
AATTACTCTCCCAGACCAGAGTCGGGTACTGTTTCAGATGCCCCACAATTGAAGGAAAATCCAAGTACTGTGGGA
GTGGAACGAGTGATTAGTACTAAAGGGTTAAATCTCCCAAGGAAATCATCCATTGTGAAAAGACCAAGAAGTGCA
GAGCTGTCAGAAGATGACCTGTTGAGTCAGTATTCTCTTTCATTTACGAAGAAGACCAAGAAAAATAGCTCTGAA
GGCAATAAATCATTGAGCTTTTCTGAAGTGTTTGTGCCTGACCTGGTAAATGGACCTACTAACAAAAAGAGTGTA
AGCACTCCACCTAGGACGAGAAATAAATTTGCAACATTTTTACAAAGGAAAAATGAAGAAAGTGGTGCAGTTGTG
GTTCCAGGGACCAGAAGCAGGTTTTTTTGCAGTTCAGATTCTACTGACTGTGTATCAAACAAAGTGAGCATCCAG
CCTCTGGATGAAACTGCTGTCACAGATAAAGAGAACAATCTGCATGAATCAGAGTATGGAGACCAAGAAGGCAAG
AGACTGGTTGACACAGATGTAGCACGTAATTCAAGTGATGACATTCCGAATAATCATATTCCAGGTGATCATATT
CCAGACAAGGCAACAGTGTTTACAGATGAAGAGTCCTACTCTTTTGAGAGCAGCAAATTTACAAGGACCATTTCA
CCACCCACTTTGGGAACACTAAGAAGTTGTTTTAGTTGGTCTGGAGGTCTTGGAGATTTTTCAAGAACGCCGAGC
CCCTCTCCAAGCACAGCATTGCAGCAGTTCCGAAGAAAGAGCGATTCCCCCACCTCTTTGCCTGAGAATAATATG
TCTGATGTGTCGCAGTTAAAGAGCGAGGAGTCCAGTGACGATGAGTCTCATCCCTTACGAGAAGGGGCATGTTCT
TCACAGTCCCAGGAAAGTGGAGAATTCTCACTGCAGAGTTCAAATGCATCAAAGCTTTCTCAGTGCTCTAGTAAG
GACTCTGATTCAGAGGAATCTGATTGCAATATTAAGTTACTTGACAGTCAAAGTGACCAGACCTCCAAGCTATGT
TTATCTCATTTCTCAAAAAAAGACACACCTCTAAGGAACAAGGTTCCTGGGCTATATAAGTCCAGTTCTGCAGAC
TCTCTTTCTACAACCAAGATCAAACCTCTAGGACCTGCCAGAGCCAGTGGGCTGAGCAAGAAGCCGGCAAGCATC
CAGAAGAGAAAGCATCATAATGCCGAGAACAAGCCGGGGTTACAGATCAAACTCAATGAGCTCTGGAAAAACTTT
GGATTTAAAAAAGATTCTGAAAAGCTTCCTCCTTGTAAGAAACCCCTGTCCCCAGTCAGAGATAACATCCAACTA
ACTCCAGAAGCGGAAGAGGATATATTTAACAAACCTGAATGTGGCCGTGTTCAAAGAGCAATATTCCAG**TAA**ATG
CAGACTGCTGCAAAGCTTTTGCCTGCAAGAGAATCTGATCAATTTGAAGTCCCTGTTTGGGAATGAGGCACTTAT
CAGCATGAAGAATTTTTTCTCATTCTGTGCCATTTTAAAAATAGAATACATTTGTATATTGACTTTAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 640

MGIQGLLQFIKEASEPIHVRKYKGQVVAVDTYCWLHKGAIACAEKLAKGEPTDRYVGFCMKFVNMLLSHGIKPIL
VFDGCTLPSKKEVERSRRERRQANLLKGKQLLREGKVSEARECFTRSINITHAMAHKVIKAARSQGVDCLVAPYE
ADAQLAYLNKAGIVQAIITEDSDLLAFGCKKVILKMDQFGNGLEIDQARLGMCRQLGDVFTEEKFRYMCILSGCD
YLSSLRGIGLAKACKVLRLANNPDIVKVIKKIGHYLKMNITVPEDYINGFIRANNTFLYQLVFDPIKRKLIPLNA
YEDDVDPETLSYAGQYVDDSIALQIALGNKDINTFEQIDDYNPDTAMPAHSRSHSWDDKTCQKSANVSSIWHRNY
SPRPESGTVSDAPQLKENPSTVGVERVISTKGLNLPRKSSIVKRPRSAELSEDDLLSQYSLSFTKKTKKNSSEGN
KSLSFSEVFVPDLVNGPTNKKSVSTPPRTRNKFATFLQRKNEESGAVVVPGTRSRFFCSSDSTDCVSNKVSIQPL
DETAVTDKENNLHESEYGDQEGKRLVDTDVARNSSDDIPNNHIPGDHIPDKATVFTDEESYSFESSKFTRTISPP
TLGTLRSCFSWSGGLGDFSRTPSPSPSTALQQFRRKSDSPTSLPENNMSDVSQLKSEESSDDESHPLREGACSSQ
SQESGEFSLQSSNASKLSQCSSKDSDSEESDCNIKLLDSQSDQTSKLCLSHFSKKDTPLRNKVPGLYKSSSADSL
STTKIKPLGPARASGLSKKPASIQKRKHHNAENKPGLQIKLNELWKNFGFKKDSEKLPPCKKPLSPVRDNIQLTP
EAEEDIFNKPECGRVQRAIFQ

FIGURE 641

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATCCAGTTGCAGGAAAACAAGCTTA
ACACGCCCACTGATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCTGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTACGTCAC
GGCAGTCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CGGCCTCTACAGTCCCAACATCTGTCTCACAGCAGATTCTTCAGGCCCAGCATCTGCCTCACTTGGACCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGTGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCCACCGAAAGTCCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCA

FIGURE 642

GTCCACATGCAGAGGCTCGCTACAGAAGCTACAGAAGAAGATGGTTACATTTCAAGTGGGCAGGTGCCGTTTGCT
TATGAGCACCATCAGCCACATCAGCCACGGTTCTTTGAATTTTACCTAATTGTCTCTAATTCTTAACAATTCTTT
GAGGTGATCTGCAACTCTTTCACCATCTGTAATGCGGAGATGCAGGAAGTTGGTGTTGGCCTATATCCCAGTATC
TCTTTGCTCAATCACAGCTGTGACCCCAACTGTTCGATTGTGTTCAATGGGCCCCACCTCTTACTGCGAGCAGTC
CGAGACATCGAGGTGGGAGAGGAGCTCACCATCTGCTACCTGGATATGCTGATGACCAGTGAGGAGCGCCGGAAG
CAGCTGAGGGACCAGTACTGCTTTGAATGTGACTGTTTCCGTTGCCAAACCCAGGACAAGGATGCTGATATGCTA
ACTGGTGATGAGCAAGTATGGAAGGAAGTTCAAGAATCCCTGAAAAAAATTGAAGAACTGAAGGCACACTGGAAG
TGGGAGCAGGTTCTGGCCATGTGCCAGGCAATCATAAGCAGCAATTCTGAACGGCTTCCCGATATCAACATCTAC
CAGCTGAAGGTGCTCGACTGCGCCATGGATGCCTGCATCAACCTCGGCCTGTTGGAGGAAGCCTTGTTCTATGGT
ACTCGGACCATGGAGCCATACAGGATTTTTTTCCCAGGAAGCCATCCCGTCAGAGGGGTTCAAGTGATGAAAGTT
GGCAAACTGCAGCTACATCAAGGCATGTTTCCCCAAGCAATGAAGAATCTGAGACTGGCTTTTGATATTATGAGA
GTGACACATGGCAGAGAACACAGCCTGATTGAAGATTTGATTCTACTTTTAGAAGAATGCGACGCCAACATCAGA
GCATCCTAAGGGAACGCAGTCAGAGGGAAATACGGCGTGTGTCTTTGTTGAATGCCTTATTGAGGTCACACACTC
TATGCTTTGTTAGCTGTGTGAACCTCTCCTATTGGAAATTCTGTTCCGTGTTTGTGTAGGTAAATAAAGGCAGAC
ATGGTTTGCAAACCACAAGAATCATTAGTTGTAGAGAAGCACGATTATAATAAATTCAAAACATTTGGTTGAGGA
TGCC

FIGURE 643

CTTGCTTCGGACGCCGGATTTTGACGTGCTCTCGCGAGATTTGGGTCTCTTCCTAAGCCGGCGCTCGGCAAGTTC
TCCCAGGAGAAAGCC**ATG**TTCAGTTCGAGCGCCAAGATCGTGAAGCCCAATGGCGAGAAGCCGGACGAGTTCGAG
TCCGGCATCTCCCAGGCTCTTCTGGAGCTGGAGATGAACTCGGACCTCAAGGCTCAGCTCAGGGAGCTGAATATT
ACGGCAGCTAAGGAAATTGAAGTTGGTGGTGGTCGGAAAGCTATCATAATCTTTGTTCCCGTTCCTCAACTGAAA
TCTTTCCAGAAAATCCAAGTCCGGCTAGTACGCGAATTGGAGAAAAAGTTCAGTGGGAAGCATGTCGTCTTTATC
GCTCAGAGGAGAATTCTGCCTAAGCCAACTCGAAAAAGCCGTACAAAAAATAAGCAAAAGCGTCCCAGGAGCCGT
ACTCTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCCCAAGCGAAATTGTGGGCAAGAGAATCCGC
GTCAAACTAGATGGCAGCCGGCTCATAAAGGTTCATTTGGACAAAGCACAGCAGAACAATGTGGAACACAAGGTT
GAAACTTTTTCTGGTGTCTATAAGAAGCTCACGGGCAAGGATGTTAATTTTGAATTCCCAGAGTTTCAATTG**TAA**
ACAAAAATGACTAAATAAAAGTATATATTCACAGTAAAAAAAAAAAAAAAAA

FIGURE 644

MFSSSAKIVKPNGEKPDEFESGISQALLELEMNSDLKAQLRELNITAAKEIEVGGGRKAIIIFVPVPQLKSFQKI
QVRLVRELEKKFSGKHVVFIAQRRILPKPTRKSRTKNKQKRPRSRTLTAVHDAILEDLVFPSEIVGKRIRVKLDG
SRLIKVHLDKAQQNNVEHKVETFSGVYKKLTGKDVNFEFPEFQL

FIGURE 645

GGCACGAGGCGGGCCAGCGACGGGCAGGACGCCCCGTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCCTGCCTGC
GCTCAGG<u>ATG</u>AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTGCCATCTGG
ACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGGCCTCAAAGGGGATGCGGAGA
GAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAA
AGGACAGAAAGGCAGTGTGGGTCGTCATGGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGG
TGACATAGGACCCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGG
GGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTCGCCGGTGTGCGCGA
GACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGACGCCCAGCTGTCCTGCCAGGGCCG
CGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCT
GGCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCG
GACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCTC
GGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATG<u>TGA</u>GC
CTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTG
CCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATG
GCCTATGCTTAAGAGGAAAATGAAAGTGTTCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATT
GTAGCCCCAATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATA
CAATAAAATCTTTAAGTAGTGCAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 646

MRGNLALVGVLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVGPTGEKGDMGDKGQ
KGSVGRHGKIGPIGSKGEKGDSGDIGPPGPNGEPGLPCECSQLRKAIGEMDNQVSQLTSELKFIKNAVAGVRETE
SKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAANGLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTF
NKWRSGEPNNAYDEEDCVEMVASGGWNDVACHTTMYFMCEFDKENM

FIGURE 647

GGCACGAGGGGCTTCTGTCACCTTCCTCACGGACCTTGGTCACGGCCGCAGGTGACCCCTTAGCCCAGCTCCAGT
GGGCGGGTGGCAGGGTCATGGAGGACGCTGGCGGCGGCGAGGAGACCCCGGCCCCGGAGGCCCCGCACCCCCCTC
AGCTCGCGCCTCCGGAGGAGCAGGGGTTGCTCTTCCAGGAGGAAACCATCGATCTTGGCGGAGATGAGTTTGGAT
CCGAAGAGAACGAGACCGCATCGGAAGGCTCGAGTCCTCTCGCGGACAAGCTGAACGAACACATGATGGAGAGCG
TCCTCATCTCTGACTCCCCCAACAGCGAGGGCGACGCGGGCGACCTGGGCCGAGTGCGGGACGAAGCTGAGCCCG
GAGGGGAAGGCGACCCAGGCCCGGAGCCCGCGGGCACCCCGAGTCCCAGCGGCGAGGCCGACGGCGACTGTGCCC
CCGAGGACGCGGCACCCAGTAGCGGAGGGGCCCCGAGGCAGGACGCGGCCCGCGAGGTCCCAGGCAGCGAAGCCG
CGCGCCCGGAGCAGGAGCCTCCCGTTGCGGAGCCGGTCCCGGTGTGCACCATCTTCAGCCAGCGCGCGCCCCCAG
CCTCCGGGGACGGCTTCGAGCCGCAGATGGTGAAGTCGCCCAGCTTCGGTGGCGCCAGCGAGGCCTCGGCCAGGA
CACCGCCCCAGGTCGTGCAGCCCAGCCCCAGCCTCAGCACGTTCTTCGGAGACACGGCCGCCAGCCACTCCTTGG
CCTCGGACTTCTTCGACTCCTTTACTACCTCCGCCTTCATTTCCGTCAGCAATCCCGGCGCGGGCTCCCCGGCCC
CCGCCAGCCCGCCTCCCCTCGCTGTGCCCGGGACCGAGGGGCGCCCCGAACCCGTGGCCATGCGAGGGCCCCAGG
CAGCTGCGCCCCCGGCGTCGCCAGAGCCTTTCGCGCACATCCAGGCAGTGTTTGCAGGGAGTGACGACCCCTTTG
CCACCGCCCTGAGCATGAGCGAGATGGACCGGAGGAACGACGCCTGGCTTCCCGGCGAGGCTACGCGTGGAGTCC
TGCGGGCCGTGGCCACCCAGCAGCGCGGCGCCGTGTTCGTGGACAAGGAGAACCTCACCATGCCGGGCCTCAGGT
TCGACAACATCCAGGGAGATGCAGTTAAAGACTTG<u>ATG</u>CTTCGCTTTCTGGGTGAAAAAGCTGCAGCAAAGAGAC
AAGTCCTAAATGCCGACTCAGTGGAACAATCTTTTGTTGGATTGAAACAGCTAATCAGCTGCAGAAACTGGAGGG
CAGCAGTGGACCTGTGCGGACGTCTCCTCACAGCCCACGGCCAGGGCTACGGCAAGAGCGGGCTGCTCACCAGCC
ACACGACAGATTCACTGCAGCTCTGGTTTGTCAGGCTGGCACTACTAGTGAAGTTGGGCCTTTTCCAGAATGCTG
AGATGGAATTTGAACCCTTCGGAAATCTTGATCAGCCAGATCTTTATTACGAGTACTACCCGCACGTGTACCCTG
GGCGCAGGGGCTCCATGGTCCCCTTCTCGATGCGCATCTTGCACGCGGAGCTTCAGCAGTACCTGGGGAACCCAC
AGGAGTCGCTGGATAGACTGCACAAGGTGAAGACTGTCTGCAGCAAGATCCTGGCCAATTTGGAGCAAGGCTTAG
CAGAAGACGGCGGCATGAGCAGCGTGACTCAGGAGGGCAGACAAGCCTCTATCCGGCTGTGGAGGTCACGTCTGG
GCCGGGTGATGTACTCCATGGCAAACTGTCTGCTCCTGATGAAGGATTATGTGCTGGCCGTGGATGCGTATCATT
CGGTTATCAAGTATTACCCAGAGCAAGAGCCCCAGCTGCTCAGCGGCATCGGCCGGATTTCCCTCCAGATTGGAG
ACATAAAAACAGCTGAAAAGTATTTTCAAGACGTTGAGAAAGTAACACAGAAATTAGACGGACTACAGGGTAAAA
TCATGGTTTTGATGAACAGCGCGTTCCTTCACCTCGGGCAGAATAACTTTGCAGAAGCCCACAGGTTCTTCACAG
AGATCTTAAGGATGGATCCAAGAAACGCAGTGGCCAACAACAACGCTGCCGTGTGTCTGCTCTACCTGGGCAAGC
TCAAGGACTCCCTGCGGCAGCTGGAGGCCATGGTCCAGCAGGACCCCAGGCACTACCTGCACGAGAGCGTGCTCT
TCAACCTGACCACCATGTACGAGCTGGAGTCCTCACGGAGCATGCAGAAGAAACAGGCCCTGCTGGAGGCTGTCG
CCGGCAAGGAGGGGGACAGCTTCAACACACAGTGCCTCAAGCTGGCC<u>TAG</u>CTGCCTCCAACACACTACGTCAGAA
GGACCCGGGTCTTTGAAACTGTGTCTTGAAGCTAATGTATTAATGTGACATGGAGGAACTCAATAAAACTCCTGC
TTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 648

MLRFLGEKAAAKRQVLNADSVEQSFVGLKQLISCRNWRAAVDLCGRLLTAHGQGYGKSGLLTSHTTDSLQLWFVR
LALLVKLGLFQNAEMEFEPFGNLDQPDLYYEYYPHVYPGRRGSMVPFSMRILHAELQQYLGNPQESLDRLHKVKT
VCSKILANLEQGLAEDGGMSSVTQEGRQASIRLWRSRLGRVMYSMANCLLLMKDYVLAVDAYHSVIKYYPEQEPQ
LLSGIGRISLQIGDIKTAEKYFQDVEKVTQKLDGLQGKIMVLMNSAFLHLGQNNFAEAHRFFTEILRMDPRNAVA
NNNAAVCLLYLGKLKDSLRQLEAMVQQDPRHYLHESVLFNLTTMYELESSRSMQKKQALLEAVAGKEGDSFNTQC
LKLA

FIGURE 649

AATTCGGCACGAGAAGACTTCCAGTTTGGAGTCGTTTGCTGCGGGGAGGGAATGAATGGGCGCTGGGAACACGCC
CGCGAGGTGGGGACGCGCCGGCCGTAGCGAGGTCCTTAGCGTGTGAGTGGCCGGGGTCGGGTCGCTTCCCCGCAG
C**ATG**GAGGACGATGCACCAGTGATCTACGGGCTGGAGTTCCAGGCACGTGCCTTAACACCTCAAACTGCAGAAAC
AGATGCCATTCGGTTTTTGGTTGGGACGCAGTCTCTTAAATATGATAATCAGATCCATATCATAGATTTTGACGA
TGAAAACAACATTATAAATAAAAATGTCCTCCTCCATCAAGCGGGTGAAATCTGGCATATTAGCGCTAGCCCTGC
AGACAGAGGTGTGCTGACGACCTGCTACAACAGAACTTCAGACAGCAAAGTCCTGACATGTGCAGCCGTGTGGAG
GATGCCGAAGGAATTGGAATCAGGCAGCCACGAGTCCCCTGATGATTCATCCAGCACTGCACAGACCCTGGAGCT
GCTCTGTCACCTTGACAACACAGCCCATGGCAACATGGCCTGTGTCGTGTGGGAGCCAATGGGAGATGGGAAGAA
AATCATTTCCTTGGCTGATAACCATATCCTGCTGTGGGATTTACAGGAAAGCTCGAGCCAGGCTGTGCTGGCCAG
CTCAGCGTCCCTGGAAGGGAAGGGACAACTGAAGTTCACCTCAGGACGGTGGAGCCCACATCATAACTGCACCCA
GGTGGCCACAGCGAACGACACCACCCTCCGTGGCTGGGACACCCGGAGCATGAGCCAGATCTACTGCATAGAGAA
TGCCCACGGACAGCTGGTGCGGGACCTTGACTTTAATCCCAATAAGCAGTACTACTTGGCCAGCTGCGGAGACGA
CTGTAAGGTGAAGTTCTGGGACACCCGAAATGTCACCGAACCCGTGAAGACCCTGGAGGAGCACTCCCACTGGGT
GTGGAACGTCCGCTACAACCACTCTCATGACCAGCTGGTCCTCACGGGCAGCAGTGACAGCAGAGTCATCCTTTC
CAACATGGTGTCCATCTCGTCGGAGCCCTTCGGCCACTTGGTAGACGACGATGACATCAGTGACCAGGAGGACCA
CCGTTCTGAAGAGAAGAGCAAGGAGCCCCTGCAGGACAACGTGATCGCCACCTACGAGGAGCACGAGGACAGCGT
CTATGCCGTGGACTGGTCCTCGGCTGACCCGTGGCTGTTTGCCTCCCTGAGCTATGACGGGAGGCTCGTGATCAA
CAGGGTGCCCAGGGCCCTGAAGTACCACATCCTGCTA**TGA**CTCCCGGGCCTGGGTTATCCAGGTCCCATTGAGTG
GTTTTCCTCTTGGCAGATTCTCAAACAGTCGCAGCTCTTTGGAGGTGACTCGTGTTCCAGGTGGATCCCTCTCTG
GGAGAGCCGCTGTTCCCTTCCTGTAGCAGCAGCATTTATGAATGGGGTGAATGGGGCTATTGTCGACGGCACAGC
TAATGCCCGAACCCAGCCCCTGTCGGCAGAGACAGAGCCCCACATTATTATGTGAATAACAATGTTTTCTGTTTT
AAGGGTGTCAGGAGTTTCGCTTTTTAAAAAAATGTCTGTTCCTGCAGTAGTAACTCTTCTTTCTCTTGAGAGTAA
AAAATGAAATAAAATAAATCCACGCTGACAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 650

MEDDAPVIYGLEFQARALTPQTAETDAIRFLVGTQSLKYDNQIHIIDFDDENNIINKNVLLHQAGEIWHISASPA
DRGVLTTCYNRTSDSKVLTCAAVWRMPKELESGSHESPDDSSSTAQTLELLCHLDNTAHGNMACVVWEPMGDGKK
IISLADNHILLWDLQESSSQAVLASSASLEGKGQLKFTSGRWSPHHNCTQVATANDTTLRGWDTRSMSQIYCIEN
AHGQLVRDLDFNPNKQYYLASCGDDCKVKFWDTRNVTEPVKTLEEHSHWVWNVRYNHSHDQLVLTGSSDSRVILS
NMVSISSEPFGHLVDDDDISDQEDHRSEEKSKEPLQDNVIATYEEHEDSVYAVDWSSADPWLFASLSYDGRLVIN
RVPRALKYHILL

FIGURE 651

CCCAGGCGCAGCCAATGGGAAGGGTCGGAGGCATGGCACAGCCAATGGGAAGGGCCGGGGCACCAAAGCCAATGG
GAAGGGCCGGGAGCGCGCGGCGCGGGAGATTTAAAGGCTGCTGGAGTGAGGGGTCGCCCGTGCACCCTGTCCCAG
CCGTCCTGTCCTGGCTGCTCGCTCTGCTTCGCTGCGCCTCCACT**ATG**CTCTCCCTCCGTGTCCCGCTCGCGCCCA
TCACGGACCCGCAGCAGCTGCAGCTCTCGCCGCTGAAGGGGCTCAGCTTGGTCGACAAGGAGAACACGCCGCCGG
CCCTGAGCGGGACCCGCGTCCTGGCCAGCAAGACCGCGAGGAGGATCTTCCAGGAGCCCACGGAGCCGAAAACTA
AAGCAGCTGCCCCCGGCGTGGAGGATGAGCCGCTGCTGAGAGAAAACCCCCGCCGCTTTGTCATCTTCCCCATCG
AGTACCATGATATCTGGCAGATGTATAAGAAGGCAGAGGCTTCCTTTTGGACCGCCGAGGAGGTTGACCTCTCCA
AGGACATTCAGCACTGGGAATCCCTGAAACCCGAGGAGAGATATTTTATATCCCATGTTCTGGCTTTCTTTGCAG
CAAGCGATGGCATAGTAAATGAAAACTTGGTGGAGCGATTTAGCCAAGAAGTTCAGATTACAGAAGCCCGCTGTT
TCTATGGCTTCCAAATTGCCATGGAAAACATACATTCTGAAATGTATAGTCTTCTTATTGACACTTACATAAAAG
ATCCCAAAGAAAGGGAATTTCTCTTCAATGCCATTGAAACGATGCCTTGTGTCAAGAAGAAGGCAGACTGGGCCT
TGCGCTGGATTGGGGACAAAGAGGCTACCTATGGTGAACGTGTTGTAGCCTTTGCTGCAGTGGAAGGCATTTTCT
TTTCCGGTTCTTTTGCGTCGATATTCTGGCTCAAGAAACGAGGACTGATGCCTGGCCTCACATTTTCTAATGAAC
TTATTAGCAGAGATGAGGGTTTACACTGTGATTTTGCTTGCCTGATGTTCAAACACCTGGTACACAAACCATCGG
AGGAGAGAGTAAGAGAAATAATTATCAATGCTGTTCGGATAGAACAGGAGTTCCTCACTGAGGCCTTGCCTGTGA
AGCTCATTGGGATGAATTGCACTCTAATGAAGCAATACATTGAGTTTGTGGCAGACAGACTTATGCTGGAACTGG
GTTTTAGCAAGGTTTTCAGAGTAGAGAACCCATTTGACTTTATGGAGAATATTTCACTGGAAGGAAAGACTAACT
TCTTTGAGAAGAGAGTAGGCGAGTATCAGAGGATGGGAGTGATGTCAAGTCCAACAGAGAATTCTTTTACCTTGG
ATGCTGACTTC**TAA**ATGAACTGAAGATGTGCCCTTACTTGGCTGATTTTTTTTTTCCATCTCATAAGAAAAATCA
GCTGAAGTGTTACCAACTAGCCACACCATGAATTGTCCGTAATGTTCATTAACAGCATCTTTAAAACTGTGTAGC
TACCTCACAACCAGTCCTGTCTGTTTATAGTGCTGGTAGTATCACCTTTTGCCAGAAGGCCTGGCTGGCTGTGAC
TTACCATAGCAGTGACAATGGCAGTCTTGGCTTTAAAGTGAGGGGTGACCCTTTAGTGAGCTTAGCACAGCGGGA
TTAAACAGTCCTTTAACCAGCACAGCCAGTTAAAAGATGCAGCCTCACTGCTTCAACGCAGATTTTAATGTTTAC
TTAAATATAAACCTGGCACTTTACAAACAAATAAACATTGTTTTGTACTCACGGCGGCGATAATAGCTTGATTTA
TTTGGTTTCTACACCAAATACATTCTCCTGACCACTAATGGGAGCCAATTCACAATTCACTAAGTGACTAAAGTA
AGTTAAACTTGTGTAGACTAAGCATGTAATTTTTAAGTTTTATTTTAATGAATTAAAATATTTGTTAACCAACTT
TAAAGTCAGTCCTGTGTATACCTAGATATTAGTCAGTTGGTGCCAGATAGAAGACAGGTTGTGTTTTTATCCTGT
GGCTTGTGTAGTGTCCTGGGATTCTCTGCCCCCTCTGAGTAGAGTGTTGTGGGATAAAGGAATCTCTCAGGGCAA
GGAGCTTCTTAAGTTAAATCACTAGAAATTTAGGGGTGATCTGGGCCTTCATATGTGTGAGAAGCCGTTTCATTT
TATTTCTCACTGTATTTTCCTCAACGTCTGGTTGATGAGAAAAAAATTCTTGAAGAGTTTTCATATGTGGGAGCTA
AGGTAGTATTGTAAAATTTCAAGTCATCCTTAAACAAAATGATCCACCTAAGATCTTGCCCCTGTTAAGTGGTGA
AATCAACTAGAGGTGGTTCCTACAAGTTGTTCATTCTAGTTTTGTTTGGTGTAAGTAGGTTGTGTGAGTTAATTC
ATTTATATTTACTATGTCTGTTAAATCAGAAATTTTTTATTATCTATGTTCTTCTAGATTTTACCTGTAGTTCAT
AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 652

MLSLRVPLAPITDPQQLQLSPLKGLSLVDKENTPPALSGTRVLASKTARRIFQEPTEPKTKAAAPGVEDEPLLRE
NPRRFVIFPIEYHDIWQMYKKAEASFWTAEEVDLSKDIQHWESLKPEERYFISHVLAFFAASDGIVNENLVERFS
QEVQITEARCFYGFQIAMENIHSEMYSLLIDTYIKDPKEREFLFNAIETMPCVKKKADWALRWIGDKEATYGERV
VAFAAVEGIFFSGSFASIFWLKKRGLMPGLTFSNELISRDEGLHCDFACLMFKHLVHKPSEERVREIIINAVRIE
QEFLTEALPVKLIGMNCTLMKQYIEFVADRLMLELGFSKVFRVENPFDFMENISLEGKTNFFEKRVGEYQRMGVM
SSPTENSFTLDADF

FIGURE 653

GTCGCTGAGGCGCCC**ATG**GCCTTCGCCCGCCGGCTCCTGCGCGGGCCACTGTCGGGGCCGCTGCTCGGGCGGCGC
GGGGTCTGCGCTGGGGCCATGGCTCCGCCGCGCCGCTTCGTCCTGGAGCTTCCCGACTGCACCCTGGCTCACTTC
GCCCTAGGCGCCGACGCCCCCGGCGACGCAGACGCCCCCGACCCCCGCCTGGCGGCGCTGCTGGGGCCCCCGGAG
CGCAGCTACTCGCTGTGCGTGCCCGTGACCCCGGACGCCGGCTGCGGGGCCCGGGTCCGGGCGGCGCGGCTGCAC
CAGCGCCTGCTGCACCAGCTGCGCCGCGGCCCCTTCCAGCGGTGCCAGCTGCTCAGGCTGCTCTGCTACTGCCCG
GGCGGCCAGGCCGGCGGCGCACAGCAAGGCTTCCTGCTGCGCGACCCCCTGGATGACCCTGACACCCGGCAAGCG
CTGCTCGAGCTGCTGGGCGCCTGTCAGGAGGCACCACGCCCGCACTTGGGCGAGTTCGAGGCCGACCCGCGCGGC
CAGCTGTGGCAGCGCCTCTGGGAGGTGCAAGACGGCAGGCGGCTGCAGGTGGGCTGCGCACAGGTCGTGCCCGTC
CCGGAGCCCCCGCTGCACCCGGTGGTGCCAGACTTGCCCAGTTCCGTGGTCTTCCCGGACCGGGAAGCCGCCCGG
GCCGTTTTGGAGGAGTGTACCTCCTTTATTCCTGAAGCCCGGGCAGTGCTTGACCTGGTCGACCAGTGCCCAAAA
CAGATCCAGAAAGGAAAGTTCCAGGTTGTTGCCATCGAAGGACTGGATGCCACGGGTAAAACCACGGTGACCCAG
TCAGTGGCAGATTCACTTAAGGCTGTCCTCTTAAAGTCACCACCCTCTTGCATTGGCCAGTGGAGGAAGATCTTT
GATGATGAACCAACTATCATTAGAAGAGCTTTTTACTCTTTGGGCAATTATATTGTGGCCTCCGAAATAGCTAAA
GAATCTGCCAAATCTCCTGTGATTGTAGACAGGTACTGGCACAGCACGGCCACCTATGCCATAGCCACTGAGGTG
AGTGGGGGTCTCCAGCACCTGCCCCCAGCCCATCACCCTGTGTACCAGTGGCCAGAGGACCTGCTCAAACCTGAC
CTTATCCTGCTGCTCACTGTGAGTCCTGAGGAGAGGTTGCAGAGGCTGCAGGGCCGGGGCATGGAGAAGACCAGG
GAAGAAGCAGAACTTGAGGCCAACAGTGTGTTTCGTCAAAAGGTAGAAATGTCCTACCAGCGGATGGAGAATCCT
GGCTGCCATGTGGTTGATGCCAGCCCCTCCAGAGAAAAGGTCCTGCAGACGGTATTAAGCCTAATCCAGAATAGT
TTTAGTGAACCG**TAG**TTACTCTGGCCAGGTGCCACGTCTAACTAGATTAGATGTTGTTTGAAACATCTACATCCA
CCATTTGTTATGCAGTGTTCCCAAATTTCTGTTCTACAAGCATGTTGTGTGGCAGAAAACTGGAGACCAGGCATC
TTAATTTTACTTCAGCCATCGTACCCTCTTCTGACTGATGGACCCGTCATCACAAAGGTCCCTCTCATCATGTTC
CAGTGAGAGGCCAGCGATTGCTTTCTTCCTGGCATAGTAAACATTTTCTTGGAACATATGTTTCACTTAATCACT
ACCAAATATCTGGAAGACCTGTCTTACTCAGACAGCACCAGGTGTACAGAAGCAGCAGACAAGATCTTCCAGATC
AGCAGGGAGACCCCGGAGCCTCTGCTTCTCCTACACTGGCATGCTGATGAGATCGTGACATGCCCACATTGGCTT
CTTCCACATCTGGTTGCACTCGTCATGATGGGCTCGCTGCATCTCCCTCAGTCCCAAATTCTAGAGCCAAGTGTT
CCTGCAGAGGCTGTCTATGTGTCCTGGCTGCCCAAGGACACTCCTGCAGAGCCATTTTTGGGTAAGGAACACTTA
CAAAGAAGGCATTGATCTTGTGTCTGAGGCTCAGAGCCCTTTTGATAGGCTTCTGAGTCATATATAAAGACATTC
AAGCCAAGATGCTCCAACTGCAAATATACCAACCTTCTCTGAATTATATTTGCTTATTTATATTTCTTTTCTTT
TTTTCTAAAGTATGGCTCTGAATAGAATGCACATTTTCCATTGAACTGGATGCATTTCATTTAGCCAATCCAGTA
ATTTATTTATATTAATCTATACATAATATGTTTCCTCAGCATAGGAGCTATGATTCATTAATTAAAAGTGGAGTC
AAAACGCTAAATGCAATGTTTGTTGTGTATTTTCATTACACAAACTTAATTTGTCTTGTTAAATAAGTACAGTGG
ATCTTGGAGTGGGATTTCTTGGTAAATTATCTTGCACTTGAATGTCTCATGATTACATATGAAATCGCTTTGACA
TATCTTTAGACAGAAAAAAGTAGCTGAGTGAGGGGGAAATTATAGAGCTGTGTGACTTTAGGGAGTAGGTTGAAC
CAGGTGATTACCTAAAATTCCTTCCAGTTCAAAGGCAGATAAATCTGTAAATTATTTTATCCTATCTACCATTTC
TTAAGAAGACATTACTCCAAAATAATTAAATTTAAGGCTTTATCAGGTCTGCATATAGAATCTTAAATTCTAATA
AAGTTTCATGTTAATGTCATAGGATTTTTAAAAGAGCTATAGGTAATTTCTATATAATATGTGTATATTAAAATG
TAATTGATTTCAGTTGAAAGTATTTTAAAGCTGATAAATAGCATTAGGGTTCTTTGCAATGTGGTATCTAGCTGT
ATTATTGGTTTTATTTACTTTAAACATTTTGAAAAGCTTATACTGGCAGCCTAGAAAAACAAACAATTAATGTAT
CTTTATGTCCCTGGCACATGAATAAACTTTGCTGTGGTTTACT

FIGURE 654

MAFARRLLRGPLSGPLLGRRGVCAGAMAPPRRFVLELPDCTLAHFALGADAPGDADAPDPRLAALLGPPERSYSL
CVPVTPDAGCGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCPGGQAGGAQQGFLLRDPLDDPDTRQALLELL
GACQEAPRPHLGEFEADPRGQLWQRLWEVQDGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEE
CTSFIPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPT
IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLL
TVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNSFSEP

FIGURE 655

GTGGTGGGACTCGCGTCGCGGCCGCGGAGACGTGAAGCTCTCGAGGCTCCTCCCGCTGCGGGTCGGCGCTCGCCC
TCGCTCTCCTCGCCCTCCGCCCCGGCCCCGGCCCCGCGCCCGCCATGGAGAAGACTGAGCTGATCCAGAAGGCCA
AGCTGGCCGAGCAGGCCGAGCGCTACGACGACATGGCCACCTGCATGAAGGCAGTGACCGAGCAGGGCGCCGAGC
TGTCCAACGAGGAGCGCAACCTGCTCTCCGTGGCCTACAAGAACGTGGTCGGGGGCCGCAGGTCCGCCTGGAGGG
TCATCTCTAGCATCGAGCAGAAGACCGACACCTCCGACAAGAAGTTGCAGCTGATTAAGGACTATCGGGAGAAAG
TGGAGTCCGAGCTGAGATCCATCTGCACCACGGTGCTGGAATTGTTGGATAAATATTTAATAGCCAATGCAACTA
ATCCAGAGAGTAAGGTCTTCTATCTGAAAATGAAGGGTGATTACTTCCGGTACCTTGCTGAAGTTGCGTGTGGTG
ATGATCGAAAACAAACGATAGATAATTCCCAAGGAGCTTACCAAGAGGCATTTGATATAAGCAAGAAAGAGATGC
AACCCACACACCCAATCCGCCTGGGGCTTGCTCTTAACTTTTCTGTATTTTACTATGAGATTCTTAATAACCCAG
AGCTTGCCTGCACGCTGGCTAAAACGGCTTTTGATGAGGCCATTGCTGAACTTGATACACTGAATGAAGACTCAT
ACAAAGACAGCACCCTCATCATGCAGTTGCTTAGAGACAACCTAACACTTTGGACATCAGACAGTGCAGGAGAAG
AATGTGATGCGGCAGAAGGGGCTGAAAACTAAATCCATACAGGGTGTCATCCTTCTTTCCTTCAAGAAACCTTTT
TACACATCTCCATTCCTTATTCCACTTGGATTTCCTATAGCAAAGAAACCCATTCATGTGTATGGAATCAACTGT
TTATAGTCTTTTCACACTGCAGCTTTGGGAAAACTTCATTCCTTGATTTGTGTTTGTCTTGGCCTTCCTGGTGTG
CAGTACTGCTGTAGAAAAGTATTAATAGCTTCATTTCATATAAACATAAGTAACTCCCAAACACTTATGTAGAGG
ACTAAAAATGTATCTGGTATTTAAGTAATCTGAACCAGTTCTGCAAGTGACTGTGTTTTGTATTACTGTGAAAAT
AAGAAAATGTAGTTAATTACAATTTAAAGAGTATTCCACATAACTTCTTAATTTCTACATTCCCTCCCTTACTCT
TCGGGGGTTTCCTTTCAGTAAGCAACTTTTCCATGCTCTTAATGTATTCCTTTTTAGTAGGAATCCGGAAGTATT
AGATTGAATGGAAAAGCACTTGCCATCTCTGTCTAGGGGTCACAAATTGAAATGGCTCCTGTATCACATACGGAG
GTCTTGTGTATCTGTGGCAACAGGGAGTTTCCTTATTCACTCTTTATTTGCTGCTGTTTAAGTTGCCAACCTCCC
CTCCCAATAAAAATTCACTTACACCTCCTGCCTTTGTAGTTCTGGTATTCACTTTACTATGTGATAGAAGTAGCA
TGTTGCTGCCAGAATACAAGCATTGCTTTTGGCAAATTAAAGTGCATGTCATTTCTTAATACACTAGAAAGGGGA
AATAAATTAAAGTACACAAGTCCAAGTCTAAAACTTTAGTACTTTTCCATGCAGATTTGTGCACATGTGAGAGGG
TGTCCAGTTTGTCTAGTGATTGTTATTTAGAGAGTTGGACCACTATTGTGTGTTGCTAATCATTGACTGTAGTCC
CAAAAAAGCCTTGTGAAAATGTTATGCCCTATGTAACAGCAGAGTAACATAAAATAAAAGTACATTTTATAAACC
ATTTACTATGGCTTTGTAACAATTGCATACCCATATTTTAAGGGACAGGTGAATTTACTACTTTCTAAAGTTTAT
TGATACTTCCCTTTTATGTAAAATGTAGTAGTGATACCTATATTTCCACATTGTGCATTGTGACACACTTGTCTA
GGGATGCCTGGAAGTGTATAAAATTGGACTGCATTTCTTAGAGTGTTTTACTATAGATCAGTCTCATGGGCCATC
TCTTCCTCAGATGTAAATGATATCTGGTTAAGTGTTATATGGAATAAAGTGGACATTTTAAAACTA

FIGURE 656

MEKTELIQKAKLAEQAERYDDMATCMKAVTEQGAELSNEERNLLSVAYKNVVGGRRSAWRVISSIEQKTDTSDKK
LQLIKDYREKVESELRSICTTVLELLDKYLIANATNPESKVFYLKMKGDYFRYLAEVACGDDRKQTIDNSQGAYQ
EAFDISKKEMQPTHPIRLGLALNFSVFYYEILNNPELACTLAKTAFDEAIAELDTLNEDSYKDSTLIMQLLRDNL
TLWTSDSAGEECDAAEGAEN

FIGURE 657

GGCACGAGGCTCCGGTGTGTCTGTCGGTTGCAGTGTTGGAGGTCGGCGCCGGCCCCCGCCTTCCGCGCCCCCCAC
GGGAAGGAAGCACCCCCGGTATTAAAACGAACGGGGCGGAAAGAAGCCCTCAGTCGCCGGCCGGGAGGCGAGCCG
ATGCCGAGCTGCTCCACGTCCACCATGCCGGGCATGATCTGCAAGAACCCAGACCTCGAGTTTGACTCGCTACAG
CCCTGCTTCTACCCGGACGAAGATGACTTCTACTTCGGCGGCCCCGACTCGACCCCCCCGGGGGAGGACATCTGG
AAGAAGTTTGAGCTGCTGCCCACGCCCCCGCTGTCGCCCAGCCGTGGCTTCGCGGAGCACAGCTCCGAGCCCCCG
AGCTGGGTCACGGAGATGCTGCTTGAGAACGAGCTGTGGGGCAGCCCGGCCGAGGAGGACGCGTTCGGCCTGGGG
GGACTGGGTGGCCTCACCCCCAACCCGGTCATCCTCCAGGACTGCATGTGGAGCGGCTTCTCCGCCCGCGAGAAG
CTGGAGCGCGCCGTGAGCGAGAAGCTGCAGCACGGCCGCGGGCCGCCAACCGCCGGTTCCACCGCCCAGTCCCCG
GGAGCCGGCGCCGCCAGCCCTGCGGGTCGCGGGCACGGCGGGGCTGCGGGAGCCGGCCGCGCCGGGGCCGCCCTG
CCCGCCGAGCTCGCCCACCCGGCCGCCGAGTGCGTGGATCCCGCCGTGGTCTTCCCCTTTCCCGTGAACAAGCGC
GAGCCAGCGCCCGTGCCCGCAGCCCCGGCCAGTGCCCCGGCGGCGGGCCCTGCGGTCGCCTCGGGGGCGGGTATT
GCCGCCCCAGCCGGGGCCCCGGGGGTCGCCCCTCCGCGCCCAGGCGGCCGCCAGACCAGCGGCGGCGACCACAAG
GCCCTCAGTACCTCCGGAGAGGACACCCTGAGCGATTCAGATGATGAAGATGATGAAGAGGAAGATGAAGAGGAA
GAAATCGACGTGGTCACTGTGGAGAAGCGGCGTTCCTCCTCCAACACCAAGGCTGTCACCACATTCACCATCACT
GTGCGTCCCAAGAACGCAGCCCTGGGTCCCGGGAGGGCTCAGTCCAGCGAGCTGATCCTCAAACGATGCCTTCCC
ATCCACCAGCAGCACAACTATGCCGCCCCCTCTCCCTACGTGGAGAGTGAGGATGCACCCCCACAGAAGAAGATA
AAGAGCGAGGCGTCCCCACGTCCGCTCAAGAGTGTCATCCCCCCAAAGGCTAAGAGCTTGAGCCCCCGAAACTCT
GACTCGGAGGACAGTGAGCGTCGCAGAAACCACAACATCCTGGAGCGCCAGCGCCGCAACGACCTTCGGTCCAGC
TTTCTCACGCTCAGGGACCACGTGCCGGAGTTGGTAAAGAATGAGAAGGCCGCCAAGGTGGTCATTTTGAAAAAG
GCCACTGAGTATGTCCACTCCCTCCAGGCCGAGGAGCACCAGCTTTTGCTGGAAAAGGAAAAATTGCAGGCAAGA
CAGCAGCAGTTGCTAAAGAAAATTGAACACGCTCGGACTTGC**TAG**ACGCTTCTCAAAACTGGACAGTCACTGCCA
CTTTGCACATTTTGATTTTTTTTTAAACAAACATTGTGTTGACATTAAGAATGTTGGTTTACTTTCAAATCGGT
CCCCTGTCGAGTTCGGCTCTGGGTGGGCAGTAGGACCACCAGTGTGGGGTTCTGCTGGGACCTTGGAGAGCCTGC
ATCCCAGGATGCTGGGTGGCCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGACGGTTG
GGAGCCTCTGGGGCTGTTGAAGTCACCTTGTGTGTTCCAAGTTTCCAAACAACAGAAAGTCATTCCTTCTTTTTA
AAATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATACCCCTGGGGAACATTTCTGTAAA
TACCATTGACACATCCGCCTTTTGTATACATCCTGGGTAATGAGAGGTGGCTTTTGCGGCCAGTATTAGACTGGA
AGTTCATACCTAAGTACTGTAATAATACCTCAATGTTTGAGGAGCATGTTTTGTATACAAATATATTGTTAATCT
CTGTTATGTACTGTACTAATTCTTACACTGCCTGTATACTTTAGTATGACGCTGATACATAACTAAATTTGATAC
TTATATTTCGTATGAAAATGAGTTGTGAAAGTTTTGAGTAGATATTACTTTATCACTTTTTGAACTAAGAAACT
TTTGTAAAGAAATTTACTATATATATATGCCTTTTTCCTAGCCTGTTTCTTCCTGTTAATGTATTTGTTCATGTT
TGGTGCATAGAACTGGGTAAATGCAAAGTTCTGTGTTTAATTTCTTCAAAATGTATATATTTAGTGCTGCATCTT
ATAGCACTTTGAAATACCTCATGTTTATGAAAATAAATAGCTTAAAATTAAAAAAAAAAAAAAAAA

FIGURE 658

MPSCSTSTMPGMICKNPDLEFDSLQPCFYPDEDDFYFGGPDSTPPGEDIWKKFELLPTPPLSPSRGFAEHSSEPP
SWVTEMLLENELWGSPAEEDAFGLGGLGGLTPNPVILQDCMWSGFSAREKLERAVSEKLQHGRGPPTAGSTAQSP
GAGAASPAGRGHGGAAGAGRAGAALPAELAHPAAECVDPAVVFPFPVNKREPAPVPAAPASAPAAGPAVASGAGI
AAPAGAPGVAPPRPGGRQTSGGDHKALSTSGEDTLSDSDDEDDEEEDEEEEIDVVTVEKRRSSSNTKAVTTFTIT
VRPKNAALGPGRAQSSELILKRCLPIHQQHNYAAPSPYVESEDAPPQKKIKSEASPRPLKSVIPPKAKSLSPRNS
DSEDSERRRNHNILERQRRNDLRSSFLTLRDHVPELVKNEKAAKVVILKKATEYVHSLQAEEHQLLEKEKLQAR
QQQLLKKIEHARTC

FIGURE 659

GTCAGTCCCTCCTGTAGCCGCCGCCGCCGCCGCCCGCCGCCCCTCTGCCAGCAGCTCCGGCGCCACCTCGGGCCG
GCGTCTCCGGCGGGCGGGAGCCAGGCGCTGACGGGCGCGGCGGGGGCGGCCGAGCGCTCCTGCGGCTGCGACTCA
GGCTCCGGCGTCTGCGCTTCCCCATGGGGCTGGCCTGCGGCGCCTGGGCGCTCTGAGATTGTCACTGCTGTTCCA
AGGGCACACGCAGAGGGATTTGGAATTCCTGGAGAGTTGCCTTTGTGAGAAGCTGGAAATATTTCTTTCAATTCC
ATCTCTTAGTTTTCCATAGGAACATCAAGAAATCATGAACAACTTTGGTAATGAAGAGTTTGACTGCCACTTCCT
CGATGAAGGTTTTACTGCCAAGGACATTCTGGACCAGAAAATTAATGAAGTTTCTTCTTCTGATGATAAGGATGC
CTTCTATGTGGCAGACCTGGGAGACATTCTAAAGAAACATCTGAGGTGGTTAAAAGCTCTCCCTCGTGTCACCCC
CTTTTATGCAGTCAAATGTAATGATAGCAAAGCCATCGTGAAGACCCTTGCTGCTACCGGGACAGGATTTGACTG
TGCTAGCAAGACTGAAATACAGTTGGTGCAGAGTCTGGGGGTGCCTCCAGAGAGGATTATCTATGCAAATCCTTG
TAAACAAGTATCTCAAATTAAGTATGCTGCTAATAATGGAGTCCAGATGATGACTTTTGATAGTGAAGTTGAGTT
GATGAAAGTTGCCAGAGCACATCCCAAAGCAAAGTTGGTTTTGCGGATTGCCACTGATGATTCCAAAGCAGTCTG
TCGTCTCAGTGTGAAATTCGGTGCCACGCTCAGAACCAGCAGGCTCCTTTTGGAACGGGCGAAAGAGCTAAATAT
CGATGTTGTTGGTGTCAGCTTCCATGTAGGAAGCGGCTGTACCGATCCTGAGACCTTCGTGCAGGCAATCTCTGA
TGCCCGCTGTGTTTTTGACATGGGGGCTGAGGTTGGTTTCAGCATGTATCTGCTTGATATTGGCGGTGGCTTTCC
TGGATCTGAGGATGTGAAACTTAAATTTGAAGAGATCACCGGCGTAATCAACCCAGCGTTGGACAAATACTTTCC
GTCAGACTCTGGAGTGAGAATCATAGCTGAGCCCGGCAGATACTATGTTGCATCAGCTTTCACGCTTGCAGTTAA
TATCATTGCCAAGAAAATTGTATTAAAGGAACAGACGGGCTCTGATGACGAAGATGAGTCGAGTGAGCAGACCTT
TATGTATTATGTGAATGATGGCGTCTATGGATCATTTAATTGCATACTCTATGACCACGCACATGTAAAGCCCCT
TCTGCAAAAGAGACCTAAACCAGATGAGAAGTATTATTCATCCAGCATATGGGGACCAACATGTGATGGCCTCGA
TCGGATTGTTGAGCGCTGTGACCTGCCTGAAATGCATGTGGGTGATTGGATGCTCTTTGAAAACATGGGCGCTTA
CACTGTTGCTGCTGCCTCTACGTTCAATGGCTTCCAGAGGCCGACGATCTACTATGTGATGTCAGGGCCTGCGTG
GCAACTCATGCAGCAATTCCAGAACCCCGACTTCCCACCCGAAGTAGAGGAACAGGATGCCAGCACCCTGCCTGT
GTCTTGTGCCTGGGAGAGTGGGATGAAACGCCACAGAGCAGCCTGTGCTTCGGCTAGTATTAATGTGTAGATAGC
ACTCTGGTAGCTGTTAACTGCAAGTTTAGCTTGAATTAAGGGATTTGGGGGGACCATGTAACTTAATTACTGCTA
GTTTTGAAATGTCTTTGTAAGAGTAGGGTCGCCATGATGCAGCCATATGGAAGACTAGGATATGGGTCACACTTA
TCTGTGTTCCTATGGAAACTATTTGAATATTTGTTTTATATGGATTTTTATTCACTCTTCAGACACGCTACTCAA
GAGTGCCCCTCAGCTGCTGAACAAGCATTTGTAGCTTGTACAATGGCAGAATGGGCCAAAAGCTTAGTGTTGTGA
CCTGTTTTTAAAATAAAGTATCTTGAAATAATTAGGC

FIGURE 660

MNNFGNEEFDCHFLDEGFTAKDILDQKINEVSSSDDKDAFYVADLGDILKKHLRWLKALPRVTPFYAVKCNDSKA
IVKTLAATGTGFDCASKTEIQLVQSLGVPPERIIYANPCKQVSQIKYAANNGVQMMTFDSEVELMKVARAHPKAK
LVLRIATDDSKAVCRLSVKFGATLRTSRLLLERAKELNIDVVGVSFHVGSGCTDPETFVQAISDARCVFDMGAEV
GFSMYLLDIGGGFPGSEDVKLKFEEITGVINPALDKYFPSDSGVRIIAEPGRYYVASAFTLAVNIIAKKIVLKEQ
TGSDDEDESSEQTFMYYVNDGVYGSFNCILYDHAHVKPLLQKRPKPDEKYYSSSIWGPTCDGLDRIVERCDLPEM
HVGDWMLFENMGAYTVAAASTFNGFQRPTIYYVMSGPAWQLMQQFQNPDFPPEVEEQDASTLPVSCAWESGMKRH
RAACASASINV

FIGURE 661

ATGAGTCAGCAGCGGCCGGCGAGGAAGTTACCCAGTCTCCTCCTGGACCCGACGGAGGAGACGGTTCGCCGTCGG
TGCCGAGACCCCATCAACGTGGAGGGCCTGCTGCCATCAAAAATAAGGATTAATTTAGAAGATAATGTACAATAT
GTGTCCATGAGAAAAGCTCTAAAAGTGAAGAGACCTCGTTTTGATGTATCGCTGGTTTATTTAACTCGAAAATTT
ATGGATCTTGTCAGATCTGCTCCCGGGGGTATTCTTGACTTAAACAAGGTTGCAACGAAACTGGGAGTCCGAAAG
CGGAGAGTGTATGACATCACCAATGTCTTAGATGGAATCGACCTCGTTGAAAAGAAATCCAAGAACCATATTAGA
TGGATAGGATCTGATCTTAGCAATTTTGGAGCAGTTCCCCAACAAAAGAAGCTACAGGAGGAACTTTCTGACTTA
TCAGCAATGGAAGATGCTTTGGATGAGTTAATTAAGGATTGTGCTCAGCAGCTGTTTGAGTTAACAGATGACAAA
GAAAATGAAAGACTAGCATATGTGACCTATCAAGACATTCATAGCATTCAGGCCTTCCATGAACAGATCGTCATT
GCAGTTAAAGCTCCAGCAGAAACCAGATTGGATGTTCCAGCTCCCAGAGAAGACTCTATCACAGTGCACATAAGG
AGCACCAACGGACCTATCGATGTCTATTTGTGTGAAGTGGAGCAGGGTCAGACCAGTAACAAAAGGTCTGAAGGT
GTCGGGACCTCTTCATCTGAGAGCACTCATCCAGAAGGCCCTGAGGAAGAAGAAAATCCTCAGCAAAGTGAAGAA
TTGCTTGAAGTAAGCAACTGATGGCATTTGAGAATTTATGTATCACTGAGTTTTTTGGGAATATCTTCGTGGAGA
ATTACGCATCAAATTTGATTCTCAGAGCAATAAATTATCCATGAAGTGCTCTCGTTCTCAGTAGCGGCATCATGG
CCAGTAGTGTCTTTGAGGAGTTCACCACTTAGATTACTGAGTAATTGTGGTTTCCACATTTGAAAACAACTCCTT
TTATAATTATTCACTGCTTTTTGTCAGTGAAATAGACATCTTGCCTCCTGAAGTAGCTTCATCACAGAGTGTCAT
GAAGACAGACAGTCAGGCTGAAATGGACAGTTCTTTGTGGACTCTACCCTTCCCTTCAAGGAGTATGTCATATAT
CACAAAAGAAATTGCCTTACACTGGTTCATGTTTGCAGTTACTGTTGTACATTGCATAGATGTACACACGAATTT
AAATGTGATGTCTTTGTATATATCTGTATAATGTTGAGATTACTTACGAAATATGTCTGAGTGACACTTTTCACC
CTTGTACAGCCAAAATAATGTATATATGGAAAGTGACAGACAAATTCTCTAATCTCTTTGGTACCTATAACTTAT
TAGAATCCTCTGGATGAGGGTTAGAAGAGACTTTTTCCAAACTTCTACATGTAGAAGTATCATAAATGTGCTACA
CATTTATGTTTGTGGATTTAATTAAAGTATTTTAATATGGTTTTCAGTGCTAAAATTGGAGTCAGATACTTCTTG
GTTTTAAGCTGTCTACCTAATTGCTGTCTCCCAGCAGACTGGTGGCATGCCCAGTGGCTTTGGGGGCAAGGATAG
AAATGCCATCAGGAAATAGCTGAATTCATTGTGAAACATGAATTCAGTCATGGTGATAATTGGAAACTCCTTTCA
GGTTTTTGCAAGTAGATTTTGTAATGTTTGTGTATGCAGCCTTGCTGTTGAGTCAGTCCAAGGGGTTTTACTTAG
GACAAGTTGTACCTTGCCCTCTCTCCAGCTCTGCTCCCACATTTTCACATACCTAGCTGTTTCTACCTCATTGGG
TAAGTCATTTACCACTCTGTGCCTCAGTTTACTCTGTAGTTTACCATTAGACTGTGAGCTCCTTGAGGGACTTTG
TCATAATCACTGTTACATCCCAGTGCCTCACACCATGCCTGGCCCTTAAGAAGTGCTCAATAAATGTCTGAACAA
ATAA

FIGURE 662

CTCTGTAGCTGTGACCCTGATACCGCGTGGTGTGCTCCGAACACATGGTGCCCAGAACGAAGGCGGCGTCCAGAA
GCCCTAGGTCCCAGAGGTCCGCTCAGCGGCAGGCGCATAAGGCGGGGCCGGCGCGGGCCTTTCCTTCCATCGGAA
CCGTTCTCCCGGGGCTGAGTCCCTGCCCGGACTCCGAACGCCGAAGACCAGGGGCCGGAAGCGCGCGCCGCCACT
GCCACGCCGTGTCAGTCGGGAGGGAGGGAGCGAGCAGGCGAAGCCGCGGAGGACGGGGTGAAG**ATG**GCGGCCTTC
TCCGAGATGGGTGTAATGCCTGAGATTGCACAAGCTGTGGAAGAGATGGATTGGCTCCTCCCAACTGATATCCAG
GCTGAATCTATCCCATTGATCTTAGGAGGAGGTGATGTACTTATGGCTGCAGAAACAGGAAGTGGCAAAACTGGT
GCTTTTAGTATTCCAGTTATCCAGATAGTTTATGAAACTCTGAAAGACCAACAGGAAGGCAAAAAAGGAAAAACA
ACAATTAAAACTGGTGCTTCAGTGCTGAACAAATGGCAGATGAACCCATATGACAGAGGATCTGCTTTTGCAATT
GGGTCAGATGGTCTTTGTTGTCAAAGCAGAGAAGTAAAGGAATGGCATGGGTGTAGAGCTACTAAAGGATTAATG
AAAGGGAAACACTACTATGAAGTATCCTGTCATGACCAAGGGTTATGCAGGGTCGGGTGGTCTACCATGCAGGCC
TCTTTGGACCTAGGTACTGACAAGTTTGGATTTGGCTTTGGTGGAACAGGAAAGAAATCCCATAACAAACAATTT
GATAATTATGGAGAGGAATTCACTATGCATGATACCATTGGATGTTACCTGGATATAGATAAGGGACATGTCAAG
TTCTCCAAAAATGGAAAAGATCTTGGTCTGGCATTTGAAATACCACCACATATGAAAAACCAAGCCCTCTTTCCT
GCCTGTGTTTTGAAGAATGCTGAACTGAAATTTAACTTCGGTGAAGAGGAATTTAAGTTTCCACCAAAAGATGGC
TTTGTTGCTCTTTCCAAGGCACCGGATGGTTACATTGTCAAATCACAGCACTCAGGTAATGCACAGGTGACACAA
ACAAAGTTTCTCCCCAATGCTCCGAAAGCTCTCATTGTTGAACCTTCCCGGGAGTTAGCTGAACAAACTTTGAAC
AACATCAAGCAGTTTAAGAAATACATTGATAATCCTAAATTAAGGGAGCTTCTGATAATTGGAGGTGTTGCAGCC
CGGGATCAGCTCTCTGTTTTGGAAAATGGAGTAGATATAGTTGTAGGTACTCCGGGAAGACTAGATGACTTGGTG
TCAACTGGAAAGCTGAACTTATCTCAAGTTAGATTCCTGGTCCTGGATGAAGCTGATGGGCTTCTTTCTCAAGGT
TATTCTGATTTTATAAATAGGATGCACAATCAGATTCCTCAGGTTACCTCTGATGGAAAAAGACTTCAGGTGATT
GTTTGCTCTGCCACTTTGCATTCTTTCGATGTAAAGAAACTGTCCGAGAAGATAATGCATTTTCCTACATGGGTT
GACTTAAAAGGAGAAGACTCTGTTCCAGATACTGTACACCATGTTGTTGTCCCAGTAAATCCCAAAACTGACAGA
CTCTGGGAAAGGCTTGGAAAGAGCCACATTAGAACTGATGATGTACATGCAAAAGATAACACAAGACCTGGTGCT
AATAGTCCAGAGATGTGGTCTGAAGCTATTAAAATCCTGAAAGGGGAGTATGCTGTCCGGGCAATCAAGGAACAT
AAGATGGATCAAGCAATTATCTTCTGTAGAACCAAAATTGACTGTGATAACTTGGAGCAGTACTTTATACAACAA
GGAGGAGGACCTGATAAAAAAGGACACCAGTTCTCATGTGTTTGTCTTCATGGTGACAGAAAGCCTCATGAGAGA
AAGCAAAACTTGGAAAGATTTAAGAAAGGAGATGTAAGATTCTTGATTTGCACAGATGTAGCTGCTAGAGGAATT
GATATCCACGGTGTTCCTTATGTTATAAATGTCACTCTGCCCGATGAAAAGCAAAACTACGTACATCGAATTGGC
AGAGTAGGAAGAGCTGAAAGGATGGGTCTGGCAATTTCCCTGGTGGCAACAGAAAAAGAAAAGGTTTGGTACCAT
GTATGTAGCAGCCGTGGAAAAGGGTGTTATAACACAAGACTCAAGGAAGATGGAGGCTGTACCATATGGTACAAC
GAGATGCAGTTACTATCTGAGATAGAAGAACACCTGAACTGTACCATTTCTCAGGTTGAGCCGGATATAAAGGTA
CCAGTGGATGAATTTGATGGGAAAGTTACCTACGGTCAGAAAAGGGCTGCTGGTGGTGGAAGCTATAAAGGCCAT
GTGGATATTTTGGCACCTACTGTTCAAGAGTTGGCTGCCCTTGAAAAGGAGGCGCAGACATCTTTCCTGCATCTT
GGCTACCTTCCTAACCAGCTGTTCAGAACCTTC**TGA**TTTTTACATTTACTGAATAAGATTTGAGTAATGAAAGTC
TGTAGTCTTAAAACTCTAAAACAGTTGTACTGCTTCCAAGCAGCAGTATTTATAGTAACGTAAGCTATTAATGCT
AACTCTTGCATGTCAAGAAACATTAGTCTTAGGAATTCTTCAAAAAATGGCATCCCAATGAAAATAAATTTGATG
ACTATA

FIGURE 663

MAAFSEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAETGSGKTGAFSIPVIQIVYETLKDQQEGK
KGKTTIKTGASVLNKWQMNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYEVSCHDQGLCRVGWS
TMQASLDLGTDKFGFGFGGTGKKSHNKQFDNYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKNQ
ALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVKSQHSGNAQVTQTKFLPNAPKALIVEPSRELAE
QTLNNIKQFKKYIDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVSTGKLNLSQVRFLVLDEADGL
LSQGYSDFINRMHNQIPQVTSDGKRLQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHVVVPVNP
KTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEAIKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQY
FIQQGGGPDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAARGIDIHGVPYVINVTLPDEKQNYV
HRIGRVGRAERMGLAISLVATEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEEHLNCTISQVEP
DIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDILAPTVQELAALEKEAQTSFLHLGYLPNQLFRTF

FIGURE 664A

GAACATGGCGGCCCCCGAGTCAGGGCCGGCTTTGAGTCCAGGCACTGCAGAGGCCTAGAGGCAACCAAAAACATG
GTGCATCCTTTATCATCACGAAAGCAATTCGAGATCGTTTATTATTTTACGCCAATACATCTGGTACAGCCCGG
CACCTTTTTGCTCCCTGATGGACTGGTTCGCTTGGTTAATAAACAGATAAACTGGCATTTGGTACTTGCAAGCA
ATAGCACTAGAGTGCATCTATACCTGTGAACGAAATGATCAACTCTGTCTTTGCTATGACCTACTAGAATGTCTG
CCAGAAAGAGGATATGGTGATAAGACAGAGGCAACCACAAAGCTTCATGACATGGTAGACCAACTGGAACAAATT
CTCAGTGTGTCAGAGCTTTTGGAAAAACATGGACTCGAGAAACCAATTTCATTTGTTAAAAACACTCAATCTAGC
TCAGAAGAGGCACGCAAGCTGATGGTTAGATTGACGAGGCACACTGGCCGGAAGCAGCCTCCTGTCAGTGAGTCT
CATTGGAGAACGTTGCTGCAAGACATGTTAACTATGCAGCAGAATGTATACACATGTCTAGATTCTGATGCCTGC
TATGAGATATTTACAGAAAGCCTTCTGTGCTCTAGTCGCCTTGAAAACATCCACCTGGCTGGACAGATGATGCAC
TGCAGTGCTTGTTCAGAAAATCCTCCAGCTGGTATAGCCCATAAAGGGAAACCCCACTACAGGGTCAGCTACGAA
AAGAGTATTGACTTGGTTTTGGCTGCCAGCAGAGAGTACTTCAATTCTTCTACCAACCTCACTGATAGCTGCATG
GATCTAGCCAGGTGCTGCTTACAACTGATAACAGACAGACCCCCTGCCATTCAAGAGGAGCTAGATCTTATCCAA
GCCGTTGGATGTCTTGAAGAATTTGGGGTAAAGATCCTGCCTTTGCAAGTGCGATTGTGCCCTGATCGGATCAGT
CTCATCAAGGAGTGTATTTCCCAGTCCCCCACATGCTATAAACAATCCACCAAGCTTCTGGGCCTTGCTGAGCTG
CTGAGGGTTGCAGGTGAGAACCCAGAAGAAAGGCGGGGACAGGTTCTAATCCTTTTAGTGGAGCAGGCACTTCGC
TTCCATGACTACAAAGCAGCCAGTATGCATTGTCAGGAGCTGATGGCCACAGGTTATCCTAAAAGTTGGGATGTT
TGTAGCCAGTTAGGACAATCAGAAGGTTACCAGGACTTGGCCACTCGTCAAGAGCTCATGGCTTTTGCTTTGACA
CATTGCCCTCCTAGCAGCATTGAACTTCTTTTGGCAGCTAGCAGCTCTCTGCAGACAGAAATTCTTTATCAAAGA
GTGAATTTCCAGATCCATCATGAAGGAGGGGAAAATATCAGTGCTTCACCATTAACTAGTAAAGCAGTACAAGAG
GATGAAGTAGGTGTTCCAGGTAGCAATTCAGCTGACCTATTGCGCTGGACCACTGCTACCACCATGAAAGTCCTT
TCCAACACCACAACCACCACCAAAGCGGTGCTGCAGGCCGTCAGTGATGGGCAGTGGTGGAAGAAGTCTTTAACT
TACCTTCGACCCCTTCAGGGGCAAAAATGTGGTGGTGCATATCAAATCGGAACTACAGCCAATGAAGATCTAGAG
AAACAAGGGTGTCATCCTTTTTATGAATCTGTCATCTCAAATCCTTTTGTCGCTGAGTCTGAAGGGACCTATGAC
ACCTATCAGCATGTTCCAGTGGAAAGCTTTGCAGAAGTATTGCTGAGAACTGGAAAATTGGCAGAGGCTAAAAAT
AAAGGAGAAGTATTTCCAACAACTGAAGTTCTCTTGCAACTAGCAAGTGAAGCCTTGCCAAATGACATGACCTTG
GCTCTTGCTTACCTTCTTGCCTTACCACAAGTGTTAGATGCTAACCGGTGCTTTGAAAAGCAGTCCCCCTCTGCA
TTATCTCTCCAGCTGGCAGCGTATTACTATAGCCTCCAGATCTATGCCCGATTGGCCCCATGTTTCAGGGACAAG
TGCCATCCTCTTTACAGGGCTGATCCCAAAGAACTAATCAAGATGGTCACCAGGCATGTGACTCGACATGAGCAC
GAAGCCTGGCCTGAAGACCTTATTTCACTGACCAAGCAGTTACACTGCTACAATGAACGTCTCCTGGATTTCACT
CAGGCGCAGATCCTTCAGGGCCTTCGGAAGGGTGTGGACGTGCAGCGGTTTACTGCAGATGACCAGTATAAAAGG
GAAACTATCCTTGGTCTGGCAGAAACTCTAGAGGAAAGCGTCTACAGCATTGCTATTTCTCTGGCACAACGTTAC
AGTGTCTCCCGCTGGGAAGTTTTTATGACCCATTTGGAGTTCCTCTTCACGGACAGTGGTTTGTCCACACTAGAA
ATTGAAAATAGAGCCCAAGACCTTCATCTCTTTGAGACTTTGAAGACTGATCCAGAAGCCTTTCACCAGCACATG
GTCAAGTATATTTACCCTACTATTGGTGGCTTTGATCACGAAAGGCTGCAGTATTATTTCACTCTTCTGGAAAAC
TGTGGCTGTGCAGATTTGGGGAACTGTGCCATTAAACCAGAAACCCACATTCGACTGCTGAAGAAGTTTAAGGTT
GTTGCATCAGGTCTTAATTACAAAAAGCTGACAGATGAAAACATGAGTCCTCTTGAAGCATTGGAGCCAGTTCTT
TCAAGTCAAAATATCTTGTCTATTTCCAAACTTGTTCCCAAAATCCCTGAAAAGGATGGACAGATGCTTTCCCCA
AGCTCTCTGTACACCATCTGGTTACAGAAGTTGTTCTGGACTGGAGACCCTCATCTCATTAAACAAGTCCCAGGC
TCTTCACCGGAGTGGCTTCATGCCTATGATGTCTGCATGAAGTACTTTGATCGTCTCCACCCAGGTGACCTCATC
ACTGTGGTAGATGCAGTTACATTTTCTCCAAAAGCTGTGACCAAGCTGTCTGTGGAAGCCCGTAAAGAGATGACT
AGAAAGGCTATTAAGACAGTCAAACATTTTATTGAGAAGCCAAGGAAAAGAAACTCAGAAGACGAAGCTCAAGAA
GCTAAGGATTCTAAAGTTACCTATGCAGATACTTTGAATCATCTGGAGAAATCACTTGCCCACCTGGAAACCCTG
AGCCACAGCTTCATCCTTTCTCTGAAGAATAGTGAGCAGGAAACACTGCAAAAATACAGTCACCTCTATGATCTG
TCCCGATCAGAAAAAGAGAAACTTCATGATGAAGCTGTGGCTATTTGTTTAGATGGTCAGCCTCTAGCAATGATT
CAGCAGCTGCTAGAGGTGGCAGTTGGCCCTCTTGACATCTCACCCAAGGATATAGTGCAGAGTGCAATCATGAAA
ATAATTTCTGCATTGAGTGGTGGCAGTGCTGACCTTGGTGGGCCAAGGGACCCACTGAAGGTCCTGGAAGGTGTT
GTTGCAGCAGTCCACGCCAGTGTGGACAAGGGTGAGGAGCTGGTTTCACCTGAGGACCTGCTGGAGTGGCTGCGG
CCTTTCTGTGCTGATGACGCCTGGCCGGTGCGGCCCCGCATTCACGTGCTGCAGATTTTGGGGCAATCATTTCAC

FIGURE 664B

CTGACTGAGGAGGACAGCAAGCTCCTCGTGTTCTTTAGAACTGAAGCCATTCTCAAAGCCTCCTGGCCCCAGAGA
CAGGTAGACATAGCTGACATTGAGAATGAAGAGAACCGCTACTGTCTATTCATGGAACTCCTGGAATCTAGTCAC
CACGAGGCTGAATTTCAGCACTTGGTTTTACTTTTGCAAGCTTGGCCACCTATGAAAAGTGAATATGTCATAACC
AATAATCCATGGGTGAGACTAGCTACAGTGATGCTAACCAGATGTACGATGGAGAACAAGGAAGGATTGGGGAAT
GAAGTTTTGAAAATGTGTCGCTCTTTGTATAACACCAAGCAGATGCTGCCTGCAGAGGGTGTGAAGGAGCTGTGT
CTGCTGCTGCTTAACCAGTCCCTCCTGCTTCCATCTCTGAAACTTCTCCTCGAGAGCCGAGATGAGCATCTGCAC
GAGATGGCACTGGAGCAAATCACGGCAGTCACTACGGTGAATGATTCCAATTGTGACCAAGAACTTCTTTCCCTG
CTCCTGGATGCCAAGCTGCTGGTGAAGTGTGTCTCCACTCCCTTCTATCCACGTATTGTTGACCACCTCTTGGCT
AGCCTCCAGCAAGGGCGCTGGGATGCAGAGGAGCTGGGCAGACACCTGCGGGAGGCCGGCCATGAAGCCGAAGCC
GGGTCTCTCCTTCTGGCCGTGAGGGGGACTCACCAGGCCTTCAGAACCTTCAGTACAGCCCTCCGCGCAGCACAG
CACTGGGTGTGAGGGCCACCTGTGGCCCTGCTCCTTAGCAGAAAAAGCATCTGGAGTTGAATGCTGTTCCCAGAA
GCAACATGTGTATCTGCCGATTGTTCTCCATGGTTCCAACAAATTGCAAATAAAACTGTATGGAAACG

FIGURE 665

ATGAGATCTCGGCTGCGAAGTGTGTCATCAGCATCTGGCTTTCTGGGTTATGATGTGGTCAGGGATGTGTCTTCT
GGCCCATTTTGGAGGCGCAAAAATGGTGATCCATGTTTGGATTTATGTGGAAGGGACAGTTCCACAGTATGGAAA
AGGGGAGACAGTCCCAGGAAGCGTGAAGAGGAAAGGTCATTGGGAATCTCTCAGTACCTCTGCCCTAATCTCTTC
TCTCCTACGGAGGCAGTTAAGTCTAAAGCCATTTGTCTGGTTTCCATATCTGAACTTCAAGCAGCATCTTCTGGA
CTTAGTTCTTGGTGGCTGGAGCAGGGAAAGTGTGGCCTCATTGAAATGGGATCAGGTTTCAGGATGTTTCATGTG
TCTGTGTCTTTCTCACACATTGTGAGGAACAGGACAGTCCCTCTGATGCGCTGGTACCTGGCCGCCATGCAGATC
ATGAGGGGAGAGAAGCAGGCTGCTTCGGGGAATCCTGCCATAGAGGCTGGAGCTTCATGTGCATCTCAGCCAGCC
CTGCAGCAGCCCTCAGCAGCCCTTCTGTGGGGCTGGGGTATCTGTTGCCCAGGAAATCACTGGGCTGAGGAAGTA
GGAGATGAATGGCTCTGTGCTATCACACCATCTTCTGCATTGAGTCTTCTTCGCTTTCTTATCATCGTCATCATG
ATTATCATCAATAAATTTGTAAGGAAGGAAACAGGACTGCTTATTGATTTTCATTTCTATGCTACTGAGAGCCAA
GGCTACGGATTTCTTTCCCCAGGAATGGAGAGAGGAAAGAGATGTGAGATTGGCTACCCAACTGTTGCATCAGTA
CCCCATTCTATCATCAACGGGTACAAACGAGTCCTGGCCTTGTCTGTGGAGACGGATTACACCTTCCCACTCGCT
GAAAAGGTCAAGGCCTTCTTGGCTGATCCATCTGCCTTTGAGATGGAGGAGTGGAGGGGTGATGATAAAATGGAA
GCTCCCGTGTCAAGAGATCAGGCAAATGGGGAGACTCCGTGGGATCCTCTGAAGAATCTACATGCACGTACTTAC
GAGAATCAGATTAGGGATGCCTACCACACAGGAGTACCAATGTTTAGTATTAGCCCGTAA

FIGURE 666

MRSRLRSVSSASGFLGYDVVRDVSSGPFWRRKNGDPCLDLCGRDSSTVWKRGDSPRKREEERSLGISQYLCPNLF
SPTEAVKSKAICLVSISELQAASSGLSSWWLEQGKCGLIEMGSGFRMFHVSVSFSHIVRNRTVPLMRWYLAAMQI
MRGEKQAASGNPAIEAGWERTGAQM

FIGURE 667

CGCGAAGAAGCTGGCAGGGGCACGAGCCGGGGGCGGGTTTGAAGACGCGTCGTTGGGTTTTGGAGGCCGTGAAAC
AGCCGTTTGAGTTTGGCTGCGGGTGGAGAACGTTTGTCAGGGGCCCGGCCAAGAAGGAGGCCCGCCTGTTACG**AT**
GGTGTCCATGAGTTTCAAGCGGAACCGCAGTGACCGGTTCTACAGCACCCGGTGCTGCGGCTGTTGCCATGTCCG
CACCGGGACGATCATCCTGGGGACCTGGTACATGGTAGTAAACCTATTGATGGCAATTTTGCTGACTGTGGAAGT
GACTCATCCAAACTCCATGCCAGCTGTCAACATTCAGTATGAAGTCATCGGTAATTACTATTCGTCTGAGAGAAT
GGCTGATAATGCCTGTGTTCTTTTTGCCGTCTCTGTTCTTATGTTTATAATCAGTTCAATGCTGGTTTATGGAGC
AATTTCTTATCAAGTGGGTTGGCTGATTCCATTCTTCTGTTACCGACTTTTTGACTTCGTCCTCAGTTGCCTGGT
TGCTATTAGTTCTCTCACCTATTTGCCAAGAATCAAAGAATATCTGGATCAACTACCTGATTTTCCCTACAAAGA
TGACCTCCTGGCCTTGGACTCCAGCTGCCTCCTGTTCATTGTTCTTGTGTTCTTTGCCTTATTCATCATTTTTAA
GGCTTATCTAATTAACTGTGTTTGGAACTGCTATAAATACATCAACAACCGAAACGTGCCGGAGATTGCTGTGTA
CCCTGCCTTTGAAGCACCTCCTCAGTACGTTTTGCCAACCTATGAAATGGCCGTGAAAATGCCTGAAAAAGAACC
ACCACCTCCTTACTTACCTGCC**TGA**AGAAATTCTGCCTTTGACAATAAATCCTATACCAGCTTTTTGTTTGTTTA
TGTTACAGAATGCTGCAATTCAGGGCTCTTCAAACTTGTTTGATATAAAATATGTTGTCTTTTGTTTAAGCATTT
ATTTTCAAACACTAAGGAGCTTTTTGACATCTGTTAAACGTCTTTTTGTTTTTTTGTTAAGTCTTTTACATTTTA
ATAGTTTTTGAAGACAATCTAGGTTAAGCAAGAGCAAAGTGCCATTGTTTGCCTTTAATTGGGGGGTGGGAAGGG
AAAGAGGGTACTTGCCACATAGTTTCCTTTTTAACTGCACTTTCTTTATATAATCGTTTGCATTTTGTTACTTGC
TACCCTGAGTACTTTCAGGAAGACTGACTTAAATATTCGGGGTGAGTAAGTAGTTGGGTATAAGATCTGAACTTT
TCATCTGCAGAGGCAAGAAAAATATTTGACATTGTGACTTGACTGTGGAAGATGATGGTTGCATGTTTCTAGTTT
GTATATGTTTCCATCTTTGTGATAAGATGATTTAATAAATCTCTTTAAATACTT

FIGURE 668

MVSMSFKRNRSDRFYSTRCCGCCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAVNIQYEVIGNYYSSER
MADNACVLFAVSVLMFIISSMLVYGAISYQVGWLIPFFCYRLFDFVLSCLVAISSLTYLPRIKEYLDQLPDFPYK
DDLLALDSSCLLFIVLVFFALFIIFKAYLINCVWNCYKYINNRNVPEIAVYPAFEAPPQYVLPTYEMAVKMPEKE
PPPPYLPA

FIGURE 669

GCGGCTTGCGGGGACCACAGCTCCCGAAAGCGACGTTCGGCCACCGGAGGAGCGGGAGCCAAGCAGGCGGAGCTC
GGCGGGAGAGGTGCGGGCCGAATCCGAGCCGAGCGGAGAGGAATCCGGCAGTAGAGAGCGGACTCCAGCCGGCGG
ACCCTGCAGCCCTCGCCTGGGACAGCGGCGCGCTGGGCAGGCGCCCAAGAGAGCATCGAGCAGCGGAACCCGCGA
AGCCGGCCCGCAGCCGCGACCCGCGCAGCCTGCCGCTCTCCCGCCGCCGGTCCGGGCAGCATGAGGCGCGCGGCG
CTCTGGCTCTGGCTGTGCGCGCTGGCGCTGAGCCTGCAGCCGGCCCTGCCGCAAATTGTGGCTACTAATTTGCCC
CCTGAAGATCAAGATGGCTCTGGGGATGACTCTGACAACTTCTCCGGCTCAGGTGCAGGTGCTTTGCAAGATATC
ACCTTGTCACAGCAGACCCCCTCCACTTGGAAGGACACGCAGCTCCTGACGGCTATTCCCACGTCTCCAGAACCC
ACCGGCCTGGAGGCTACAGCTGCCTCCACCTCCACCCTGCCGGCTGGAGAGGGGCCCAAGGAGGGAGAGGCTGTA
GTCCTGCCAGAAGTGGAGCCTGGCCTCACCGCCCGGGAGCAGGAGGCCACCCCCCGACCCAGGGAGACAGCATCA
GGGTTAAGAAGACTTTTTTTTTTTTTTTTTAAACTAGGAGAACCAAATCTGGAAGCCAAAATGTAGGCTTAGTTT
GTGTGTTGTCTCTTGAGTTTGTCGCTCATGTGTGCAACAGGGTATGGACTATCTGTCTGGTGGCCCCGTTTCTGG
TGGTCTGTTGGCAGGCTGGCCAGTCCAGGCTGCCGTGGGGCCGCCGCCTCTTTCAAGCAAGGCCAGAGGCCCCCA
GCCCAGGGCTCCTGCACTTACTTGCTTATTTGACAACGTTTCAGCGACTCCGTTGGCCACTCCGAGAGGTGGGCC
AGTCTGTGGATCAGAGATGCACCACCAAGCCAAGGGAACCTGTGTCCGGTATTCGATACTGCGACTTTCTGCCTG
GAGTGTATGACTGCACATGACTCGGGGGTGGGGAAAGGGGTCGGCTGACCATGCTCATCTGCTGGTCCGTGGGAC
GGTGCCCAAGCCAGAGGCTGGGTTCATTTGTGTAACGACAATAAACGGTACTTGTCATTTCGGGC

FIGURE 670

ACTGCGCGCCCCGCCCGGAGTCCCCGCCGCCGTC**ATG**CAGTCCCCGGCGGTGCTCGTCACCTCCAGGCGACTTCA
GAATGCCCACACTGGCCTCGACCTGACTGTGCCCCAGCACCAGGAGGTACGGGGCAAGATGATGTCTGGACACGT
GGAGTACCAGATCCTGGTGGTGACCCGTCTGGCTGCGTTCAAGTCGGCCAAGCACAGGCCCGAGGATGTCGTCCA
GTTCTTGGTCTCCAAAAAGTACAGCGAGATTGAGGAGTTTTACCAGAAACTGAGCAGTCGTTATGCAGCAGCCAG
CCTCCCCCCACTACCCAGGAAGGTCCTGTTTGTTGGGGAGTCTGACATCCGGGAGAGGAGAGCCGTGTTCAATGA
GATCCTGCGCTGTGTCTCCAAGGATGCCGAGTTGGCAGGCAGCCCAGAGCTGCTAGAGTTCTTAGGTACCAGATC
CCCAGGGGCTGCAGGGCTCACCAGCAGAGATTCCTCTGTCCTGGATGGCACAGACAGTCAGACAGGGAATGATGA
AGAGGCTTTCGACTTTTTTGAGGAGCAAGACCAAGTGGCAGAAGAGGGTCCGCCCGTCCAGAGCCTGAAGGGCGA
GGATGCTGAGGAATCCTTGGAGGAGGAGGAGGCGCTGGACCCTCTGGGCATTATGCGCTCCAAGAAGCCCAAGAA
ACATCGGTGTGAAGGGAAGGGACTGGGCCCTGCAGGGTCAGAACCTCCCCACCCCCAGGGGAGGCCAGGCAGAAG
CCTGGGTCACAGCACCCAGAACTGCATGGTTCCATTTTCTCCGGGGCTGTGGGGCCAAAGTAGAAGCCTGCGGGC
TGCGGGAGCGGCTCTCACCCTAGGAGCCAGAGCCCAATGTGTCTTATTCCCCGTGGACATGAAGGGGAGGGAGGG
TGTGGGGATGCCTTGCCAACCAGAAGCCCAGCCCCAAGGA**TGA**AGCAAGACATGTGGGGCCGTAGCGAGGTGTCA
CATGGGGCAGGGAAGCTTCATGCCCACGGGTTCTGCCAGCCCCAGCACAGACCCAAACTGGGGCTGGGCCTCTAT
CCCTCCTCTGCCTCTGTTCGCATAGTAAGAAGGAGTGACCGGTATCCTCCCCTTCCCCTACCCTAAGCTGTAGCC
TGGGTGACTGACTGGCCTGGGCCTGGGGTGGGGACGTCCCCAAGCCAAATTACTCCAGGGCCTCTGCTCCTCGTG
GCTGCCAGGGGCCTGCAGGGTCTGGGTGGGTCTCCCAGGAGAGGAATACTGAGTGGGAGATCGGCTGTCTGGAGT
GTTCTGATGCAAGTCTCTCTCTCCTGAGCCTCCTCTTGATGCAAGCTCTAAAGGGAGAAGTCAGGCCCTGCCTCT
CCAGGGTATAGACGGCCCTGCTAGGCCCCAGTTCTTCCTCCTTCCCCCTTTCCCAGGAAAGGCCAGCCCAGTCCA
TGGCCTTCTTGGGCCTCTGGGCACAGAGCCAATGTTCGTCATTGCAGCTCTCAGCAAACTGGGTCATAGCTTTCC
CCACAGCTCAGCCTGGGGCCTGGGCAGGGCTCCCAGCCTGCACCGCCTCCCACTGCCAGTGGGGCATGATTCTCT
CAGGCTTCTGCCCCGAGGCCTTCGTCGTCCTCAGGGTCTGGACTTGGTCAGTGGCCTTTCACCAGTGGAGCTGCC
TTCCCAGGGAGAAGGAGCCGTGCGCCAGGGCAGGGCCCGTGCCTTAGACTTCTCCCGACCCCCAGAGCGCTGGTA
CACAGGTCTAGGCACCACACAGTGCTTTGGAAATTCTCAGTGAATGATGTTTAATAAAGCAAAAAATGTC

FIGURE 671

MQSPAVLVTSRRLQNAHTGLDLTVPQHQEVRGKMMSGHVEYQILVVTRLAAFKSAKHRPEDVVQFLVSKKYSEIE
EFYQKLSSRYAAASLPPLPRKVLFVGESDIRERRAVFNEILRCVSKDAELAGSPELLEFLGTRSPGAAGLTSRDS
SVLDGTDSQTGNDEEAFDFFEEQDQVAEEGPPVQSLKGEDAEESLEEEEALDPLGIMRSKKPKKHRCEGKGLGPA
GSEPPHPQGRPGRSLGHSTQNCMVPFSPGLWGQSRSLRAAGAALTLGARAQCVLFPVDMKGREGVGMPCQPEAQP
QG

FIGURE 672

ATGGGTCAAAGTCAGAGTGGTGGTCATGGTCCTGGAAGTGGCAAGAAGGATGACAAGGACAAAAAAAAGAAATAT
GAACCTTCTGTACCAACTAGAGTGAGGAAAAAGAAGAAGAAAACAAAGGGACCAGATGCAGTCAGCAAACTGCCA
CTGGTGACACCTCACACTCAGTGCCGGTTAAAATTACTGACATTAGAGAGAATTAAAGACTATCTTCTCATGGAG
GAAGAATTCATTAGAAATCAGGAACAGATGAAACCATTAGAAGAAAAGCAAAAGGAGGAAAGATCAAAAGTGGAT
GATCTGAGGGGGACCCCGATACAAGGATCTTCTGGAAACTGGCTGCTCGGTCCTGCTCAACCACAAGGTGCATGC
CGTGATGGGGTGCTGATGGATGACACGGATCCCCTGGTCACAGTGATGAAGATGGAAAAGACCCCCCAGGAGACC
TATGCCAATATTGGGGGGCTGGACAACCAAATTCAGGAAATAAAGGAAGCTGTGGAGTTTCCTCTCACCCATCCT
GAATATTATGAAGAGATGGGTAAAAAGCCTCCTAAGGGGGTCATTCTCTATGGTCCACCTGGCACAGGCAAAACC
TTGTTATCCAAAGCAGTAGCAAACCAAACCTCAGCCACTTTCTTGAGAGTGGTTGGCTCTGAACTTATTCAGAAG
TACCTAGTTGCTGAAGAGCATGAACTATCCATCATGTTTACTGATGAAATTGGAGCCATTGGGACAAAAAGATAT
GACTCAAATTCTGGTGGCCGCATTGACAGGAAGATCAAGTTCTCCCTGCCTGATGAAAGGACTAAGAAGCGTATC
TTTCAGAATCACACAAGCAGGATGACACTGGCCGATGAAGTAACCCTGGACGACTTGATCATGGTTAAAGATGAC
CTCTCTGGTGCTGACATCAAGGCAATCTGTACAGAAGCTGGTCTGATGGCCTCAAGAGAACGTAGAATGAAAGTA
ACGAATGAATTCTTCAAAAAATATAAAGAAATGTTCTTTATAAGAAACAGGAAGGCACCCCTGAGGGGCTCTATC
TCTAGTGAACCACAGCTGCCATCAGGAAAATGGTTGGGCGATTCCTCGACCCCTGAAAAGGATGAGCAACTTGTT
CCCAAAGCTGGAGAAGACACTCCTGAGGGCTATTTAGGACAACTTATGACTCAGCTCTTTGAGCAGAAAGAGGCC
AAAAAGTTCAGCAGAAAAAGCCCTGAACTCTTGGAAGAGCTGGCTTCAAGCCTGGCT**TAG**

FIGURE 673

MGQSQSGGHGPGSGKKDDKDKKKKYEPSVPTRVRKKKKKTKGPDAVSKLPLVTPHTQCRLKLLTLERIKDYLLME
EEFIRNQEQMKPLEEKQKEERSKVDDLRGTPIQGSSGNWLLGPAQPQGACRDGVLMDDTDPLVTVMKMEKTPQET
YANIGGLDNQIQEIKEAVEFPLTHPEYYEEMGKKPPKGVILYGPPGTGKTLLSKAVANQTSATFLRVVGSELIQK
YLVAEEHELSIMFTDEIGAIGTKRYDSNSGGRIDRKIKFSLPDERTKKRIFQNHTSRMTLADEVTLDDLIMVKDD
LSGADIKAICTEAGLMASRERRMKVTNEFFKKYKEMFFIRNRKAPLRGSISSEPQLPSGKWLGDSSTPEKDEQLV
PKAGEDTPEGYLGQLMTQLFEQKEAKKFSRKSPELLEELASSLA

FIGURE 674

GACGGCGCCTTCGCGAAACACT**ATG**CTAATGGCATGGTGCCGCGGTCCTGTCTTGCTGTGCCTGCGGCAGGGGCT
CGGAACCAATTCATTCCTGCACGGCCTGGGGCAGGAGCCCTTCGAGGGAGCTCGGTCACTGTGTTGCAGGTCCTC
GCCTAGAGACCTGCGAGATGGAGAAAGAGAGCACGAGGCGGCACAAAGGAAAGCCCCAGGAGCAGAGTCTTGCCC
ATCTCTCCCTCTGAGCATCTCGGACATTGGGACTGGATGTCTTTCGTCACTGGAAAACCTCAGACTGCCGACGCT
GCGGGAAGAGTCATCACCTCGAGAGCTCGAGGACTCGAGCGGAGACCAGGGCCGGTGCGGTCCCACACACCAGGG
ATCCGAGGATCCTTCGATGCTCTCGCAGGCCCAGTCCGCTATCGAGGTCGAAGAGCGTCACGTCTCCCCTTCTTG
TTCAACTTCCAGAGAGAGACCCTTTCAGGCTGGGGAGCTGATTTTAGCTGAGACTGGGGAGGGAGAAACAAAATT
TAAGAAATTATTTAGGTTGAACAACTTCGGACTCTTAAATAGTAACTGGGGGGCAGTCCCGTTCGGCAAGATCGT
GGGGAAGTTCCCCGGCCAGATACTGAGGAGTTCCTTCGGTAAGCAGTACATGCTGAGGAGGCCAGCCTTGGAAGA
CTATGTAGTATTGATGAAAAGAGGGACTGCCATAACATTCCCAAAGGATATTAATATGATTCTCTCAATGATGGA
TATCAACCCAGGTGATACTGTTTTGGAAGCTGGCTCAGGCTCTGGTGGAATGAGCTTATTTTTATCCAAAGCAGT
TGGATCACAAGGACGAGTCATAAGTTTTGAGGTACGAAAAGACCACCATGATCTGGCTAAGAAGAATTACAAACA
CTGGCGTGATTCATGGAAATTAAGTCATGTAGAAGAGTGGCCAGACAATGTGGATTTTATTCATAAGGACATTTC
AGGAGCAACCGAAGACATAAAATCTTTAACATTTGACGCAGTAGCTTTGGATATGTTAAATCCTCATGTTACTTT
GCCTGTTTTTTACCCACATCTTAAGCATGGTGGTGTATGTGCTGTATATGTAGTAAACATCACACAGGTTATTGA
ACTTTTAGATGGAATTCGCACCTGTGAACTTGCTCTTTCATGTGAAAAGATAAGCGAGGTCATTGTCAGAGATTG
GTTGGTTTGCCTTGCAAAACAGAAAAATGGAATTTTAGCTCAAAAAGTAGAATCTAAAATCAACACAGATGTACA
ACTAGATTCTCAAGAGAAAATTGGAGTTAAAGGTGAGCTGTTTCAAGAGGATGACCATGAAGAATCGCATTCTGA
TTTTCCATATGGATCATTTCCCTATGTTGCTAGACCAGTACACTGGCAACCTGGTCATACAGCTTTTCTTGTCAA
GTTGAGGAAGGTCAAACCACAACTTAAC**TGA**GTACTCCAGATGACAGTAACTGACTTGAAGATGGAAAAATATCA
AAATAGAACTTTATATTGAAAATCACTGCTTCCATAGATTGGCATTTTTAGCTATTACTATGACTTATATAACTT
ATACATATAATTTTGAAAATAACAACTAAAAGATGTATAACATAGCAAAACTGCTTAAACATCCCATTTTGACAC
TTGTCTTGCAGTTAGTTTGACATTTTGTAGTTAATGATTCCAAATTGGTTTAGTTGGGCCATCTCATTCTTCACT
TCCTGTAAACCACTCCATAGATTTGTCTTTCTTCAAGAAATTAGTTTCTTTCCTTTATTTGATTGATGGTCATT
GACTACTGAAATAAAATATGCATTTTAAGATAAAAAAAAAAAAAAA

FIGURE 675

MLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSLCCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSIS
DIGTGCLSSLENLRLPTLREESSPRELEDSSGDQGRCGPTHQGSEDPSMLSQAQSAIEVEERHVSPSCSTSRERP
FQAGELILAETGEGETKFKKLFRLNNFGLLNSNWGAVPFGKIVGKFPGQILRSSFGKQYMLRRPALEDYVVLMKR
GTAITFPKDINMILSMMDINPGDTVLEAGSGSGGMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDSWKL
SHVEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLPVFYPHLKHGGVCAVYVVNITQVIELLDGIRT
CELALSCEKISEVIVRDWLVCLAKQKNGILAQKVESKINTDVQLDSQEKIGVKGELFQEDDHEESHSDFPYGSFP
YVARPVHWQPGHTAFLVKLRKVKPQLN

FIGURE 676

ATGCAACAAGCTTCCTACCCCCAACCCGGCCAGACAAAGCCCCGGCAGCAGGGCCGGCACTTCCGAGCCTCCGGA
CTCGGGACGCCGCGCTCTTACCCTGGCCTCATCCAGAGTGACGCCGGCGCCACCGCTTCCCCCGGCTTTGGCGGC
GGGGCAGCTGGCGGCGCGGGTCTTGGAGGAGCGGGTCCGAGAGGAGATGAAATGGCTGCTGCCTCCGGTCGCCCC
AGGCTCTGCTCCGGCCCCAGGCCCAGGCCCGGGACCAGGAGACTTGGACCCGAGAAGGCGGAGAGAGCTCTTCCG
GGTGTTCACCATGGTCCAGCCAGGGGGACGGAGTCCACGCCGCGCCCGGGAGAGCCGAGCAAGGCCGGCCCGCCG
GCCGCTGCCCCGCCCCCGGCGCGGCGTCAGCGCTCGGCGGCCGGGGAGCGACGCTCTAGGCTGTCAGCTCGGTGG
TTTCCAGCTCTCCCCGACCGCAGGGCTGGGGCGACCAGAAAAGCCAGACTAATCAGGACGAGTTCGGGCGTGGAA
TTGGGCCTGAAGCCCTCATGCCCAGCCAGGCCTGAATGCCCCAGACCCCACCGTCACCCCCGTGGCCTGGATGGA
GCAGGGGACGGCCGGCGAAGGCGCGGGGTGGAAGGGGAGCGGCGACGAAGGCGCGAGGAGCTGACTGGGAATCCC
CAAGCTACCCGAGGCAAGACACTGAACTTGAGTCGCACTTTTCATGCCTGTAGAAATGAGAATGACAGCTGTGAT
AAAAAAAAAATTCATCTGGGCGGTATCTGGAACTTGGGCGTTCCGAAACTTACAGTTATGCGCAACACAATGTTT
CTATTTTCAAAGGCGAACGCTGCACGATCGCAGTCCAGTGATACAAATAATAAAAGAGTTTATTACTTGTCAGCA
ATGATGAATGTTCGTGTGGCATCCAGCGTTGAGTTCCTATTCTTACTTGGAACTCATTGGTCCCTGTGTCTGGGG
CCAGCACTGATGGACACAACTAAGTTTGCACTCGTCTTCCCTCTCATGTATCATACCTGGAATGGGATCCAACAC
TTGATGTGGGACCTAGGAAAAGGCCTGAAGATTCCCCAGCTATACCAGTCTGGAGTGGTTGTCCTGGTTCTTACT
GTGTTATTTGTAGGGCTGGCAGCTGTG**TGA**

FIGURE 677

MQQASYPQPGQTKPRQQGRHFRASGLGTPRSYPGLIQSDAGATASPGFGGGAAGGAGLGGAGPRGDEMAAASGRP
RLCSGPRPRPGTRRLGPEKAERALPGVHHGPARGTESTPRPGEPSKAGPPAAAPPPARRQRSAAGERRSRLSARW
FPALPDRRAGATRKARLIRTSSGVELGLKPSCPARPECPRPHRHPRGLDGAGDGRRRRGVEGERRRRREELTGNP
QATRGKTLNLSRTFHACRNENDSCDKKKIHLGGIWNLGVPKLTVMRNTMFLFSKANAARSQSSDTNNKRVYYLSA
MMNVRVASSVEFLFLLGTHWSLCLGPALMDTTKFALVFPLMYHTWNGIQHLMWDLGKGLKIPQLYQSGVVVLVLT
VLFVGLAAV

FIGURE 678A

ACAGAGAGATTGGTGTTTTTGTGAGGCAGTGAGACCTAAGGTAACCTTTATCAAAAGG**ATG**GAGTTGGGAAAAGG
AAAACTACTCAGGACTGGACTGAATGCGTTGCATCAAGCAGTGCATCCGATCCATGGCCTTGCCTGGACCGATGG
GAATCAAGTTGTCCTAACTGATTTGCGGCTTCACAGTGGAGAGGTCAAGTTTGGGGACTCCAAAGTCATTGGACA
GTTTGAATGTGTCTGTGGGTTGTCCTGGGCCCCACCTGTTGCAGATGATACACCTGTTCTACTCGCTGTCCAGCA
TGAGAAGCATGTCACTGTGTGGCAGCTGTGTCCCAGCCCTATGGAGTCAAGCAAATGGCTGACGTCTCAGACTTG
TGAGATTAGAGGATCACTACCTATCCTTCCCCAGGGCTGTGTGTGGCACCCAAAATGTGCTATTCTGACTGTGTT
GACTGCTCAGGATGTCTCCATTTTCCCTAATGTTCACTCTGATGATTCCCAGGTAAAGGCAGACATCAACACCCA
GGGCCGCATTCACTGTGCATGTTGGACCCAGGATGGCCTGAGGCTGGTGGTGGCAGTAGGCAGCAGCCTGCATTC
TTATATTTGGGACAGCGCTCAGAAGACTCTTCACAGGTGCTCCTCCTGCCTGGTGTTTGATGTGGACAGCCACGT
CTGCTCCATCACAGCAACTGTGGACTCACAGGTTGCTATAGCTACTGAGCTTCCATTGGATAAGATCTGTGGCTT
AAATGCATCTGAAACCTTTAATATCCCACCTAACAGTAAAGACATGACTCCGTATGCTTTACCAGTTATTGGTGA
AGTACGCTCTATGGATAAAGAGGCAACTGATTCTGAAACAAATTCTGAAGTATCAGTTTCTTCTTCCTATTTAGA
ACCTCTGGATCTAACTCACATACATTTCAATCAACATAAGTCTGAGGGTAATTCTCTTATTTGTCTAAGAAAAAA
GGACTACTTGACAGGAACTGGCCAAGATTCTTCACATTTGGTCCTTGTGACCTTTAAGAAGGCAGTTACCATGAC
GAGAAAAGTCACTATTCCAGGCATTCTGGTTCCTGATCTGATAGCATTTAATCTTAAAGCCCACGTAGTGGCAGT
GGCTTCCAACACTTGTAATATAATTTTGATCTACTCTGTCATTCCATCTTCAGTCCCAAACATCCAGCAAATTCG
ATTAGAGAACACTGAAAGACCAAAAGGGATATGTTTCTTGACAGACCAACTATTACTAATTTTGGTAGGAAAACA
AAAACTCACTGATACAACATTTCTTCCTTCTTCAAAGTCTGATCAGTATGCCATTAGCTTGATTGTTAGAGAAAT
AATGTTGGAAGAAGAACCTTCAATAACATCAGGTGAAAGCCAGACTACCTACTCTACTTTCAGTGCTCCGTTAAA
TAAAGCAAATAGAAAAAAGTTAATTGAAAGTCTTTCCCCAGATTTTTGTCACCAAAACAAAGGGCTGTTGCTGAC
AGTTAATACCAGTAGTCAGAATGGAAGGCCTGGAAGAACACTTATTAAAGAAATCCAGAGTCCTCTGTCTAGTAT
CTGTGATGGCTCCATAGCTCTAGATGCTGAGCCTGTTACCCAGCCAGCATCGCTGCCCAGACACAGCAGCACACC
AGACCACACCAGCACACTGGAGCCTCCTCGTTTGCCTCAAAGAAAGAACTTACAAAGTGAAAAGGAAACTTATCA
GCTGTCTAAGGAGGTGGAAATTTTATCTAGGAACCTGGTTGAAATGCAACGGTGTCTTTCTGAACTTACAAACCG
TCTGCATAATGGGAAGAAATCCTCTTCAGTGTATCCACTCTCTCAAGATCTTCCTTATGTTCACATCATTTACCA
GAAACCTTATTATCTAGGTCCTGTTGTTGAAAAAAGAGCGGTGCTTCTCTGTGATGGTAAACTAAGGCTCAGTAC
AGTTCAGCAGACTTTTGGCCTTTCTCTCATTGAAATGCTACATGATTCCCACTGGATTCTTCTCTCTGCTGACAG
TGAGGGCTTTATCCCGTTAACCTTCACAGCCACACAGGAAATAATCATAAGAGATGGCAGCCTGTCCAGGTCAGA
TGTCTTCAGAGACTCTTTTTCTCACAGTCCAGGTGCTGTTTCTTCTCTTAAAGTCTTTACAGGCCTTGCTGCCCC
CAGTTTAGATACCACTGGCTGTTGTAACCATGTAGATGGCATGGCT**TGA**TATCTGCAGTGTCCTTGCTGTGTAGC
TCTTCAGATGAGACCATTACAAACAAGGCCTGCTTGACACTGGACACTCGCCAATGAGACTCCCACTGCACTCAG
GCGAAGCGCTTGCCATGGTCGGCTCTCCTGGTTTCCCCCTGTTTCCCCTGAGCTGAGGCTCGCTGCTGTGTAGCA
GAGCTCAGTCTTTATTAGATGGCTCCGAAAGTGGTGTTTATGTATTCATGACTGTGTGGTTTTGACTAAGGGCAG
AATTCTCAGAACAAAACAATATTATGGTGCCATATGGATGGTGTTTTATGGTTTCTCTGAGGCTTTGTGTCCCTT
GTCCAAAGCTGCATTGAAGCTGTCTTAGGAGCACTTAAAAGATACCTTGGCATTGTTATAGGTCTTTTTCTTGGC
TTCAAGAGGAGGTTGAGGAGTCTGCTGGGGGGCATGTGCTCTAGCATATTAACCTCAAACCAGCAAGAATTAGCA
GAGCTCCAAGGAGGACCAGAGACCCACTGGCTTCTGCTCTCAGGAACAGGAAGTGGCTCTGATGTTGCCTGGACC
TCCCAGAATTTAAACCAAACCCTCTTGCTTCCTTAACAAATTCTGGCTGACGAAGGTCCAGGTACTCTTAAAAAC
TGGCCCTGGGAAAATTTTGAATGAAATTTCAAGGGAATTTGTCCCCTCTGGGTTCCACTTGAGGTTGTGCCGATG
CTGCTACCACACTGTCGAGCCCAGGTAAGTCCTACTGCAGGATTTTGTGCTGTGGCCACTCATGAGTGTCCCTGA
AATAACTTTTTTTTTTTTTAAATCCAGTTTTGGGATCACGCAACTTTCCTATTTTTCTCCCAGTAGTCAGCTCCC
TTAGTTAACTTGTCACTTTAATTTGATATTTTTATTTTCTCTCCTTTTAAGTCTTAGAGACCAGCAGAGAATCTG
TGAGAGAAAGTATTTCAGGAAGTTAGAAATTCAACCGAATCTGAGGTAGTCCTAAAAAGTGCCATTTTGTTTCAC
TTATGGGCTAAAGTACCAGCTTAGTCAGGTAAGAGCCCTGACCCACTTCAGATGGTAACACCACTTCTCACTGCC
TTCAGATGGAATCACAGATTTCAGTCACGGCGCATAACAAATTGATCAGTGAGTGGCTAGGCATCTGCAGATAAA
TTGTTTCAGCCATAGAAGCTCCATTAGCACATATGCTTCCTTTTCCCCCCTTCCTTTAAAATCATCTGGAAAGAA
ACTATTTTGTGCCCTTGGGGACTCCTGTCTGTCTGTTACAGTTTACCAAGATGGAGCTGGGTTAGGAAAGAAGTG
AGGGCCCATTTTGTGGTTCAAGTGCACTAGACAGCTGCTGGGGTAGGAAGCACAGGCAATGTCTGCAATCAGCTG

FIGURE 678B

TGGGAGAGCGGTGACTGAGAACAGTCTGAGGCCTGGCTCCACTTGGAAGTATCTGGGGTGCGATGAAATCACAAT
TATCTTGAAGCCTAAAGAGGGAACTACAAGACTGTTAACTAAGATCAATGTGGCACCTAAAAGGGTATGTTAAA
ATCACCATTTCTCAGGTCAAAATACTGTGAAATAAAAATGGAAACGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

FIGURE 679

MELGKGKLLRTGLNALHQAVHPIHGLAWTDGNQVVLTDLRLHSGEVKFGDSKVIGQFECVCGLSWAPPVADDTPV
LLAVQHEKHVTVWQLCPSPMESSKWLTSQTCEIRGSLPILPQGCVWHPKCAILTVLTAQDVSIFPNVHSDDSQVK
ADINTQGRIHCACWTQDGLRLVVAVGSSLHSYIWDSAQKTLHRCSSCLVFDVDSHVCSITATVDSQVAIATELPL
DKICGLNASETFNIPPNSKDMTPYALPVIGEVRSMDKEATDSETNSEVSVSSSYLEPLDLTHIHFNQHKSEGNSL
ICLRKKDYLTGTGQDSSHLVLVTFKKAVTMTRKVTIPGILVPDLIAFNLKAHVVAVASNTCNIILIYSVIPSSVP
NIQQIRLENTERPKGICFLTDQLLLILVGKQKLTDTTFLPSSKSDQYAISLIVREIMLEEEPSITSGESQTTYST
FSAPLNKANRKKLIESLSPDFCHQNKGLLLTVNTSSQNGRPGRTLIKEIQSPLSSICDGSIALDAEPVTQPASLP
RHSSTPDHTSTLEPPRLPQRKNLQSEKETYQLSKEVEILSRNLVEMQRCLSELTNRLHNGKKSSSVYPLSQDLPY
VHIIYQKPYYLGPVVEKRAVLLCDGKLRLSTVQQTFGLSLIEMLHDSHWILLSADSEGFIPLTFTATQEIIIRDG
SLSRSDVFRDSFSHSPGAVSSLKVFTGLAAPSLDTTGCCNHVDGMA

FIGURE 680

TTCTCTTAGCAGCACCCAGCTTGCCCACCCATGCTCAAGATGGGCGGGATGCCAGCCTGTTACATAAATGTGCCA
AAAGCCTGGCCATGCCTGGAAAATGGACCAATCCGCCCGCCAAGAGGTTGGGTCTCGTTCCCTAGAGAGAAGGAA
GTTTCCTCTCCTTGAAGTGAGAGCTAGAATCGCACTTTCTGTCAAGCTGAGAGAAAGACTCTTTTCCAGAGGCTA
AAAGGACAAGAAAATCTGATTTGCTTGCTTCTAACTTTGCGTTTTAAAGGGGGAAGGAGGAAAGGAAAGAGGGGG
AGGGTGGTTCTGCTTAGCCCCACCCCTCCGGCTACCCCAGGTCCAGCCGTCCATTCCGGTGGAGGCAGAGGCAGT
CCTGGGGCTCTGGGGCTCGGGCTTTGTCACCGGGACCCGCAGGAGCCAGAACCACTCGGCGCCGCCTGGTGCATG
GGAGGGGAGCCGGGCCAGGAACAATATGTTAGCCGTGCACTTTGACAAGCCGGGAGGACCGGAAAACCTCTACGT
GAAGGAGGTGGCCAAGCCGAGCCCGGGGGAGGGTGAAGTCCTCCTGAAGGTGGCGGCCAGCGCCCTGAACCGGGC
GGACTTAATGCAGAGACAAGGCCAGTATGACCCACCTCCAGGAGCCAGCAACATTTTGGGACTTGAGGCATCTGG
ACATGTGGCAGAGCTGGGGCCTGGCTGCCAGGGACACTGGAAGATCGGGGACACAGCCATGGCTCTGCTCCCCGG
TGGGGGCCAGGCTCAGTACGTCACTGTCCCCGAAGGGCTCCTCATGCCTATCCCAGAGGGATTGACCCTGACCCA
GGCTGCAGCCATCCCAGAGGCCTGGCTCACCGCCTTCCAGCTGTTACATCTTGTGGGAAATGTTCAGGCTGGAGA
CTATGTGCTAATCCATGCAGGACTGAGTGGTGTGGGCACAGCTGCTATCCAACTCACCCGGATGGCTGGAGCTAT
TCCTCTGGTCACAGCTGGCTCCCAGAAGAAGCTTCAAATGGCAGAAAAGCTTGGAGCAGCTGCTGGATTCAATTA
CAAAAAAGAGGATTTCTCTGAAGCAACGCTGAAATTCACCAAAGGTGCTGGAGTTAATCTTATTCTAGACTGCAT
AGGCGGATCCTACTGGGAGAAGAACGTCAACTGCCTGGCTCTTGATGGTCGATGGGTTCTCTATGGTCTGATGGG
AGGAGGTGACATCAATGGGCCCCTGTTTTCAAAGCTACTTTTTAAGCGAGGAAGTCTGATCACCAGTTTGCTGAG
GTCTAGGGACAATAAGTACAAGCAAATGCTGGTGAATGCTTTCACGGAGCAAATTCTGCCTCACTTCTCCACGGA
GGGCCCCCAACGTCTGCTGCCGGTTCTGGACAGAATCTACCCAGTGACCGAAATCCAGGAGGCCCATAAGTACAT
GGAGGCCAACAAGAACATAGGCAAGATCGTCCTGGAACTGCCCCAGTGAAGGAGGATGGGGCAGGACAGGACGCG
GCCACCCCAGGCCTTTCCAGAGCAAACCTGGAGAAGATTCACAATAGACAGGCCAAGAAACCCGGTGCTTCCTCC
AGAGCCGTTTAAAGCTGATATGAGGAAATAAAGAGTGAACTGG

FIGURE 681

GGCACGAGGGTCCCGTTACCGCCTCCTGCTCCTGCCGCGCGCACCCCCGGGGCTTCGGCTCCGGCACGGGTCGCG
CCCAGCTTTCCTGCACCTGAGGCCGCCGGCCAGCCGCCGCC**ATG**GGTGCCTACCTCTCCCAGCCCAACACGGTGA
AGTGCTCCGGGGACGGGGTCGGCGCCCCGCGCCTGCCGCTGCCCTACGGCTTCTCCGCCATGCAAGGCTGGCGCG
TCTCCATGGAGGATGCTCACAACTGTATTCCTGAGCTGGACAGTGAGACAGCCATGTTTTCTGTCTACGATGGAC
ATGGAGGGGAGGAAGTTGCCTTGTACTGTGCCAAATATCTTCCTGATATCATCAAAGATCAGAAGGCCTACAAGG
AAGGCAAGCTACAGAAGGCTTTAGAAGATGCCTTCTTGGCTATTGACGCCAAATTGACCACTGAAGAAGTCATTA
AAGAGCTGGCACAGATTGCAGGGCGACCCACTGAGGATGAAGATGAAAAAGAAAAAGTAGCTGATGAAGATGATG
TGGACAATGAGGAGGCTGCACTGCTGCATGAAGAGGCTACCATGACTATTGAAGAGCTGCTGACACGCTACGGGC
AGAACTGTCACAAGGGCCCTCCCCACAGCAAATCTGGAGGTGGGACAGGCGAGGAACCAGGGTCCCAGGGCCTCA
ATGGGGAGGCAGGACCTGAGGACTCAACTAGGGAAACTCCTTCACAAGAAAATGGCCCCACAGCCAAGGCCTACA
CAGGCTTTTCCTCCAACTCGGAACGTGGGACTGAGGCAGGCCAAGTTGGTGAGCCTGGCATTCCCACTGGTGAGG
CTGGGCCTTCCTGCTCTTCAGCCTCTGACAAGCTGCCTCGAGTTGCTAAGTCCAAGTTCTTTGAGGACAGTGAGG
ATGAGTCAGATGAGGCGGAGGAAGAAGAGGAAGACAGTGAGGAATGCAGCGAGGAAGAGGATGGCTACAGCAGTG
AGGAGGCAGAGAATGAGGAAGATGAGGATGACACCGAGGAGGCTGAAGAGGACGATGAAGAAGAAGAAGAAGAGA
TGATGGTGCCAGGGATGGAAGGCAAAGAGGAGCCTGGCTCTGACAGTGGTACAACAGCGGTGGTGGCCCTGATAC
GAGGGAAGCAGTTGATTGTAGCCAACGCAGGAGACTCTCGCTGTGTGGTATCTGAGGCTGGCAAAGCTTTAGACA
TGTCCTATGATCACAAACCAGAGGATGAAGTAGAACTAGCACGCATCAAGAATGCTGGTGGCAAGGTCACCATGG
ATGGGCGAGTCAACGGGGGCCTCAACCTCTCCAGAGCCATTGGGGACCACTTCTATAAGAGAAACAAGAACCTGC
CACCTGAGGAACAGATGATTTCAGCCCTTCCTGACATCAAGGTGCTGACTCTCACTGACGACCATGAATTCATGG
TCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGCCAGGAAGTTGTAGATTTCATTCAATCAAAGATCAGCC
AGCGTGATGAAAATGGGGAGCTTCGGTTATTGTCATCCATTGTGGAAGAGCTGCTGGATCAGTGCCTGGCACCAG
ACACTTCTGGGGATGGTACAGGGTGTGACAACATGACCTGCATCATCATTTGCTTCAAGCCCCGAAACACAGCAG
AGCTCCAGCCAGAGAGTGGCAAGCGAAAACTAGAGGAGGTGCTCTCTACTGAGGGGGCTGAAGAAAATGGCAACA
GCGACAAGAAGAAGAAGGCCAAGCGAGAC**TAG**CAGTCATCCAGACCCCTGCCCACCTAGACTGTTTTCTGAGCCC
TCCGGACCTGAGACTGAGTTTTGTCTTTTTCCTTTAGCCTTAGCAGTGGGTATGAGGTGTGCAGGGGGAGCTGGG
TGGCTTCACTCCGCCCATTCCAAAGAGGGCTCTCCCTCCACACTGCAGCCGGGAGCCTCTGCTGTCCTTCCCAGC
CGCCTCTGCTCCTCGGGCTCATCACCGGTTCTGTGCCTGTGCTCTGTTGTGTTGGAGGGAAGGACTGGCGGTTCT
GGTTTTTACTCTGTGAACTTTATTTAAGGACATTCTTTTTATTGGCGGCTCCATGGCCCTCGGCCGCTTGCACC
CGCTCTCTGTTGTACACTTTCAATCAACACTTTTTCAGACTAAAGGCCAAAACCTAAAAAAAAAAAAAA

FIGURE 682

MGAYLSQPNTVKCSGDGVGAPRLPLPYGFSAMQGWRVSMEDAHNCIPELDSETAMFSVYDGHGGEEVALYCAKYL
PDIIKDQKAYKEGKLQKALEDAFLAIDAKLTTEEVIKELAQIAGRPTEDEDEKEKVADEDDVDNEEAALLHEEAT
MTIEELLTRYGQNCHKGPPHSKSGGGTGEEPGSQGLNGEAGPEDSTRETPSQENGPTAKAYTGFSSNSERGTEAG
QVGEPGIPTGEAGPSCSSASDKLPRVAKSKFFEDSEDESDEAEEEEEDSEECSEEEDGYSSEEAENEEDEDDTEE
AEEDDEEEEEEEMMVPGMEGKEEPGSDSGTTAVVALIRGKQLIVANAGDSRCVVSEAGKALDMSYDHKPEDEVELA
RIKNAGGKVTMDGRVNGGLNLSRAIGDHFYKRNKNLPPEEQMISALPDIKVLTLTDDHEFMVIACDGIWNVMSSQ
EVVDFIQSKISQRDENGELRLLSSIVEELLDQCLAPDTSGDGTGCDNMTCIIICFKPRNTAELQPESGKRKLEEV
LSTEGAEENGNSDKKKKAKRD

FIGURE 683

CCACTGCCGCTGCCGCCGCCTCTCCTTAGTCGCCGGCATGACGACCGCGTCTACCTCGCAGGTGCGCCAGAACTT
GCTGAGAAATTGATGAAGCTGTAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAAACCAGACTGT
GCGGGGAGAATGCGATGGAGAGCGGGCTGAATGCGATGGATTACATTTGGAAAAAATTGTGCATTTTGCATTAC
ATTTGGAAAAAAATGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCACTGACAAAAATGACCCCCATTTGT
GTGACTTCATTGAGACACATTACCTGAATGAACAAGTGAAGGCCATCAAAGAATTGGGTGACCACGTGACCAACA
TGCACGAGATGGGAGCGCCCGAATCTGGCGTGGCAGAATACCTCTTTGACAAGCACACCCTGGGAGACAGTGATA
ATGAAAGCTAAGCCTCAGGCTAATTTCCCCATAGCCATAGGGTGACTTACCTTGTCACCAAGGCAGCGCATGTAT
GTTGGGGTTTCCTTTACCTTTTCTATAAGTTGTTCCAAGACACCCACTTAAGTTCTTTGATTTGTACCATTCCTT
CAAATAAATAAATTTGGTACCC

FIGURE 684

CCCTATCCGGACAGGTGGCTCTTGCCCTTTAGACTACAGTTCCCAGCATGCCCAGGCGATTGCGTCCCAGAACCG
ACGTCCCACCGCCTTCCCACATCGGATCGCAGGGCTCCCAAAATGGCGAGTGAGGCTGCGGGGACTCGCTGAGCA
GCGGAGGGGGAGCGTGCAGAGCCGCTGCGGCCCTCACAGTCCGGAGCCCGGCCGTGCCGTGCCGTAGGGAAC**ATG**

CACTTTTCCATTCCCGAAACCGAGTCCCGCAGCGGGGACAGCGGCGGCTCCGCCTACGTGGCCTATAACATTCAC
GTGAATGGAGTCCTGCACTGTCGGGTGCGCTACAGCCAGCTCCTGGGGCTGCACGAGCAGCTTCGGAAGGAGTAT
GGGGCCAATGTGCTTCCTGCATTCCCCCCAAAGAAGCTTTTCTCTCTGACTCCTGCTGAGGTAGAACAGAGGAGA
GAGCAGTTAGAGAAGTACATGCAAGCTGTTCGGCAAGACCCATTGCTTGGGAGCAGCGAGACTTTCAACAGTTTC
CTGCGTCGGGCACAACAGGAGACACAGCAGGTCCCCACAGAGGAAGTGTCCTTGGAAGTGCTGCTCAGCAACGGG
CAGAAAGTTCTGGTCAACGTGCTAACTTCAGATCAGACTGAGGATGTCCTGGAGGCTGTAGCTGCAAAGCTGGAT
CTTCCAGATGACTTGATTGGATACTTTAGTCTATTCTTAGTTCGAGAAAAAGAGGATGGAGCCTTTTCTTTTGTA
CGGAAGTTGCAAGAGTTTGAGCTGCCTTATGTGTCTGTCACCAGCCTTCGGAGTCAAGAGTATAAGATTGTGCTA
AGGAAGAGTTATTGGGACTCTGCCTATGATGACGATGTCATGGAGAACCGGGTTGGCCTGAACCTGCTTTATGCT
CAGACGGTATCAGATATTGAGCGTGGGTGGATCTTGGTCACCAAGGAACAGCACCGGCAACTCAAATCTCTGCAA
GAGAAAGTCTCCAAGAAGGAGTTCCTGAGACTGGCCCAGACGCTGCGGCACTATGGCTACTTGCGCTTTGATGCC
TGTGTGGCTGACTTCCCAGAAAAGGACTGTCCTGTGGTGGTGAGCGCGGGCAACAGTGAGCTCAGCCTGCAGCTC
CGCCTGCCTGGCCAGCAACTCCGAGAAGGCTCCTTCCGGGTCACCCGCATGCGATGCTGGCGGGTCACCTCCTCT
GTACCATTGCCCAGTGGAAGCACGAGCAGCCCAGGCCGGGGCCGGGGTGAGGTGCGCCTGGAACTGGCTTTTGAA
TACCTCATGAGCAAGGACCGGCTACAGTGGGTCACCATCACTAGCCCCCAGGCTATCATGATGAGCATCTGCTTG
CAGTCCATGGTTGATGAACTGATGGTGAAGAAATCTGGCGGCAGTATCAGGAAGATGCTGCGCCGGCGGGTGGGG
GGTACTCTGAGACGCTCAGACAGCCAGCAAGCAGTGAAGTCCCCACCACTGCTTGAGTCACCTGATGCCACCCGG
GAGTCTATGGTCAAACTCTCAAGTAAGCTGAGTGCCGTGAGCTTGCGGGGAATTGGCAGTCCCAGCACAGATGCC
AGTGCCAGTGATGTCCACGGCAATTTCGCCTTCGAGGGCATTGGAGATGAGGATCTG**TAA**TCTCCACTGCTTGGA
TGTCTGCCCTCTACCCCAGAGGAATTTACAGAAACTTGCCCTGTGCCTGTGTCCCCCATGCTAGGGGCGGAGGGG
TCTTTTCCTTCTTCTTTCCTACCTACCCCTTTTCTCTTGGCCAGGGGCCTCGTATCCTACCTTTCCTTGTCCCCT
GGGCTGGCTGCACAGAGGATTGCCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTT
GCACAAAGTCTAAGGGACCATGGCTGCCTGCCTTGGGGAGGAACCATAGCTCCCTCTGGGCCGCTTCTGGCCTCT
TGGAGCCATGGGCCAAAGGCCAAGGGGATGGGCAGAGGTCTGTGTTTGGTCTGGCCCAGTTCCCCATCATTAAAC
TCAGCCTGACTGCTGCCT

FIGURE 685

MHFSIPETESRSGDSGGSAYVAYNIHVNGVLHCRVRYSQLLGLHEQLRKEYGANVLPAFPPKKLFSLTPAEVEQR
REQLEKYMQAVRQDPLLGSSETFNSFLRRAQQETQQVPTEEVSLEVLLSNGQKVLVNVLTSDQTEDVLEAVAAKL
DLPDDLIGYFSLFLVREKEDGAFSFVRKLQEFELPYVSVTSLRSQEYKIVLRKSYWDSAYDDDVMENRVGLNLLY
AQTVSDIERGWILVTKEQHRQLKSLQEKVSKKEFLRLAQTLRHYGYLRFDACVADFPEKDCPVVVSAGNSELSLQ
LRLPGQQLREGSFRVTRMRCWRVTSSVPLPSGSTSSPGRGRGEVRLELAFEYLMSKDRLQWVTITSPQAIMMSIC
LQSMVDELMVKKSGGSIRKMLRRRVGGTLRRSDSQQAVKSPPLLESPDATRESMVKLSSKLSAVSLRGIGSPSTD
ASASDVHGNFAFEGIGDEDL

FIGURE 686

G**ATG**GCTGCTGTGGCCGTGGCTGTTCGCGAGGACTCGGGATCCGGGATGAAGGCGGAGCTTCCCCCTGGGCCTGG
GGCAGTGGGGAGGGAAATGACCAAAGAAGAAAAGCTGCAGCTTCGGAAGGAAAAGAAACAGCAGAAGAAGAAACG
GAAGGAAGAAAAGGGGGCAGAACCAGAGACTGGCTCTGCTGTATCTGCAGCCCAATGTCAAGTAGGCCCAACCAG
AGAACTGCCAGAATCGGGCATTCAGTTGGGCACTCCTCGGGAGAAAGTTCCAGCTGGTCGGAGTAAGGCCGAACT
TCGGGCTGAGCGTCGAGCCAAGCAGGAGGCCGAGCGGGCCCTGAAACAGGCAAGAAAAGGGGAACAAGGAGGACC
ACCTCCTAAGGCCAGCCCCAGCACAGCTGGAGAAACCCCCTCAGGAGTGAAGCGTCTCCCTGAGTACCCTCAGGT
TGATGACCTACTTCTGAGAAGGCTTGTTAAAAAACCAGAGCGTCAACAGGTTCCTACACGAAAGGATTATGGATC
CAAAGTCAGTCTCTTCTCTCACCTACCCCAGTACAGCAGACAAAACTCTCTGACCCAGTTTATGAGCATCCCATC
CTCTGTGATCCACCCAGCCATGGTGCGACTCGGCCTGCAGTACTCCCAGGGCCTGGTCAGTGGCTCCAATGCCCG
GTGTATTGCCCTGCTTCGTGCCTTGCAGCAGGTGATTCAGGATTACACAACACCGCCTAATGAAGAACTCTCCAG
GGATCTAGTGAATAAACTAAAACCCTACATGAGCTTCCTGACTCAGTGCCGTCCCCTGTCAGCGAGCATGCACAA
CGCCATCAAGTTCCTTAACAAGGAAATCACCAGTGTGGGCAGTTCCAAGCGGGAAGAGGAGGCCAAGTCAGAACT
TCGAGCAGCCATTGATCGGTATGTGCAAGAGAAGATTGTGCTAGCAGCTCAGGCAATTTCACGCTTTGCTTACCA
GAAGATCAGTAATGGAGATGTGATCCTGGTATATGGATGCTCATCTCTGGTATCACGAATTCTTCAGGAGGCTTG
GACAGAGGGCCGGCGGTTTCGGGTGGTAGTGGTGGACAGCCGGCCATGGCTGGAAGGAAGGCACACACTACGTTC
TCTAGTCCATGCTGGTGTCCCAGCCTCCTACCTGCTGATTCCTGCAGCCTCCTATGTGCTCCCAGAGGTTTCCAA
GGTGCTATTGGGAGCTCATGCACTCTTGGCCAACGGGTCTGTGATGTCACGGGTAGGGACAGCACAGTTAGCCCT
GGTGGCTCGAGCCCATAATGTACCAGTGCTGGTTTGCTGTGAAACATACAAGTTCTGTGAGCGTGTGCAGACTGA
TGCCTTTGTCTCTAATGAGCTAGATGACCCTGATGATCTGCAATGTAAGCGGGGAGAACATGTTGCGCTGGCTAA
CTGGCAGAACCACGCATCCCTACGGTTGTTGAATCTAGTCTATGATGTGACTCCCCCAGAGCTTGTGGATCTGGT
GATCACGGAGCTGGGGATGATCCCTTGCAGTTCTGTACCTGTTGTTCTACGAGTCAAGAGCAGTGACCAG**TGA**CG
GGGGAAACACAGGGTTAATAAATGCCATACTCCCTACCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAC

FIGURE 687

MAAVAVAVREDSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKKRKEEKGAEPETGSAVSAAQCQVGPTR
ELPESGIQLGTPREKVPAGRSKAELRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKRLPEYPQV
DDLLLRRLVKKPERQQVPTRKDYGSKVSLFSHLPQYSRQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVSGSNAR
CIALLRALQQVIQDYTTPPNEELSRDLVNKLKPYMSFLTQCRPLSASMHNAIKFLNKEITSVGSSKREEEAKSEL
RAAIDRYVQEKIVLAAQAISRFAYQKISNGDVILVYGCSSLVSRILQEAWTEGRRFRVVVVDSRPWLEGRHTLRS
LVHAGVPASYLLIPAASYVLPEVSKVLLGAHALLANGSVMSRVGTAQLALVARAHNVPVLVCCETYKFCERVQTD
AFVSNELDDPDDLQCKRGEHVALANWQNHASLRLLNLVYDVTPPELVDLVITELGMIPCSSVPVVLRVKSSDQ

FIGURE 688

AGGACTTTGGCGAGGGGGCAGCCATTTTGGGGGGTGCTG**ATG**GATACCTGCGGGGTCGGCTATGTTGCCCTGGGG
GAGGCCGGCCCCGTGGGGAACATGACTGTGGTAGACTCTCCTGGACAAGAGGTGCTAAATCAGCTTGATGTCAAG
ACCTCTTCAGAAATGACCAGTGCAGAGGCTTCCGTAGAGATGTCATTACCTACCCCTTTGCCTGGATTTGAGGAT
TCTCCTGATCAGAGGAGGCTCCCTCCAGAGCAGGAAAGCCTCTCCAGACTGGAACAGCCAGATCTTTCTTCAGAG
ATGTCAAAGGTCTCAAAGCCTAGGGCCTCAAAGCCTGGCCGGAAGAGAGGTGGTAGGACACGAAAAGGCCCCAAA
AGGCCCCAACAGCCTAATCCTCCATCAGCCCCACTGGTTCCTGGTCTCTTAGATCAATCCAACCCTCTGTCCACC
CCCATGCCTAAGAAACGAGGTCGAAAGTCCAAGGCAGAGCTGCTGCTGCTGAAGTTGTCAAAAGACCTAGATCGG
CCAGAATCTCAATCTCCAAAGAGGCCCCCTGAGGACTTTGAGACCCCTTCTGGGGAACGACCCCGCCGAAGGGCT
GCCCAAGTGGCACTTCTGTATCTTCAGGAACTGGCTGAAGAGCTCTCAACAGCCCTGCCTGCCCCTGTGTCCTGT
CCTGAGGGCCCCAAGGTGAGCAGCCCCACCAAACCGAAGAAGATCCGGCAGCCAGCAGCCTGTCCAGGTGGAGAA
GAGGTGGATGGTGCTCCACGGGATGAAGACTTTTTCTCCAGGTTGAGGCTGAAGATGTGGAAGAAAGTGAGGGC
CCAAGTGAGAGCTCATCTGAACCTGAGCCTGTAGTGCCCCGAAGCACCCCACGAGGATCTACTTCAGGGAAACAG
AAACCACACTGCCGAGGAATGGCTCCCAATGGCTTACCAAATCATATCATGGCTCCTGTTTGGAAGTGCCTCCAT
CTCACCAAGGACTTCCGAGAGCAGAAACATTCATACTGGGAGTTTGCTGAGTGGATTCCTTTAGCCTGGAAGTGG
CACTTGTTATCTGAGCTTGAGGCCGCTCCCTACCTGCCCCAGGAGGAGAAGTCTCCATTGTTTTCTGTACAACGT
GAAGGGCTACCTGAAGATGGCACCCTCTACCGAATAAACAGATTTAGCTCGATCACAGCACATCCAGAGCGCTGG
GATGTGTCCTTCTTCACGGGGGGACCGCTCTGGGCTCTGGACTGGTGCCCAGTGCCAGAGGGGGCAGGAGCCTCG
CAATATGTGGCTCTTTTCTCCAGCCCTGACATGAATGAGACACACCCACTGAGCCAGCTTCATTCGGGTCCTGGG
CTGCTCCAGCTCTGGGGCCTTGGGACCTTGCAGCAAGAAAGCTGTCCTGGCAACAGGGCCCACTTTGTCTATGGG
ATTGCTTGTGACAACGGCTGCATCTGGGACCTCAAGTTCTGCCCCAGTGGAGCATGGAACTTCCAGGCACCCCT
CGGAAGGCTCCTCTCCTGCCCCGGTTGGGTCTCTTGGCTCTGGCCTGCTCAGACGGGAAAGTACTGCTATTCAGT
CTACCCCATCCGGAGGCCCTGCTGGCTCAGCAACCCCCAGATGCAGTGAAGCCTGCCATATATAAGGTACAATGT
GTGGCAACTCTGCAGGTGGGGTCTATGCAAGCTACAGACCCCTCTGAGTGTGGTCAGTGCCTTAGCCTGGCCTGG
ATGCCTACCAGGCCCCACCAACACCTAGCTGCTGGATATTATAATGGCATGGTGGTTTTCTGGAACCTTCCCACT
AACTCACCCCTGCAGCGGATACGGCTCTCTGATGGCTCCTTAAAGCTCTACCCCTTCCAGTGTTTCCTAGCCCAT
GACCAGGCTGTGCGTACCCTTCAATGGTGCAAAGCTAACAGCCATTTCCTTGTCTCTGCGGGGAGTGACCGGAAA
ATCAAATTCTGGGACCTTCGACGTCCTTACGAACCCATAAACTCTATCAAGCGCTTCTTGAGTACAGAACTGGCC
TGGCTGCTTCCCTACAATGGTGTCACTGTGGCTCAGGACAACTGCTATGCCTCTTATGGACTCTGTGGGATTCAT
TATATTGACGCTGGTTACCTTGGTTTCAAGGCCTACTTCACTGCTCCTCGAAAAGGCACCGTTTGGAGTCTTTCA
GGATCCGACTGGCTTGGGACAATAGCTGCAGGAGATATATCCGGGGAGCTCATTGCTGCTATATTACCAGATATG
GCACTGAATCCAATAAATGTCAAGCGACCTGTAGAGCGAAGATTTCCTATATATAAAGCAGATCTGATACCGTAT
CAGGACAGTCCTGAAGGTCCAGACCATTCTTCTGCTTCATCTGGGGTCCCCAACCCTCCCAAGGCTCGAACTTAC
ACTGAAACTGTCAACCATCACTACTTGCTCTTTCAAGACACAGATTTGGGTTCATTCCATGATCTGCTCCGTAGA
GAACCAATGCTGCGCATGCAGGAGGGAGAGGGGCATTCTCAACTCTGCCTGGACAGGCTGCAGCTGGAGGCTATT
CATAAGGTACGTTTCAGCCCAAACCTGGACTCCTATGGATGGCTGGTATCTGGGGGGCAGTCAGGGCTGGTTCGA
ATCCATTTTGTCCGTGGACTCGCCTCCCCACTGGGCCACCGTATGCAGCTTGAAAGCCGAGCCCACTTCAATGCT
ATGTTCCAACCATCCTCCCCCACTAGACGGCCTGGCTTCTCTCCAACCAGCCATCGCCTTCTGCCCACTCCC**TAG**

CCTTGGCCCACACCAGATCCTTGGAGTGAAGTCGGTCAAGAACAAATGGCCCCTATGCACAGAGCCATAGGAACT
GGGGGCCTTCCCTGGACAGTGATCATGCCAGGCCTGGACCTTTAGGCCTGCCTCCCCAGGACTCCTTAGATCCCA
CTCTTTCTACAGACTTCTGTGATCACAGCCCCCTGCGGGCAGGGGGGCTCTCCCTCCACCAACTCTCAAGGCTCC
TCAGCCTAAGACTATGGCTCATGAGAAACACTCAGGCCTGACCTAGGCTTGGGAGTCAAACTGCTCATATTGAGC
ATATTGTTAAGTGGGTAAAGCCAAGTAAAGGTACTGGGTGTTTTTGTGACCACTTGTGAATGGGTGTATGGAGAA
CTGAAAAGGGTATCTGCATGAAGGCTCCTGTCTGACTATTCCAGGATCCAATATTACTGCCTTCTGAAACTTCCT
CTTTAGGGTAACCATCATGTATGCCCACGAGGGTGATAGTAATTCGTGAGACTGAAGTTGCTTAGAGTACTTCTT
TGACCAAGGAATACCACAGACACCCTACCGATAGAACAGTGGCTCAGATCTTACTTGCTCCTGCTTACGAAGTAT
TCCCAATCACTGGTCATCTGACCCTACTTGAACACTCCTGAACAGTCATGTTTTTTAAAATCTTCCTTTATATCA
AGTCAGAGAGTATACTTCTATAAATTTCACTCATGGATGTTAGGAAATCTAGTCATCTTCCCTGTGATTGCCCTG
TTAAGTATTTAACCATAGCTATCATGTGTTTCCCAAATCTTCTCTAGATTAAATATCTTCAGTTACTTC

FIGURE 689

MDTCGVGYVALGEAGPVGNMTVVDSPGQEVLNQLDVKTSSEMTSAEASVEMSLPTPLPGFEDSPDQRRLPPEQES
LSRLEQPDLSSEMSKVSKPRASKPGRKRGGRTRKGPKRPQQPNPPSAPLVPGLLDQSNPLSTPMPKKRGRKSKAE
LLLLKLSKDLDRPESQSPKRPPEDFETPSGERPRRRAAQVALLYLQELAEELSTALPAPVSCPEGPKVSSPTKPK
KIRQPAACPGGEEVDGAPRDEDFFLQVEAEDVEESEGPSESSSEPEPVVPRSTPRGSTSGKQKPHCRGMAPNGLP
NHIMAPVWKCLHLTKDFREQKHSYWEFAEWIPLAWKWHLLSELEAAPYLPQEEKSPLFSVQREGLPEDGTLYRIN
RFSSITAHPERWDVSFFTGGPLWALDWCPVPEGAGASQYVALFSSPDMNETHPLSQLHSGPGLLQLWGLGTLQQE
SCPGNRAHFVYGIACDNGCIWDLKFCPSGAWELPGTPRKAPLLPRLGLLALACSDGKVLLFSLPHPEALLAQQPP
DAVKPAIYKVQCVATLQVGSMQATDPSECGQCLSLAWMPTRPHQHLAAGYYNGMVVFWNLPTNSPLQRIRLSDGS
LKLYPFQCFLAHDQAVRTLQWCKANSHFLVSAGSDRKIKFWDLRRPYEPINSIKRFLSTELAWLLPYNGVTVAQD
NCYASYGLCGIHYIDAGYLGFKAYFTAPRKGTVWSLSGSDWLGTIAAGDISGELIAAILPDMALNPINVKRPVER
RFPIYKADLIPYQDSPEGPDHSSASSGVPNPPKARTYTETVNHHYLLFQDTDLGSFHDLLRREPMLRMQEGEGHS
QLCLDRLQLEAIHKVRFSPNLDSYGWLVSGGQSGLVRIHFVRGLASPLGHRMQLESRAHFNAMFQPSSPTRRPGF
SPTSHRLLPTP

FIGURE 690

GAGGGACGGTGGGGGTGACCCCCTCTCCTCTTGGCTTGACAGGAAGCATGGCACTCTGGCGGGCATACCAGCGGG
CCCTGGCCGCTCACCCGTGGAAAGTACAGGTCCTGACAGCTGGGTCCCTGATGGGCCTGGGTGACATTATCTCAC
AGCAGCTGGTGGAGAGGCGGGGTCTGCAGGAACACCAGAGAGGCCGGACTCTGACCATGGTGTCCCTGGGCTGTG
GCTTTGTGGGCCCTGTGGTAGGAGGCTGGTACAAGGTTTTGGATCGGTTCATCCCTGGCACCACCAAAGTGGATG
CACTGAAGAAGATGTTGTTGGATCAGGGGGGCTTTGCCCCGTGTTTTCTAGGCTGCTTTCTCCCACTGGTAGGGG
CACTTAATGGACTGTCAGCCCAGGACAACTGGGCCAAACTACAGCGGGATTATCCTGATGCCCTTATCACCAACT
ACTATCTATGGCCTGCTGTGCAGTTAGCCAACTTCTACCTGGTCCCCCTTCATTACAGGTTGGCCGTTGTCCAAT
GTGTTGCTGTTATCTGGAACTCCTACCTGTCCTGGAAGGCACATCGGCTCTAAGCCTGCCTCACTCCATCGTTTC
CACCTTGCAGTGATGCAGCTTGACCCTGGAACGGTCAGACAACCTCCTCAAAGTGGGCATACCAGTTTCCACGGG
GTTGGGTTGCCGGTCAGAGCTTAAGAGGACTAGCACCCTGCAATGCCCCTCTTCACTCTAAAATGTACACTGACT
GCTTTAGAGCCCTTGATAATAGTCTTATTCCCACCACATACTAGGCACTCCATAAATATCTGTTGAACCTTCATG
ACCTTATCAACTTTACACCCATATCCCAGCAAATGCCACTCATCCCCACTCTTCATAGACACATTTGTTACTCTA
ACCCTGCCTAGGCTTCTTGTAGCTCCAGCTCTTTAGAGACTCCCGGAACCCTTTATATGGTGCCTCAGTAAATAT
GTTATTAAATATGTAATCCGG

FIGURE 691

MALWRAYQRALAAHPWKVQVLTAGSLMGLGDIISQQLVERRGLQEHQRGRTLTMVSLGCGFVGPVVGGWYKVLDR
FIPGTTKVDALKKMLLDQGGFAPCFLGCFLPLVGALNGLSAQDNWAKLQRDYPDALITNYYLWPAVQLANFYLVP
LHYRLAVVQCVAVIWNSYLSWKAHRL

FIGURE 692A

CGCCCCCGCCTCTGAGCTCCCTTCCC**ATG**GCGGCCCTAGTGTTGGAGGACGGGTCGGTCCTGCGGGGCCAGCCCT
TTGGGGCCGCCGTGTCGACTGCCGGGGAAGTGGTGTTTCAAACCGGCATGGTCGGCTACCCCGAGGCCCTCACTG
ATCCCTCCTACAAGGCACAGATCTTAGTGCTCACCTATCCTCTGATCGGCAACTATGGCATCCCCCCAGATGAAA
TGGATGAGTTCGGTCTCTGCAAGTGGTTTGAATCCTCGGGCATCCACGTAGCAGCACTGGTAGTGGGAGAGTGCT
GTCCTACTCCCAGCCACTGGAGTGCCACCCGCACCCTGCATGAGTGGCTGCAGCAGCATGGCATCCCTGGCTTGC
AAGGAGTAGACACTCGGGAGCTGACCAAGAAGTTGCGGGAACAGGGGTCTCTGCTGGGGAAGCTGGTCCAGAATG
GAACAGAACCTTCATCCCTGCCATTCTTGGACCCCAATGCCCGCCCCCTGGTACCAGAGGTCTCCATTAAGACTC
CACGGGTATTCAATACAGGGGGTGCCCCTCGGATCCTTGCTTTGGACTGTGGCCTCAAGTATAATCAGATCCGAT
GCCTCTGCCAGCGTGGGGCTGAGGTCACTGTGGTACCCTGGGACCATGCACTAGACAGCCAAGAGTATGAGGGTC
TCTTCTTAAGTAATGGGCCTGGTGACCCTGCCTCCTATCCCAGTGTCGTATCCACACTGAGCCGTGTTTTATCTG
AGCCTAATCCCCGACCTGTCTTTGGGATCTGCCTGGGACACCAGCTATTGGCCTTAGCCATTGGGGCCAAGACTT
ACAAGATGAGATATGGGAACCGAGGCCATAACCAGCCCTGCTTGTTGGTGGGCTCTGGGCGCTGCTTTCTGACAT
CCCAGAACCATGGGTTTGCTGTGGAGACAGACTCACTGCCAGCAGACTGGGCTCCTCTCTTCACCAACGCCAATG
ATGGTTCCAATGAAGGCATTGTGCACAACAGCTTGCCTTTCTTCAGTGTCCAGTTTCACCCAGAGCACCAAGCTG
GCCCTTCAGATATGGAACTGCTTTTCGATATCTTTCTGGAAACTGTGAAAGAGGCCACAGCTGGGAACCCTGGGG
GCCAGACAGTTAGAGAGCGGCTGACTGAGCGCCTCTGTCCCCCTGGGATTCCCACTCCCGGCTCTGGACTTCCAC
CACCACGAAAGGTTCTGATCCTGGGCTCAGGGGGCCTCTCCATTGGCCAAGCTGGAGAATTTGACTACTCGGGCT
CTCAGGCAATTAAGGCCCTGAAGGAGGAAAACATCCAGACGTTGCTGATCAACCCCAATATTGCCACAGTGCAGA
CCTCCCAGGGGCTGGCCGACAAGGTCTATTTTCTTCCCATAACACCTCATTATGTAACCCAGGTGATACGTAATG
AACGCCCCGATGGTGTGTTACTGACTTTGGGGGCCAGACTGCTCTGAACTGTGGTGTGGAGCTGACCAAGGCCG
GGGTGCTGGCTCGGTATGGGGTCCGGGTCCTGGGCACACCAGTGGAGACCATTGAGCTGACCGAGGATCGACGGG
CCTTTGCTGCCAGAATGGCAGAGATCGGAGAGCATGTGGCCCCGAGCGAGGCAGCAAATTCTCTTGAACAGGCCC
AGGCAGCCGCTGAACGGCTGGGGTACCCTGTGCTAGTGCGTGCAGCCTTTGCCCTGGGTGGCCTGGGCTCTGGCT
TTGCCTCTAACAGGGAGGAGCTCTCTGCTCTCGTGGCCCCAGCTTTTGCCCATACCAGCCAAGTGCTAGTAGACA
AGTCTCTGAAGGGATGGAAGGAGATTGAGTACGAGGTGGTGAGAGACGCCTATGGCAACTGTGTCACGGTGTGTA
ACATGGAGAACTTGGACCCACTGGGCATCCACACTGGTGAGTCCATAGTGGTGGCCCCTAGCCAGACACTGAATG
ACAGGGAGTATCAGCTCCTGAGGCAGACAGCTATCAAGGTGACCCAGCACCTGGGAATTGTTGGGGAGTGCAATG
TGCAGTATGCCTTGAACCCTGAGTCTGAGCAGTATTACATCATTGAAGTGAATGCCAGGCTCTCTCGCAGCTCTG
CCCTGGCCAGTAAGGCCACAGGTTATCCACTGGCTTATGTGGCAGCCAAGCTAGCATTGGGCATCCCTTTGCCTG
AGCTCAGGAACTCTGTGACAGGGGGTACAGCAGCCTTTGAACCCAGCGTGGATTATTGTGTGGTGAAGATTCCTC
GATGGGACCTTAGCAAGTTCCTGCGAGTCAGCACAAAGATTGGGAGCTGCATGAAGAGCGTTGGTGAAGTCATGG
GCATTGGGCGTTCATTTGAGGAGGCCTTCCAGAAGGCCCTGCGCATGGTGGATGAGAACTGTGTGGGCTTTGATC
ACACAGTGAAACCAGTCAGCGATATGGAGTTGGAGACTCCAACAGATAAGCGGATTTTTGTGGTGGCAGCTGCTT
TGTGGGCTGGTTATTCAGTGGACCGCCTGTATGAGCTCACACGCATCGACCGCTGGTTCCTGCACCGAATGAAGC
GTATCATCGCACATGCCCAGCTGCTAGAACAACACCGTGGACAGCCTTTGCCGCCAGACCTGCTGCAACAGGCCA
AGTGTCTTGGCTTCTCAGACAAACAGATTGCCCTTGCAGTTCTGAGCACAGAGCTGGCTGTTCGCAAGCTGCGTC
AGGAACTGGGGATCTGTCCAGCAGTGAAACAGATTGACACAGTTGCAGCTGAGTGGCCAGCCCAGACAAATTACC
TATACCTAACGTATTGGGGCACCACCCATGACCTCACCTTTCGAACACCTCATGTCCTAGTCCTTGGCTCTGGCG
TCTACCGTATTGGCTCTAGCGTTGAATTTGACTGGTGTGCTGTAGGCTGCATCCAGCAGCTCCGAAAGATGGGAT
ATAAGACCATCATGGTGAACTATAACCCAGAGACAGTCAGCACCGACTATGACATGTGTGATCGACTCTACTTTG
ATGAGATCTCTTTTGAGGTGGTGATGGACATCTATGAGCTCGAGAACCCTGAAGGTGTGATCCTATCCATGGGTG
GACAGCTGCCCAACAACATGGCCATGGCGTTGCATCGGCAGCAGTGCCGGGTGCTGGGCACCTCCCCTGAAGCCA
TTGACTCGGCTGAGAACCGTTTCAAGTTTTCCCGGCTCCTTGACACCATTGGTATCAGCCAGCCTCAGTGGAGGG
AGCTCAGTGACCTCGAGTCTGCTCGCCAATTCTGCCAGACCGTGGGGTACCCCTGTGTGGTGCGCCCCTCCTATG
TGCTGAGCGGTGCTGCTATGAATGTGGCCTACACGGATGGAGACCTGGAGCGCTTCCTGAGCAGCGCAGCAGCCG
TCTCCAAAGAGCATCCCGTGGTCATCTCCAAGTTCATCCAGGAGGCTAAGGAGATTGACGTGGATGCCGTGGCCT
CTGATGGTGTGGTGGCAGCCATCGCCATCTCTGAGCATGTGGAGAATGCAGGTGTGCATTCAGGTGATGCGACGC
TGGTGACCCCCCCACAAGATATCACTGCCAAAACCCTGGAGCGGATCAAAGCCATTGTGCATGCTGTGGGCCAGG

FIGURE 692B

AGCTACAGGTCACAGGACCCTTCAATCTGCAGCTCATTGCCAAGGATGACCAGCTGAAAGTTATTGAATGCAACG
TACGTGTCTCTCGCTCCTTCCCCTTCGTTTCCAAGACACTGGGTGTGGACCTAGTAGCCTTGGCCACGCGGGTCA
TCATGGGGGAAGAAGTGGAACCTGTGGGGCTAATGACTGGTTCTGGAGTCGTGGGAGTAAAGGTGCCTCAGTTCT
CCTTCTCCCGCTTGGCGGGTGCTGACGTGGTGTTGGGTGTGGAAATGACCAGTACTGGGGAGGTGGCCGGCTTTG
GGGAGAGCCGCTGTGAGGCATACCTCAAGGCCATGCTAAGCACTGGCTTTAAGATCCCCAAGAAGAATATCCTGC
TGACCATTGGCAGCTATAAGAACAAAAGCGAGCTGCTCCCAACTGTGCGGCTACTGGAGAGCCTGGGCTACAGCC
TCTATGCCAGTCTCGGCACAGCTGACTTCTACACTGAGCATGGCGTCAAGGTAACAGCTGTGGACTGGCACTTTG
AGGAGGCTGTGGATGGTGAGTGCCCACCACAGCGGAGCATCCTGGAGCAGCTAGCTGAGAAAAACTTTGAGCTGG
TGATTAACCTGTCAATGCGTGGAGCTGGGGGCCGGCGTCTCTCTTCCTTTGTCACCAAGGGCTACCGCACCCGAC
GCTTGGCCGCTGACTTCTCCGTGCCCCTAATCATCGATATCAAGTGCACCAAACTCTTTGTGGAGGCCCTAGGCC
AGATCGGGCCAGCCCCTCCTTTGAAGGTGCATGTTGACTGTATGACCTCCCAAAAGCTTGTGCGACTGCCGGGAT
TGATTGATGTCCATGTGCACCTGCGGGAACCAGGTGGGACACATAAGGAGGACTTTGCTTCAGGCACAGCCGCTG
CCCTGGCTGGGGGTATCACCATGGTGTGTGCCATGCCTAATACCCGGCCCCCCATCATTGACGCCCCTGCTCTGG
CCCTGGCCCAGAAGCTGGCAGAGGCTGGCGCCCGGTGCGACTTTGCGCTATTCCTTGGGGCCTCGTCTGAAAATG
CAGGAACCTTGGGCACCGTGGCCGGGTCTGCAGCCGGGCTGAAGCTTTACCTCAATGAGACCTTCTCTGAGCTGC
GGCTGGACAGCGTGGTCCAGTGGATGGAGCATTTCGAGACATGGCCCTCCCACCTCCCCATTGTGGCTCACGCAG
AGCAGCAAACCGTGGCTGCTGTCCTCATGGTGGCTCAGCTCACTCAGCGCTCAGTGCACATATGTCACGTGGCAC
GGAAGGAGGAGATCCTGCTAATTAAAGCTGCAAAGGCACGGGGCTTGCCAGTGACCTGCGAGGTGGCTCCCCACC
ACCTGTTCCTAAGCCATGATGACCTGGAGCGCCTGGGGCCTGGGAAGGGGGAGGTCCGGCCTGAGCTTGGCTCCC
GCCAGGATGTGGAAGCCCTGTGGGAGAACATGGCTGTCATCGACTGCTTTGCCTCAGACCATGCTCCCCATACCT
TGGAGGAGAAGTGTGGGTCCAGGCCCCCACCTGGGTTCCCAGGGTTAGAGACCATGCTGCCACTACTCCTGACGG
CTGTAAGCGAGGGCCGGCTCAGCCTGGACGACCTGCTGCAGCGATTGCACCACAATCCTCGGCGCATCTTTCACC
TGCCCCCGCAGGAGGACACCTATGTGGAGGTGGATCTGGAGCATGAGTGGACAATTCCCAGCCACATGCCCTTCT
CCAAGGCCCACTGGACACCTTTTGAAGGGCAGAAAGTGAAGGGCACCGTCCGCCGTGTGGTCCTGCGAGGGGAGG
TTGCCTATATCGATGGGCAGGTTCTGGTACCCCCGGGCTATGGACAGGATGTACGGAAGTGGCCACAGGGGGCTG
TTCCTCAGCTCCCACCCTCAGCCCCTGCCACTAGTGAGATGACCACGACACCTGAAAGACCCCGCCGTGGCATCC
CAGGGCTTCCTGATGGCCGCTTCCATCTGCCGCCCCGAATCCATCGAGCCTCCGACCCAGGTTTGCCAGCTGAGG
AGCCAAAGGAGAAGTCCTCTCGGAAGGTAGCCGAGCCAGAGCTGATGGGAACCCCTGATGGCACCTGCTACCCTC
CACCACCAGTACCGAGACAGGCATCTCCCCAGAACCTGGGGACCCCTGGCTTGCTGCACCCCCAGACCTCACCCC
TGCTGCACTCATTAGTGGGCCAACATATCCTGTCCGTCCAGCAGTTCACCAAGGATCAGATGTCTCACCTGTTCA
ATGTGGCACACACACTGCGTATGATGGTGCAGAAGGAGCGGAGCCTCGACATCCTGAAGGGGAAGGTCATGGCCT
CCATGTTCTATGAAGTGAGCACACGGACCAGCAGCTCCTTTGCAGCAGCCATGGCCCGGCTGGGAGGTGCTGTGC
TCAGCTTCTCGGAAGCCACATCGTCCGTCCAGAAGGGCGAATCCCTGGCTGACTCCGTGCAGACCATGAGCTGCT
ATGCCGACGTCGTCGTGCTCCGGCACCCCCAGCCTGGAGCAGTGGAGCTGGCCGCCAAGCACTGCCGGAGGCCAG
TGATCAATGCTGGGGATGGGGTCGGAGAGCACCCCACCCAGGCCCTGCTGGACATCTTCACCATCCGTGAGGAGC
TGGGAACTGTCAATGGCATGACGATCACGATGGTGGGTGACCTGAAGCACGGACGCACAGTACATTCCCTGGCCT
GCCTGCTCACCCAGTATCGTGTCAGCCTGCGCTACGTGGCACCTCCCAGCCTGCGCATGCCACCCACTGTGCGGG
CCTTCGTGGCCTCCCGCGGCACCAAGCAGGAGGAATTCGAGAGCATTGAGGAGGCGCTGCCTGACACTGATGTGC
TCTACATGACTCGAATCCAGAAGGAACGATTTGGCTCTACCCAGGAGTACGAAGCTTGCTTTGGTCAGTTCATCC
TCACTCCCCACATCATGACCCGGGCCAAGAAGAAGATGGTGGTGATGCACCCGATGCCCCGTGTCAACGAGATAA
GCGTGGAAGTGGACTCGGATCCCCGCGCAGCCTACTTCCGCCAGGCTGAGAACGGCATGTACATCCGCATGGCTC
TGTTAGCCACCGTGCTGGGCCGTTTCTAGGGGCCTGGCTTCCTCAGCCTCTTCTCTTTAGGCCCAGCTGCTGGGC
AAGGAATTCCAGTGCCTCCTACGGGGGCAGCACACTTAGATATTCCTGGACATCCAGATTGCTCACATGTGCTGA
CCACACTTCAGGCTCTGGACTGGAGCTCTCTGGCATGGGGGTGGGGCCTCAGATGCTGGGGCCCAGTCTGCCCCA
TCTTCATTCCTGCACCTTAAACCTGTACAGTCATTTTTCTACTGACTTAATAAACAGCCGAGCTGTCCCTTG

FIGURE 693

MAALVLEDGSVLRGQPFGAAVSTAGEVVFQTGMVGYPEALTDPSYKAQILVLTYPLIGNYGIPPDEMDEFGLCKW
FESSGIHVAALVVGECCPTPSHWSATRTLHEWLQQHGIPGLQGVDTRELTKKLREQGSLLGKLVQNGTEPSSLPF
LDPNARPLVPEVSIKTPRVFNTGGAPRILALDCGLKYNQIRCLCQRGAEVTVVPWDHALDSQEYEGLFLSNGPGD
PASYPSVVSTLSRVLSEPNPRPVFGICLGHQLLALAIGAKTYKMRYGNRGHNQPCLLVGSGRCFLTSQNHGFAVE
TDSLPADWAPLFTNANDGSNEGIVHNSLPFFSVQFHPEHQAGPSDMELLFDIFLETVKEATAGNPGGQTVRERLT
ERLCPPGIPTPGSGLPPPRKVLILGSGGLSIGQAGEFDYSGSQAIKALKEENIQTLLINPNIATVQTSQGLADKV
YFLPITPHYVTQVIRNERPDGVLLTFGGQTALNCGVELTKAGVLARYGVRVLGTPVETIELTEDRRAFAARMAEI
GEHVAPSEAANSLEQAQAAAERLGYPVLVRAAFALGGLGSGFASNREELSALVAPAFAHTSQVLVDKSLKGWKEI
EYEVVRDAYGNCVTVCNMENLDPLGIHTGESIVVAPSQTLNDREYQLLRQTAIKVTQHLGIVGECNVQYALNPES
EQYYIIEVNARLSRSSALASKATGYPLAYVAAKLALGIPLPELRNSVTGGTAAFEPSVDYCVVKIPRWDLSKFLR
VSTKIGSCMKSVGEVMGIGRSFEEAFQKALRMVDENCVGFDHTVKPVSDMELETPTDKRIFVVAAALWAGYSVDR
LYELTRIDRWFLHRMKRIIAHAQLLEQHRGQPLPPDLLQQAKCLGFSDKQIALAVLSTELAVRKLRQELGICPAV
KQIDTVAAEWPAQTNYLYLTYWGTTHDLTFRTPHVLVLGSGVYRIGSSVEFDWCAVGCIQQLRKMGYKTIMVNYN
PETVSTDYDMCDRLYFDEISFEVVMDIYELENPEGVILSMGGQLPNNMAMALHRQQCRVLGTSPEAIDSAENRFK
FSRLLDTIGISQPQWRELSDLESARQFCQTVGYPCVVRPSYVLSGAAMNVAYTDGDLERFLSSAAAVSKEHPVVI
SKFIQEAKEIDVDAVASDGVVAAIAISEHVENAGVHSGDATLVTPPQDITAKTLERIKAIVHAVGQELQVTGPFN
LQLIAKDDQLKVIECNVRVSRSFPFVSKTLGVDLVALATRVIMGEEVEPVGLMTGSGVVGVKVPQFSFSRLAGAD
VVLGVEMTSTGEVAGFGESRCEAYLKAMLSTGFKIPKKNILLTIGSYKNKSELLPTVRLLESLGYSLYASLGTAD
FYTEHGVKVTAVDWHFEEAVDGECPPQRSILEQLAEKNFELVINLSMRGAGGRRLSSFVTKGYRTRRLAADFSVP
LIIDIKCTKLFVEALGQIGPAPPLKVHVDCMTSQKLVRLPGLIDVHVHLREPGGTHKEDFASGTAAALAGGITMV
CAMPNTRPPIIDAPALALAQKLAEAGARCDFALFLGASSENAGTLGTVAGSAAGLKLYLNETFSELRLDSVVQWM
EHFETWPSHLPIVAHAEQQTVAAVLMVAQLTQRSVHICHVARKEEILLIKAAKARGLPVTCEVAPHHLFLSHDDL
ERLGPGKGEVRPELGSRQDVEALWENMAVIDCFASDHAPHTLEEKCGSRPPPGFPGLETMLPLLLTAVSEGRLSL
DDLLQRLHHNPRRIFHLPPQEDTYVEVDLEHEWTIPSHMPFSKAHWTPFEGQKVKGTVRRVVLRGEVAYIDGQVL
VPPGYGQDVRKWPQGAVPQLPPSAPATSEMTTTPERPRRGIPGLPDGRFHLPPRIHRASDPGLPAEEPKEKSSRK
VAEPELMGTPDGTCYPPPPVPRQASPQNLGTPGLLHPQTSPLLHSLVGQHILSVQQFTKDQMSHLFNVAHTLRMM
VQKERSLDILKGKVMASMFYEVSTRTSSSFAAAMARLGGAVLSFSEATSSVQKGESLADSVQTMSCYADVVVLRH
PQPGAVELAAKHCRRPVINAGDGVGEHPTQALLDIFTIREELGTVNGMTITMVGDLKHGRTVHSLACLLTQYRVS
LRYVAPPSLRMPPTVRAFVASRGTKQEEFESIEEALPDTDVLYMTRIQKERFGSTQEYEACFGQFILTPHIMTRA
KKKMVVMHPMPRVNEISVEVDSDPRAAYFRQAENGMYIRMALLATVLGRF

FIGURE 694

GGAGCACCAAGGGAACGGAAAATGGCGCCTCACGGCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCC
CTGCTCCTCGCTCTGGGCGTGGAAAGGGCTCTGGCGCTACCCGAGGTACAGAAGCAAGTTTGAGGTCGGGCTGAA
GCAGGGTCACTGGCCAGCCGTGCGTCGCGCTCGCCAGCGGCTCCCCCTTCTCCTCGGCGGGCCTGCGGTTCTGAT
TTCGTCCCTGACGCTTCCCGACCCTGCCCAGCCAGATATGCACCCAATGTCCAGGGAGCGTGCAAAATTTGTCAA
AAGTGGCCTTTTATTGTAAAACGACACGAGAGCTA**ATG**CTGCATGCCCGTTGCTGCCTGAATCAGAAGGGCACCA
TCTTGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCTGGTCCAAACTTTCATCAGGCACATACCACTGTCA
TCATAGACCTGCAAGCAAACCCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTACTCAGCTCCAGACTC
TGATACTGCCACAACATGTCAACTGTCCTGGAGGAATTAATGCCTGGAATACTATCACCTCTTATATAGACAACC
AAATCTGTCAAGGGCAAAAGAACCTTTGCAATAACACTGGGGACCCAGAAATGTGTCCTGAGAATGGATCTTGTG
TACCTGATGGTCCAGGTCTTTTGCAGTGTGTTTGTGCTGATGGTTTCCATGGATACAAGTGTATGCGCCAGGGCT
CGTTCTCACTGCTTATGTTCTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTTTGGGCGACCC
AGCGCCGAAAAGCCAAGACTTCA**TGA**ACTACATAGGTCTTACCATTGACCTAAGATCAATCTGAACTATCTTAGC
CCAGTCAGGGAGCTCTGCTTCCTAGAAAGGCATCTTTCGCCAGTGGATTCGCCTCAAGGTTGAGGCCGCCATTGG
AAGATGAAAAATTGCACTCCCTTGGTGTAGACAAATACCAGTTCCCATTGGTGTTGTTGCCTATAATAAACACTT
TTTCTTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 695

MLHARCCLNQKGTILGLDLQNCSLEDPGPNFHQAHTTVIIDLQANPLKGDLANTFRGFTQLQTLILPQHVNCPGG
INAWNTITSYIDNQICQGQKNLCNNTGDPEMCPENGSCVPDGPGLLQCVCADGFHGYKCMRQGSFSLLMFFGILG
ATTLSVSILLWATQRRKAKTS

FIGURE 696

GGAGCACCAAGGGAACGGAAAATGGCGCCTCACGGCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCC
CTGCTCCTCGCTCTGGGCGTGGAAAGGGCTCTGGCGCTACCCGAGATATGCACCCAATGTCCAGGGAGCGTGCAA
AATTTGTCAAAAGTGGCCTTTTATTGTAAAACGACACGAGAGCTA**ATG**CTGCATGCCCGTTGCTGCCTGAATCAG
AAGGGCACCATCTTGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCTGGTCCAAACTTTCATCAGGCACAT
ACCACTGTCATCATAGACCTGCAAGCAAACCCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTACTCAG
CTCCAGACTCTGATACTGCCACAACATGTCAACTGTCCTGGAGGAATTAATGCCTGGAATACTATCACCTCTTAT
ATAGACAACCAAATCTGTCAAGGGCAAAAGAACCTTTGCAATAACACTGGGGACCCAGAAATGTGTCCTGAGAAT
GGATCTTGTGTACCTGATGGTCCAGGTCTTTTGCAGTGTGTTTGTGCTGATGGTTTCCATGGATACAAGTGTATG
CGCCAGGGCTCGTTCTCACTGCTTATGTTCTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTT
TGGGCGACCCAGCGCCGAAAAGCCAAGACTTCA**TGA**ACTACATAGGTCTTACCATTGACCTAAGATCAATCTGAA
CTATCTTAGCCCAGTCAGGGAGCTCTGCTTCCTAGAAAGGCATCTTTCGCCAGTGGATTCGCCTCAAGGTTGAGG
CCGCCATTGGAAGATGAAAAATTGCACTCCCTTGGTGTAGACAAATACCAGTTCCCATTGGTGTTGTTGCCTATA
ATAAACACTTTTCTTTTTAAAAA

FIGURE 697

MLHARCCLNQKGTILGLDLQNCSLEDPGPNFHQAHTTVIIDLQANPLKGDLANTFRGFTQLQTLILPQHVNCPGG
INAWNTITSYIDNQICQGQKNLCNNTGDPEMCPENGSCVPDGPGLLQCVCADGFHGYKCMRQGSFSLLMFFGILG
ATTLSVSILLWATQRRKAKTS

FIGURE 698

GCGCCCTAGCCCTCTTTCGGGGATACTGGCCGACCCCCTCTTCCTTTTCCCCTTTAGTGAAGGCCTCCCCCGTCG
CCGCGCGGCTTCCCGGAGCCGACTGCAGACTCCCTCAGCCCGGTGTTCCCCGCGTCCGGACGCCGAGGTCGCGGC
TTCGCAGAAACTCGGGCCCCTCCATCCGCCCTCAGAAAAGGGAGCGATGTTGATCTCAGGAAGCACAAAGGGACC
TTCCTAGCTCTGACTGAACCACGGAGCTCACCCTGGACAGTATCACTCCGTGGAGGAAGACTGTGAGACTGTGGC
TGGAAGCCAGATTGTAGCCACACATCCGCCCCTGCCCTACCCCAGAGCCCTGGAGCAGCAACTGGCTGCAGATCA
CAGACACAGTGAGGAT**ATG**AGTGTAGGGGTGAGCACCTCAGCCCCTCTTTCCCCAACCTCGGGCACAAGCGTGGG
CATGTCTACCTTCTCCATCATGGACTATGTGGTGTTCGTCCTGCTGCTGGTTCTCTCTCTTGCCATTGGGCTCTA
CCATGCTTGTCGTGGCTGGGGCCGGCATACTGTTGGTGAGCTGCTGATGGCGGACCGCAAAATGGGCTGCCTTCC
GGTGGCACTGTCCCTGCTGGCCACCTTCCAGTCAGCCGTGGCCATCCTGGGTGTGCCGTCAGAGATCTACCGATT
TGGGACCCAATATTGGTTCCTGGGCTGCTGCTACTTTCTGGGGCTGCTGATACCTGCACACATCTTCATCCCCGT
TTTCTACCGCCTGCATCTCACCAGTGCCTATGAGTACCTGGAGCTTCGATTCAATAAAACTGTGCGAGTGTGTGG
AACTGTGACCTTCATCTTTCAGATGGTGATCTACATGGGAGTTGTGCTCTATGCTCCGTCATTGGCTCTCAATGC
AGTGACTGGCTTTGATCTGTGGCTGTCCGTGCTGGCCCTGGGCATTGTCTGTACCGTCTATACAGCTCTGGGTGG
GCTGAAGGCCGTCATCTGGACAGATGTGTTCCAGACACTGGTCATGTTCCTCGGGCAGCTGGCAGTTATCATCGT
GGGGTCAGCCAAGGTGGGCGGCTTGGGGCGTGTGTGGGCCGTGGCTTCCCAGCACGGCCGCATCTCTGGGTTTGA
GCTGGATCCAGACCCCTTTGTGCGGCACACCTTCTGGACCTTGGCCTTCGGGGGTGTCTTCATGATGCTCTCCTT
ATACGGGGTGAACCAGGCTCAGGTGCAGCGGTACCTCAGTTCCCGCACGGAGAAGGCTGCTGTGCTCTCCTGTTA
TGCAGTGTTCCCCTTCCAGCAGGTGTCCCTCTGCGTGGGCTGCCTCATTGGCCTGGTCATGTTCGCGTATTACCA
GGAGTATCCCATGAGCATTCAGCAGGCTCAGGCAGCCCCAGACCAGTTCGTCCTGTACTTTGTGATGGATCTCCT
GAAGGGCCTGCCAGGCCTGCCAGGGCTCTTCATTGCCTGCCTCTTCAGCGGCTCTCTCAGCACTATATCCTCTGC
TTTTAATTCATTGGCAACTGTTACGATGGAAGACCTGATTCGACCTTGGTTCCCTGAGTTCTCTGAAGCCCGGGC
CATCATGCTTTCCAGAGGCCTTGCCTTTGGCTATGGGCTGCTTTGTCTAGGAATGGCCTATATTTCCTCCCAGAT
GGGACCTGTGCTGCAGGCAGCAATCAGCATCTTTGGCATGGTTGGGGGACCGCTGCTGGGACTCTTCTGCCTTGG
AATGTTCTTTCCATGTGCTAACCCTCCTGGTGCTGTTGTGGGCCTGTTGGCTGGGCTCGTCATGGCCTTCTGGAT
TGGCATCGGGAGCATCGTGACCAGCATGGGCTTCAGCATGCCACCCTCTCCCTCTAATGGGTCCAGCTTCTCCCT
GCCCACCAATCTAACCGTTGCCACTGTGACCACACTGATGCCCTTGACTACCTTCTCCAAGCCCACAGGGCTGCA
GCGGTTCTATTCCTTGTCTTACTTATGGTACAGTGCTCACAACTCCACCACAGTGATTGTGGTGGGCCTGATTGT
CAGTCTACTCACTGGGAGAATGCGAGGCCGGTCCCTGAACCCTGCAACCATTTACCCAGTGTTGCCAAAGCTCCT
GTCCCTCCTTCCGTTGTCCTGTCAGAAGCGGCTCCACTGCAGGAGCTACGGCCAGGACCACCTCGACACTGGCCT
GTTTCCTGAGAAGCCGAGGAATGGTGTGCTGGGGGACAGCAGAGACAAGGAGGCCATGGCCCTGGATGGCACAGC
CTATCAGGGGAGCAGCTCCACCTGCATCCTCCAGGAGACCTCCCTG**TGA**TGTTGACTCAGGACCCCGCCTCTGTC
CTCACTGTGCCAGGCCATAGCCAGAGGCCACCCTGTAGTACAGGGATGAGTCTTGGTGTGTTCTGCAGGGACAGG
CCTGGATGATCTAGCTCATACCAAAGGACCTTGTTCTGAGAGGTTCTTGCCTGCAGGAGAAGCTGTCACATCTCA
AGCATGTGAGGCACCGTTTTTCTCGTCGCTTGCCAATCTGTTTTTAAAGGATCAGGCTCGTAGGGAGCAGGATC
ATGCCAGAAATAGGGATGGAAGTGCATCCTCTGGGAAAAAGATAATGGCTTCTGATTCAACATAGCCATAGTCCT
TTGAAGTAAGTGGCTAGAAACAGCACTCTGGTTATAATTGCCCCAGGGCCTGATTCAGGACTGACTCTCCACCAT
AAAACTGGAAGCTGCTTCCCCTGTAGTCCCCATTTCAGTACCAGTTCTGCCAGCCACAGTGAGCCCCTATTATTA
CTTTCAGATTGTCTGTGACACTCAAGCCCCTCTCATTTTTATCTGTCTACCTCCATTCTGAAGAGGGAGGTTTTG
GTGTCCCTGGTCCTCTGGGAATAGAAGATCCATTTGTCTTTGTGTAGAGCAAGCACGTTTTCCACCTCACTGTCT
CCATCCTCCACCTCTGAGATGGACACTTAAGAGACGGGGCAAATGTGGATCCAAGAAACCAGGGCCATGACCAGG
TCCACTGTGGAGCAGCCATCTATCTACCTGACTCCTGAGCCAGGCTGCCGTGGTGTCATTTCTGTCATCCGTGCT
CTGTTTCCTTTTGGAGTTTCTTCTCCACATTATCTTTGTTCCTGGGGAATAAAAACTACCATTGGACCTAAAAAA
AAAAAAAAAAA

FIGURE 699

MSVGVSTSAPLSPTSGTSVGMSTFSIMDYVVFVLLLVLSLAIGLYHACRGWGRHTVGELLMADRKMGCLPVALSL
LATFQSAVAILGVPSEIYRFGTQYWFLGCCYFLGLLIPAHIFIPVFYRLHLTSAYEYLELRFNKTVRVCGTVTFI
FQMVIYMGVVLYAPSLALNAVTGFDLWLSVLALGIVCTVYTALGGLKAVIWTDVFQTLVMFLGQLAVIIVGSAKV
GGLGRVWAVASQHGRISGFELDPDPFVRHTFWTLAFGGVFMMLSLYGVNQAQVQRYLSSRTEKAAVLSCYAVFPF
QQVSLCVGCLIGLVMFAYYQEYPMSIQQAQAAPDQFVLYFVMDLLKGLPGLPGLFIACLFSGSLSTISSAFNSLA
TVTMEDLIRPWFPEFSEARAIMLSRGLAFGYGLLCLGMAYISSQMGPVLQAAISIFGMVGGPLLGLFCLGMFFPC
ANPPGAVVGLLAGLVMAFWIGIGSIVTSMGFSMPPSPSNGSSFSLPTNLTVATVTTLMPLTTFSKPTGLQRFYSL
SYLWYSAHNSTTVIVVGLIVSLLTGRMRGRSLNPATIYPVLPKLLSLLPLSCQKRLHCRSYGQDHLDTGLFPEKP
RNGVLGDSRDKEAMALDGTAYQGSSSTCILQETSL

FIGURE 700

GCCTGCGCGGAGGGAGCCGCGAGACAGGTGCGCATGCGCAGTGCGCGTCTGCGAGACCGACTTGGACGGAGCCGA
GCTGAGGCTCGGCTTCCTGCTGATGGTCAGGGTTTTGGCAACTCCCCGGTGTGAGAGGGGTAGGGAGTGCTCCCG
GCGGCGACGGGGCCGAGTTCACCAGCCGCCGGGGCAGTAGTCGAAGGCCCGGCGCGGCATGTCCTGGGTGCCGCG
GTGCGGGCAGTGAACGCGCGCCGGGCGGGATGGGCCGGCGCCGGGCGCCAGAGCTGTACCGGGCTCCGTTCCCGT
TGTACGCGCTTCAGGTCGACCCCAGCACTGGGCTGCTCATCGCTGCGGGCGGAGGAGGCGCCGCCAAGACAGGCA
TAAAGAATGGCGTGCACTTTCTGCAGCTAGAGCTGATTAATGGGCGCTTGAGTGCCTCCTTGCTGCACTCCCATG
ACACAGAGACACGGGCCACCATGAACTTGGCACTGGCTGGTGACATCCTTGCTGCAGGGCAGGATGCCCACTGTC
AGCTCCTGCGCTTCCAGGCACATCAACAGCAGGGCAACAAGGCAGAGAAGGCCGGTTCCAAGGAGCAGGGGCCTC
GACAAAGGAAGGGAGCAGCCCCAGCAGAGAAGAAATGTGGAGCGGAAACCCAGCACGAGGGGCTAGAACTCAGGG
TAGAGAATTTGCAGGCGGTGCAGACAGACTTTAGCTCCGATCCACTGCAGAAAGTTGTGTGCTTCAACCACGATA
ATACCCTGCTTGCCACTGGAGGAACAGATGGCTACGTCCGTGTCTGGAAGGTGCCCAGCCTGGAGAAGGTTCTGG
AGTTCAAAGCCCACGAAGGGGAGATTGAAGACCTGGCTTTAGGGCCTGATGGCAAGTTGGTAACCGTGGGCCGGG
ACCTTAAGGCCTCTGTGTGGCAGAAGGATCAGCTGGTGACACAGCTGCACTGGCAAGAAAATGGACCCACCTTTT
CCAGCACACCTTACCGCTACCAGGCCTGCAGGTTTGGGCAGGTTCCAGACCAGCCTGCTGGCCTGCGACTCTTCA
CAGTGCAAATTCCCCACAAGCGCCTGCGCCAGCCCCCTCCCTGCTACCTCACAGCCTGGGATGGCTCCAACTTCT
TGCCCCTTCGGACCAAGTCCTGTGGCCATGAAGTCGTCTCCTGCCTCGATGTCAGTGAATCCGGCACCTTCCTAG
GCCTGGGCACAGTCACTGGCTCTGTTGCCATCTACATAGCTTTCTCTCTCCAGTGCCTCTACTACGTGAGGGAGG
CCCATGGCATTGTGGTGACGGATGTGGCCTTTCTACCTGAGAAGGGTCGTGGTCCAGAGCTCCTTGGGTCCCATG
AAACTGCCCTGTTCTCTGTGGCTGTGGACAGTCGTTGCCAGCTGCATCTGTTGCCCTCACGGCGGAGTGTTCCTG
TGTGGCTCCTGCTCCTGCTGTGTGTCGGGCTTATTATTGTGACCATCCTGCTGCTCCAGAGTGCCTTTCCAGGTT
TCCTTTAGCTTCCCTGCTTCCTGGGAATCAGGAGCCTGGACACTGCCATCTCTAGAGCAGAGTGGAGGCCTGGAC
TCCCTTTGCTCACTCCATTCGGGTCCACAGCTGAGGTTGCCGCTGACAAGATGAATGGGCACTGCCTGCCCTTCT
AGTGAAAAGGCTTGGCTATGGCCCTGTGTGACTCCAGGTCCCAGGAACCTTGCCTTCGTCATCTGTGGATCCATC
CAGAACAGCGGTATCTGAAGCCCAGGCCATACTCCCTGCCTCCTTTCTTCTGCCTACCAGAGGCTCCAGAGTTGA
GCTTGTCCTTATCTAGAAACATGTGAAGATGCCCAAGAGCCTGGAGGCACTGCTGTCCTTCCTGCAGAAACAGTT
TCTCCTCCTCCCCTCAGCCTTGTGGCCAGTTCCTCTTCACATGAAGCCCCTGGCATTTGCTGGGGAAGGGACTGG
CCTGGTACTTGCTGTTAGGGCAGGAAGGGGCAAAAGGAAGACTTGGGTAGTAATCTGGGGGTTCAGATGGGTAGC
ACTAAGCCAGCTGGCCTAAAGATGCAATAAGTTCCTAGGTAGTCTACCCTTACCTTGAGGAATGGAAAATGAAC
CTCAGCCCATTAGGCAGGAAAAGTTGATATTTAATAAACAAGGAAAGAGTGAACTGAGACCCC

FIGURE 701

GTAGCCTC**ATG**GAAGAGAAGCAGATCCTGTGCGTGGGGCTAGTGGTGCTGGACGTCATCAGCCTGGTGGACAAGT
ACCCTAAGGAGGACTCGGAGATAAGGTGTTTGTCCCAGAGATGGCAGCGCGGAGGCAACGCGTCCAACTCCTGCA
CCGTTCTCTCCCTGCTCGGAGCCCCCTGTGCCTTCATGGGCTCAATGGCTCCTGGCCATGTTGCTGATTTTGTCC
TGGATGACCTCCGCCGCTATTCTGTGGACCTACGCTACACAGTCTTTCAGACCACAGGCTCCGTCCCCATCGCCA
CGGTCATCATCAACGAGGCCAGTGGTAGCCGCACCATCCTATACTATGACAGGAGCCTGCCAGATGTGTCTGCTA
CAGACTTTGAGAAGGTTGATCTGACCCAGTTCAAGTGGATCCACATTGAGGGCCGGAACGCATCGGAGCAGGTGA
AGATGCTGCAGCGGATAGACGCACACAACACCAGGCAGCCTCCAGAGCAGAAGATCCGGGTGTCCGTGGAGGTGG
AGAAGCCACGAGAGGAGCTCTTCCAGCTGTTTGGCTACGGAGACGTGGTGTTTGTCAGCAAAGATGTGGCCAAGC
ACTTGGGGTTCCAGTCAGCAGAGGAAGCCTTGAGGGGCTTGTATGGTCGTGTGAGGAAAGGGGCTGTGCTTGTCT
GTGCCTGGGCTGAGGAGGGCGCCGACGCCCTGGGCCCTGATGGCAAATTGCTCCACTCGGATGCTTTCCCGCCAC
CCCGCGTGGTGGATACACTGGGAGCTGGAGACACCTTCAATGCCTCCGTCATCTTCAGCCTCTCCCAGGGGAGGA
GCGTGCAGGAAGCACTGAGATTCGGGTGCCAGGTGGCCGGCAAGAAGTGTGGCCTGCAGGGCTTTGATGGCATCG
TG**TGA**GAGCAGGTGCCGGCTCCTCACACACCATGGAGACTACCATTGCGGCTGCATCGCCTTCTCCCCTCCATCC
AGCCTGGCGTCCAGGTTGCCCTGTTCAGGGGACAGATGCAAGCTGTGGGGAGGACTCTGCCTGTGTCCTGTGTTC
CCCACAGGGAGAGGCTCTGGGGGGATGGCTGGGGGATGCAGAGCCTCAGAGCAAATAAATCTTCCTCAGAGCCAG
CTTCTCCTCTCAATGTCTGAACTGCTCTGGCTGGGCATTCCTGAGGCTCTGACTCTTCGATCCTCCCTCTTTGTG
TCCATTCCCCAAATTAACCTCTCCGCCCAGGCCCAGAGGAGGGGCTGCCTGGGCTAGAGCAGCGAGAAGTGCCCT
GGGCTTGCCACCAGCTCTGCCCTGGCTGGGGAGGACACTCGGTGCCCCACACCCAGTGAACCTGCCAAAGAAACC
GTGAGAGCTCTTCGGGGCCCTGCGTTGTGCAGACTCTATTCCCACAGCTCAGAAGCTGGGAGTCCACACCGCTGA
GCTGAACTGACAGGCCAGTGGGGGGCAGGGGTGCGCCTCCTCTGCCCTGCCCACCAGCCTGTGATTTGATGGGGT
CTTCATTGTCCAGAAATACCTCCTCCCGCTGACTGCCCCAGAGCCTGAAAGTCTCACCCTTGGAGCCCACCTTGG
AATTAAGGGCGTGCCTCAGCCACAAATGTGACCCAGGATACAGAGTGTTGCTGTCCTCAGGGAGGTCCGATCTGG
AACACATATTGGAATTGGGGCCAACTCCAATATAGGGTGGGTAAGGCCTTATAATGTAAAGAGCATATAATGTAA
AGGGCTTTAGAGTGAGACAGACCTGGATTCAAATCTGCCATTTAATTAGCTGCATATCACCTTAGGGTACAGCAC
TTAACGCAATCTGCCTCAATTTCTTCATCTGTCAAATGGAACCAATTCTGCTTGGCTACAGAATTATTGTGAGGA
TAAAAATCATATATAAAAAAAAAA

FIGURE 702

MEEKQILCVGLVVLDVISLVDKYPKEDSEIRCLSQRWQRGGNASNSCTVLSLLGAPCAFMGSMAPGHVADFVLDD
LRRYSVDLRYTVFQTTGSVPIATVIINEASGSRTILYYDRSLPDVSATDFEKVDLTQFKWIHIEGRNASEQVKML
QRIDAHNTRQPPEQKIRVSVEVEKPREELFQLFGYGDVVFVSKDVAKHLGFQSAEEALRGLYGRVRKGAVLVCAW
AEEGADALGPDGKLLHSDAFPPPRVVDTLGAGDTFNASVIFSLSQGRSVQEALRFGCQVAGKKCGLQGFDGIV

FIGURE 703

GTAGCCTC**ATG**GAAGAGAAGCAGATCCTGTGCGTGGGGCTAGTGGTGCTGGACGTCATCAGCCTGGTGGACAAGT
ACCCTAAGGAGGACTCGGAGATAAGGTGTTTGTCCCAGAGATGGCAGCGCGGAGGCAACGCGTCCAACTCCTGCA
CCGTTCTCTCCCTGCTCGGAGCCCCCTGTGCCTTCATGGGCTCAATGGCTCCTGGCCATGTTGCTGACTTCCTGG
TGGCCGACTTCAGGCGGCGGGGCGTGGACGTGTCTCAGGTGGCCTGGCAGAGCAAGGGGGACACCCCCAGCTCCT
GCTGCATCATCAACAACTCCAATGGCAACCGTACCATTGTGCTCCATGACACGAGCCTGCCAGATGTGTCTGCTA
CAGACTTTGAGAAGGTTGATCTGACCCAGTTCAAGTGGATCCACATTGAGGGCCGGAACGCATCGGAGCAGGTGA
AGATGCTGCAGCGGATAGACGCACACAACACCAGGCAGCCTCCAGAGCAGAAGATCCGGGTGTCCGTGGAGGTGG
AGAAGCCACGAGAGGAGCTCTTCCAGCTGTTTGGCTACGGAGACGTGGTGTTTGTCAGCAAAGATGTGGCCAAGC
ACTTGGGGTTCCAGTCAGCAGAGGAAGCCTTGAGGGGCTTGTATGGTCGTGTGAGGAAAGGGGCTGTGCTTGTCT
GTGCCTGGGCTGAGGAGGGCGCCGACGCCCTGGGCCCTGATGGCAAATTGCTCCACTCGGATGCTTTCCCGCCAC
CCCGCGTGGTGGATACACTGGGAGCTGGAGACACCTTCAATGCCTCCGTCATCTTCAGCCTCTCCCAGGGGAGGA
GCGTGCAGGAAGCACTGAGATTCGGGTGCCAGGTGGCCGGCAAGAAGTGTGGCCTGCAGGGCTTTGATGGCATCG
TG**TGA**GAGCAGGTGCCGGCTCCTCACACACCATGGAGACTACCATTGCGGCTGCATCGCCTTCTCCCCTCCATCC
AGCCTGGCGTCCAGGTTGCCCTGTTCAGGGGACAGATGCAAGCTGTGGGGAGGACTCTGCCTGTGTCCTGTGTTC
CCCACAGGGAGAGGCTCTGGGGGGATGGCTGGGGGATGCAGAGCCTCAGAGCAAATAAATCTTCCTCAGAGCCAG
CTTCTCCTCTCAATGTCTGAACTGCTCTGGCTGGGCATTCCTGAGGCTCTGACTCTTCGATCCTCCCTCTTTGTG
TCCATTCCCCAAATTAACCTCTCCGCCCAGGCCCAGAGGAGGGGCTGCCTGGGCTAGAGCAGCGAGAAGTGCCCT
GGGCTTGCCACCAGCTCTGCCCTGGCTGGGGAGGACACTCGGTGCCCCACACCCAGTGAACCTGCCAAAGAAACC
GTGAGAGCTCTTCGGGGCCCTGCGTTGTGCAGACTCTATTCCCACAGCTCAGAAGCTGGGAGTCCACACCGCTGA
GCTGAACTGACAGGCCAGTGGGGGGCAGGGGTGCGCCTCCTCTGCCCTGCCCACCAGCCTGTGATTTGATGGGGT
CTTCATTGTCCAGAAATACCTCCTCCCGCTGACTGCCCCAGAGCCTGAAAGTCTCACCCTTGGAGCCCACCTTGG
AATTAAGGGCGTGCCTCAGCCACAAATGTGACCCAGGATACAGAGTGTTGCTGTCCTCAGGGAGGTCCGATCTGG
AACACATATTGGAATTGGGGCCAACTCCAATATAGGGTGGGTAAGGCCTTATAATGTAAAGAGCATATAATGTAA
AGGGCTTTAGAGTGAGACAGACCTGGATTCAAATCTGCCATTTAATTAGCTGCATATCACCTTAGGGTACAGCAC
TTAACGCAATCTGCCTCAATTTCTTCATCTGTCAAATGGAACCAATTCTGCTTGGCTACAGAATTATTGTGAGGA
TAAAAATCATATATAAAAAAAAAA

FIGURE 704

MEEKQILCVGLVVLDVISLVDKYPKEDSEIRCLSQRWQRGGNASNSCTVLSLLGAPCAFMGSMAPGHVADFLVAD
FRRRGVDVSQVAWQSKGDTPSSCCIINNSNGNRTIVLHDTSLPDVSATDFEKVDLTQFKWIHIEGRNASEQVKML
QRIDAHNTRQPPEQKIRVSVEVEKPREELFQLFGYGDVVFVSKDVAKHLGFQSAEEALRGLYGRVRKGAVLVCAW
AEEGADALGPDGKLLHSDAFPPPRVVDTLGAGDTFNASVIFSLSQGRSVQEALRFGCQVAGKKCGLQGFDGIV

FIGURE 705

ATGGCCCCCCGCACCCTCTGGAGCTGCTACCTCTGCTGCCTGCTGACGGCAGCTGCAGGGGCCGCCAGCTACCCT
CCTCGAGGTTTCAGCCTCTACACAGGTTCCAGTGGGCCCTCAGCCCCGGGGGGCCCCAGGCCCAGATTGCCCCC
CGGCCAGCCAGCCGCCACAGGAACTGGTGTGCCTACGTGGTGACCCGGACAGTGAGCTGTGTCCTTGAGGATGGA
GTGGAGACATATGTCAAGTACCAGCCTTGTGCCTGGGGCCAGCCCCAGTGTCCCCAAAGCATCATGTACCGCCGC
TTCCTCCGCCCTCGCTACCGTGTGGCCTACAAGACAGTGACCGACATGGAGTGGAGGTGCTGTCAGGGTTATGGG
GGCGATGACTGTGCTGAGAGTCCCGCTCCAGCGCTGGGGCCTGCGTCTTCCACACCACGGCCCCTGGCCCGGCCT
GCCCGCCCCAACCTCTCTGGCTCCAGTGCAGGCAGCCCCCTCAGTGGACTGGGGGGAGAAGGTCCTGGGGAGTCA
GAGAAGGTGCAGCAGCTGGAGGAACAGGTGCAGAGCCTGACCAAGGAGCTGCAAGGCCTGCGGGGCGTCCTGCAA
GGACTGAGCGGGCGCCTGGCAGAGGATGTGCAGAGGGCTGTGGAGACGGCCTTCAACGGGAGGCAGCAGCCAGCT
GACGCGGCTGCCCGCCCTGGGGTGCATGAAACCCTCAATGAGATCCAGCACCAGCTGCAGCTCCTGGACACCCGC
GTCTCCACCCACGACCAGGAGCTGGGTCACCTCAACAACCATCATGGCGGCAGCAGCAGCAGTGGGGGCAGCAGG
GCCCCAGCCCCAGCCTCAGCCCCTCCGGGCCCCAGTGAGGAGCTGCTGCGGCAGCTGGAGCAGCGGTTGCAGGAG
TCCTGCTCCGTGTGCCTGGCCGGGCTAGATGGCTTCCGCCGGCAGCAGCAGGAGGACAGGGAGCGGCTGCGAGCG
ATGGAGAAGCTGCTGGCCTCGGTGGAGGAGCGGCAACGGCACCTCGCAGGGCTGGCGGTGGGCCGCAGGCCCCCT
CAGGAATGCTGCTCTCCAGAGCTGGGCCGGCGACTGGCAGAGCTGGAGCGCAGGCTGGATGTCGTGGCCGGCTCA
GTGACAGTGCTGAGTGGGCGGCGAGGCACAGAGCTGGGAGGAGCCGCGGGGCAGGGAGGCCACCCCCCAGGCTAC
ACCAGCTTGGCCTCCCGCCTGTCTCGCCTGGAGGACCGCTTCAACTCCACCCTGGGCCCTTCGGAGGAGCAGGAG
GAGAGCTGGCCTGGGGCTCCTGGGGGGCTGAGCCACTGGCTGCCTGCTGCCCGGGGCCGACTAGAGCAGTTGGGG
GGGCTGCTGGCCAATGTGAGCGGGGAGCTGGGGGGGCGGTTGGATCTGTTGGAGGAGCAGGTGGCAGGGGCCATG
CAGGCATGCGGGCAGCTCTGCTCTGGGGCCCCTGGGGAGCAGGACTCTCAAGTCAGCGAGATCCTCAGTGCCTTG
GAGCGCAGGGTGCTGGACAGTGAGGGGCAGCTGCGGCTGGTGGGCTCCGGCCTGCACACGGTGGAAGCAGCGGGG
GAGGCCCGGCAGGCCACGCTGGAGGGATTACAAGAGGTTGTGGGCCGGCTCCAGGATCGTGTGGATGCCCAGGAT
GAGACAGCTGCAGAGTTCACACTACGGCTGAATCTCACTGCGGCCCGGCTAGGCCAACTGGAGGGGCTGCTGCAG
GCCCATGGGGATGAGGGCTGTGGGGCCTGTGGCGGAGTCCAAGAGGAACTAGGCCGCCTTCGGGATGGTGTGGAG
CGCTGCTCCTGCCCCCTGTTGCCTCCTCGGGGTCCTGGGGCTGGTCCAGGTGTTGGGGGCCCAAGCCGTGGGCCC
CTGGACGGCTTCAGCGTGTTTGGGGGCAGCTCAGGCTCAGCCCTGCAGGCCCTGCAAGGAGAGCTCTCTGAGGTT
ATTCTCAGCTTCAGCTCCCTCAATGACTCACTGAATGAGCTCCAGACCACTGTGGAGGGCCAGGGCGCTGATCTG
GCTGACCTGGGGGCAACCAAGGACCGTATCATTTCTGAGATTAACAGGCTGCAGCAGGAGGCCACAGAGCATGCT
ACAGAGAGTGAAGAGCGCTTCCGAGGCCTAGAGGAGGGACAAGCACAGGCCGGCCAGTGCCCCAGCTTAGAGGGG
CGATTGGGCCGTCTTGAGGGTGTCTGTGAACGGTTGGACACTGTGGCTGGGGGACTGCAGGGCCTGCGCGAGGGC
CTTTCCAGACACGTGGCTGGGCTCTGGGCTGGGCTCCGGGAAACCAACACCACCAGCCAGATGCAGGCAGCCCTG
CTGGAGAAGCTGGTCGGGGGACAGGCGGGCCTGGGCAGGCGGCTGGGTGCCCTTAACAGCTCCCTGCAGCTCCTG
GAGGACCGTCTGCACCAGCTCAGCCTGAAGGACCTCACTGGGCCTGCAGGAGAGGCTGGGCCCCCAGGGCCTCCT
GGGCTGCAGGGACCCCCAGGCCCTGCTGGACCTCCAGGATCACCAGGCAAGGACGGGCAAGAGGGCCCCATCGGG
CCACCAGGTCCTCAAGGGGAACAGGGAGTGGAGGGGGCACCAGCAGCCCCTGTGCCCCAAGTGGCATTTTCAGCT
GCTCTGAGTTTGCCCCGGTCTGAACCAGGCACGGTCCCCTTCGACAGAGTCCTGCTCAATGATGGAGGCTATTAT
GATCCAGAGACAGGCGTGTTCACAGCGCCACTGGCTGGACGCTACTTGCTGAGCGCGGTGCTGACTGGGCACCGG
CACGAGAAAGTGGAGGCCGTGCTGTCCCGCTCCAACCAGGGCGTGGCCCGCGTAGACTCCGGTGGCTACGAGCCT
GAGGGCCTGGAGAATAAGCCGGTGGCCGAGAGCCAGCCCAGCCCGGGCACCCTGGGCGTCTTCAGCCTCATCCTG
CCGCTGCAGGCCGGGGACACGGTCTGCGTCGACCTGGTCATGGGGCAGCTGGCGCACTCGGAGGAGCCGCTCACC
ATCTTCAGCGGGGCCCTGCTCTATGGGGACCCAGAGCTTGAACACGCG<u>TAG</u>ACTGGGGTCCCGCCCGACGTGTCT
ACGTCGGCTGAAGAGACAGCGGGGGCGGCGGGCTCCTGGGGTCTCGCCTGAGACGGGGCACCTAGCCCTGGGCGA
GCGCCGCACCCGGGCCCGCAGCGGCACCGCGCCCAGAGCGGCCTCTCCCCACGCCCGGGGCGCGCCGGCTCAGGG
AGGCTCGGGGCCGCCCATGCAGACTTTTGGCCTGGCGCGATCCCCCAAGAACCCCTCCAGGGCCGGCCTGCGGAG
GAGCCGATCCTCGCACCCTCCGCTCCCTCCACTGGCCCTCCAGGTCGATTCCCTGGGCTCCAGGCTCCCCCGCGC
GGGCGCCGCCCACCGCCATACTAAACGATCGAGGAATAAAGACACTTGGTTTTTCT

FIGURE 706

MAPRTLWSCYLCCLLTAAAGAASYPPRGFSLYTGSSGALSPGGPQAQIAPRPASRHRNWCAYVVTRTVSCVLEDG
VETYVKYQPCAWGQPQCPQSIMYRRFLRPRYRVAYKTVTDMEWRCCQGYGGDDCAESPAPALGPASSTPRPLARP
ARPNLSGSSAGSPLSGLGGEGPGESEKVQQLEEQVQSLTKELQGLRGVLQGLSGRLAEDVQRAVETAFNGRQQPA
DAAARPGVHETLNEIQHQLQLLDTRVSTHDQELGHLNNHHGGSSSSGGSRAPAPASAPPGPSEELLRQLEQRLQE
SCSVCLAGLDGFRRQQQEDRERLRAMEKLLASVEERQRHLAGLAVGRRPPQECCSPELGRRLAELERRLDVVAGS
VTVLSGRRGTELGGAAGQGGHPPGYTSLASRLSRLEDRFNSTLGPSEEQEESWPGAPGGLSHWLPAARGRLEQLG
GLLANVSGELGGRLDLLEEQVAGAMQACGQLCSGAPGEQDSQVSEILSALERRVLDSEGQLRLVGSGLHTVEAAG
EARQATLEGLQEVVGRLQDRVDAQDETAAEFTLRLNLTAARLGQLEGLLQAHGDEGCGACGGVQEELGRLRDGVE
RCSCPLLPPRGPGAGPGVGGPSRGPLDGFSVFGGSSGSALQALQGELSEVILSFSSLNDSLNELQTTVEGQGADL
ADLGATKDRIISEINRLQQEATEHATESEERFRGLEEGQAQAGQCPSLEGRLGRLEGVCERLDTVAGGLQGLREG
LSRHVAGLWAGLRETNTTSQMQAALLEKLVGGQAGLGRRLGALNSSLQLLEDRLHQLSLKDLTGPAGEAGPPGPP
GLQGPPGPAGPPGSPGKDGQEGPIGPPGPQGEQGVEGAPAAPVPQVAFSAALSLPRSEPGTVPFDRVLLNDGGYY
DPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNQGVARVDSGGYEPEGLENKPVAESQPSPGTLGVFSLIL
PLQAGDTVCVDLVMGQLAHSEEPLTIFSGALLYGDPELEHA

FIGURE 707

GGCACGAGGGGCACCGCGGCGCTCGGGTGTTTTTGGGGGCCCGGGTGGAGGGCCCGGGTGCCGGGGCCCAAGGTG
CGGCCTCGCTAGCGGGAGAGGGAGCGGGATCACCGGCCCGGAGAGAGCTCTCAGGGCCAGAGCGGGGCAGGAGGA
TGCTTTCCCAGCCCCACCATGGAGCTGCGCTGTGGGGGATTGCTGTTCAGTTCTCGCTTTGATTCAGGGAATCTA
GCCCACGTGGAGAAGGTGGAATCTTTGTCCAGTGATGGGGAAGGGGTAGGAGGTGGGGCGTCAGCCCTGACCAGT
GGCATTGCCTCTTCCCCTGACTATGAATTCAACGTGTGGACCCGACCAGACTGTGCTGAAACGGAATTTGAGAAT
GGGAACAGGTCATGGTTCTACTTCAGCGTCCGGGGAGGAATGCCAGGAAAACTCATCAAGATCAACATT<u>ATG</u>AAC
ATGAACAAGCAGAGCAAGCTGTATTCCCAGGGCATGGCCCCCTTTGTGCGCACACTGCCCACCCGGCCACGCTGG
GAACGCATTCGAGACCGGCCCACCTTTGAGATGACAGAGACGCAGTTTGTGTTATCCTTTGTTCATCGTTTCGTG
GAGGGCCGTGGGGCCACCACCTTCTTCGCCTTCTGCTACCCCTTCTCCTACAGTGACTGCCAGGAACTGCTAAAC
CAGCTAGACCAGCGCTTTCCGGAGAACCACCCTACCCATAGCAGCCCCCTGGATACCATCTATTACCATCGGGAG
CTCCTTTGCTATTCTCTGGATGGACTTCGTGTAGATCTGCTGACGATCACTTCCTGCCATGGGCTTCGAGAAGAT
CGAGAGCCCCGTCTAGAGCAGCTATTTCCTGATACCAGCACCCCTCGACCATTCCGTTTCGCAGGCAAGAGGATA
TTCTTCTTAAGCAGTAGAGTACACCCAGGGGAGACTCCATCTAGCTTTGTCTTCAATGGCTTTCTGGACTTCATC
CTCCGACCTGATGATCCCCGGGCCCAAACCCTCCGTCGCCTCTTCGTCTTTAAGCTGATTCCCATGTTGAACCCC
GATGGTGTGGTCCGGGGACACTACCGCACAGACTCACGTGGAGTGAATCTGAACCGTCAGTACCTGAAGCCTGAT
GCCGTCCTGCACCCGGCCATCTATGGGGCCAAAGCTGTGCTTCTCTACCACCATGTGCACTCTCGTCTGAACTCC
CAGAGTTCCTCTGAGCACCAGCCCAGTTCCTGTCTCCCTCCTGATGCTCCTGTTTCTGACCTGGAGAAAGCCAAC
AATCTCCAAAATGAAGCTCAGTGTGGGCACTCAGCTGACAGGCATAACGCTGAAGCCTGGAAACAAACAGAGCCA
GCAGAACAGAAGCTCAACAGTGTGTGGATTATGCCACAACAGTCTGCGGGGCTTGAAGAGTCAGCCCCTGATACC
ATCCCCCCCAAAGAGAGTGGCGTTGCTTACTATGTGGACCTGCATGGACATGCTTCCAAAAGGGGCTGCTTCATG
TACGGAAACAGCTTTAGTGATGAGAGCACCCAGGTGGAAAACATGCTATATCCAAAGCTCATCTCCTTGAATTCA
GCCCACTTCGACTTCCAGGGCTGCAATTTCTCAGAGAAGAATATGTATGCCCGAGACCGTAGAGATGGCCAGTCT
AAAGAGGGAAGCGGCCGTGTTGCAATCTACAAAGCCTCAGGGATAATCCACAGCTACACACTTGAATGCAACTAC
AACACTGGACGCTCAGTAAACAGCATCCCTGCTGCCTGCCATGACAATGGGCGTGCCAGCCCCCCTCCCCCGCCG
GCTTTCCCCTCCAGATACACTGTGGAACTATTTGAGCAGGTGGGACGAGCTATGGCCATTGCAGCCCTGGACATG
GCGGAATGTAATCCGTGGCCCCGAATTGTACTGTCAGAGCACAGCAGCCTTACTAATCTACGGGCCTGGATGCTG
AAACATGTACGCAACAGCCGAGGCCTAAGCAGCACTCTGAATGTGGGTGTCAACAAGAAGAGGGGCCTTCGAACT
CCACCCAAAAGTCACAATGGGTTGCCTGTCTCCTGCTCCGAAAACACCTTGAGTCGGGCACGAAGTTTTAGCACC
GGCACAAGTGCCGGTGGTAGCAGCAGCAGCCAACAAAATTCTCCACAGATGAAGAATTCCCCCAGCTTTCCTTTT
CATGGCAGTCGGCCTGCAGGGCTGCCAGGCCTGGGCTCTAGTACCCAAAAGGTCACCCACCGGGTGCTGGGCCCC
GTCAGAGAGCCCCGAAGCCAGGACAGGAGACGGCAGCAGCAGCCCCTGAACCATCGTCCTGCAGGCAGCCTCGCT
CCATCCCCAGCTCCTACTAGTTCTGGCCCAGCCTCCTCACACAAGCTGGGCTCCTGTCTACTGCCTGATTCATTC
AACATACCAGGGAGCAGTTGCTCACTCTTGTCCTCTGGAGACAAACCAGAGGCTGTCATGGTAATCGGGAAAGGT
CTGCTAGGGACTGGAGCTCGGATGCCCTGCATCAAGACTCGATTGCAGACCTGTCCGAGGAGAGTTTCCGCCAGG
AGGGGTCCCGGATTCCCCAGGCTAGGCCCAGGTTGGGCCGGGGCTCACCGCCGACTCGCAGAGGGA<u>TGA</u>AAGGCT
CTTCAGGCCCCACATCCCCTACCCCCCGGACCAGGGAGAGCAGTGAGCTGGAGCTGGGATCCTGCTCTGCTACAC
CAGGGCTGCCTCAGGCCAGGCCCCCACGGCCCCGCTCTGCCCCTGCCTTTTCTCCTATATCCTGTAGTCTATCTG
ACTCCCCATCCTGGAATTGTTACAGCAGGGGTCCCTTGGGCCAACCTGAGGTTTGTTTTGTCCCTAAATCTCCCC
CACTGACTGTTTCTCCCCGGGTCTGATAATGCCTTTATGTTCAATCCCAGGATATAGCCCCAAGATGGGGTAACA
GTGGGAAATATGCTAGTTCCCCTCCAGGCCGCTGATTCCATGTGACAGCCGTTAAGTCCTTGGAATGCCAGCCAC
GCTGTCCAAGGCATTACAGAGTATCACCTTGAGACAGAACAAAACAGGGACCTGCCACCCCTTCCCTCCCTCCGC
AGCACAAGATTTTGGGACCACAAAAAAAAGTCTATATTTTTATATTGGGGGGAGGGAGTAGAAAAGCAAGCCCCT
ATACTGGGCCCTATTCAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTGAGGAAATAAAAGTTGTTTG
GAAAAATCCAAAAAAAAAAAAAAAAAA

FIGURE 708

MNMNKQSKLYSQGMAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGATTFFAFCYPFSYSDCQEL
LNQLDQRFPENHPTHSSPLDTIYYHRELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPFRFAGK
RIFFLSSRVHPGETPSSFVFNGFLDFILRPDDPRAQTLRRLFVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLK
PDAVLHPAIYGAKAVLLYHHVHSRLNSQSSSEHQPSSCLPPDAPVSDLEKANNLQNEAQCGHSADRHNAEAWKQT
EPAEQKLNSVWIMPQQSAGLEESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVENMLYPKLISL
NSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRVAIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPP
PPAFPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNLRAWMLKHVRNSRGLSSTLNVGVNKKRGL
RTPPKSHNGLPVSCSENTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGLPGLGSSTQKVTHRVL
GPVREPRSQDRRRQQQPLNHRPAGSLAPSPAPTSSGPASSHKLGSCLLPDSFNIPGSSCSLLSSGDKPEAVMVIG
KGLLGTGARMPCIKTRLQTCPRRVSARRGPGFPRLGPGWAGAHRRLAEG

FIGURE 709

CCCGCCCCACTCTGGACTCCCGCGCTGGGCGCGCTGAGGCGGCCCCCGAGCGAGCGCGCGTGCAGCCGCCGCCGC
CCCGAGCACCCGCAGCTCCGGCGCCGCGGCGAGACGGAGACGGACCGAGCCACGGGCCCCCGCGGCCGCAGCATC
TCGGAGGAGAAC**ATG**CTTGCCAACTCAGCCAGCGTGAGGATCCTCATCAAGGGAGGCAAGGTGGTGAACGATGAC
TGCACCCACGAGGCTGACGTCTACATCGAGAATGGCATCATCCAGCAGGTGGGCCGCGAGCTCATGATCCCTGGC
GGGGCCAAGGTGATTGATGCCACAGGAAAACTGGTGATCCCTGGTGGCATCGACACCAGCACCCACTTCCACCAG
ACCTTCATGAATGCCACGTGCGTGGACGACTTCTACCATGGGACCAAGGCAGCACTCGTCGGAGGCACCACCATG
ATCATCGGCCACGTCCTGCCCGACAAGGAGACCTCCCTTGTGGACGCTTATGAGAAGTGCCGAGGTCTGGCCGAC
CCCAAGGTCTGCTGTGATTACGCCCTCCACGTGGGGATCACCTGGTGGGCACCCAAGGTGAAAGCAGAAATGGAG
ACACTGGTGAGGGAGAAGGGTGTCAACTCGTTCCAGATGTTCATGACCTACAAGGACCTGTACATGCTTCGAGAC
AGTGAGCTGTACCAAGTGTTGCACGCTTGCAAGGACATTGGGGCAATCGCCCGCGTCCATGCTGAAAATGGGGAG
CTTGTGGCCGAGGGTGCTAAGGAGGCACTGGATTTGGGGATCACAGGCCCAGAAGGAATCGAGATCAGCCGTCCA
GAGGAGCTGGAAGCTGAAGCCACTCATCGTGTTATCACCATTGCAAACAGGACTCACTGTCCAATCTACCTGGTC
AACGTGTCCAGTATCTCGGCTGGTGACGTTATCGCAGCTGCTAAGATGCAAGGGAAGGTTGTGCTGGCGGAGACC
ACCACTGCACATGCCACGCTGACAGGCTTACACTACTACCACCAGGACTGGTCCCACGCGGCTGCCTATGTCACG
GTGCCTCCCCTGAGACTGGACACCAACACCTCAACCTACCTCATGAGCCTGCTGGCCAATGACACTCTGAACATC
GTGGCATCAGATCACCGGCCTTTCACCACAAAGCAGAAAGCTATGGGCAAGGAAGACTTCACCAAGATCCCACAT
GGAGTGAGTGGCGTGCAGGACCGCATGAGCGTCATCTGGGAGAGAGGAGTGGTTGGAGGAAAGATGGATGAGAAC
CGTTTTGTGGCCGTTACCAGTTCCAACGCAGCTAAGCTTCTGAACCTGTATCCCCGCAAGGGCCGCATTATTCCC
GGAGCCGATGCTGATGTGGTGGTGTGGGACCCAGAAGCCACAAAGACCATCTCAGCCAGCACGCAGGTCCAGGGA
GGAGACTTCAACCTGTATGAGAACATGCGCTGCCACGGCGTGCCACTGGTCACCATCAGCCGGGGGCGCGTCGTG
TATGAGAACGGCGTCTTCATGTGCGCCGAGGGCACCGGCAAGTTCTGTCCCCTGAGGTCCTTCCCAGACACTGTC
TACAAGAAGCTGGTCCAGAGAGAGAAGACTTTAAAGGTTAGAGGAGTGGACCGCACTCCCTACCTGGGGGATGTC
GCTGTTGTCGTGCACCCTGGGAAAAAAGAGATGGGAACCCCACTCGCAGACACTCCTACCCGGCCCGTCACCCGG
CATGGGGGCATGAGGGACCTTCACGAATCCAGCTTCAGCCTCTCTGGCTCTCAGATCGATGACCATGTTCCAAAG
CGAGCTTCAGCTCGGATCCTCGCTCCTCCCGGAGGCAGGTCGAGTGGCATTTGG**TAA**AGGCATTGCCAAGCCCCC
CGAGTGAGGACGCACCGCCGCCACCAGCCCGCAACTCTCCAGCCGAAGCTGCAGGGGCAGGAGAGGCTGGGCTGG
GTGGCACACCACCCGAGGGGGGCCCCGGGACCCACGGAGCCCTCCCTATGTCTGCAAAGTGATTCACTGTGCTTC
GAGCCAACTCTAACAGGCACTTTGAGATGTGTTCCTCCTGCTGTAGTCCTTTCTGCCTTGGCCTCGGCGGGCTTT
TCTGGGGCCCAGGAAGCCCACACTATGCACAGAGCCCAATGCATAGAGCCCTGGCCAGCCCTTCCTCTCACTCCT
GCCTCCGCTGGCTTTGGGAAAGCCCAGACTTTAGTGCCCTGCCCCCTGGCTGACTGGCCAGTTGCCCAGAGCACT
TTAGCAGATGTGGTTTCAAAGTAAAGGCCTCCTCCCCCACCCCTTAGGCCCCGTGGTGACATTTCCCAAGTCAGA
CAGATGTCAGCTTCCCAGCCATGCCCAGGACGTCCTATCTCCCCCAACCCACCTCTGGCCCTGTGTAGGGGCAGG
GATGGGGGTGGCTGGGACTCCTGGTGCCCCTCGCCAGCTTCTCCTGCGCCCCGCCCACACCCTCGGGGGGGTCAC
AGGCCCAGAAGGGTAGCTGGGCGGGGCTCGAGGCTGGTGCCAGGCGCGTGTAAATGGTTTTGTTTTGCACGTTTG
GTTTGCGCAGTAGTTTGGTTTGACTTGTTTGTGCATCCTGTGAAAAATAACGGTGCTTGTGTCACTAGCATAGAA
TAGCGACAGGAATAGATGTGGTCCTTAGGAGACGCTGCACTTGACACCAACCAGACAGCACAGGGCAGGGGTGGT
GGAGGGGGCTGGGCTCACAGGCCTCTCTTTTCCCCGCCTGCAGTCTTCTGGGCTGCGGGAGGCCCTGGCCCTTTC
CCCTTCCCCTCCCCTCCTTGTCTAGTTTCCCACATTCCAAAAGGGGGCCTGGGATGCTAGCCCCAGAGATGCCAG
CCCTTCAGGAAGCAGGTGTCCTTTCCCCTCTCTGCCCCTGATCACTCCCAGCACTCCCCTTGCCTTCCCCTGTCT
TCACCTGCCACCACACACACACACACACACACACACACACACACACGCATGGCTTCCTATAACTTCTTCCTGCTG
GACAGAGACTCAGCGCTCCTCCTGTGTGACTGGCAAGAGGCCTCATGCCTGCTGAGAGAGGGTCGACGCGGCCG

FIGURE 710

MLANSASVRILIKGGKVVNDDCTHEADVYIENGIIQQVGRELMIPGGAKVIDATGKLVIPGGIDTSTHFHQTFMN
ATCVDDFYHGTKAALVGGTTMIIGHVLPDKETSLVDAYEKCRGLADPKVCCDYALHVGITWWAPKVKAEMETLVR
EKGVNSFQMFMTYKDLYMLRDSELYQVLHACKDIGAIARVHAENGELVAEGAKEALDLGITGPEGIEISRPEELE
AEATHRVITIANRTHCPIYLVNVSSISAGDVIAAAKMQGKVVLAETTTAHATLTGLHYYHQDWSHAAAYVTVPPL
RLDTNTSTYLMSLLANDTLNIVASDHRPFTTKQKAMGKEDFTKIPHGVSGVQDRMSVIWERGVVGGKMDENRFVA
VTSSNAAKLLNLYPRKGRIIPGADADVVVWDPEATKTISASTQVQGGDFNLYENMRCHGVPLVTISRGRVVYENG
VFMCAEGTGKFCPLRSFPDTVYKKLVQREKTLKVRGVDRTPYLGDVAVVVHPGKKEMGTPLADTPTRPVTRHGGM
RDLHESSFSLSGSQIDDHVPKRASARILAPPGGRSSGIW

FIGURE 711

CTTGCTCCGAGAGGGAGTCCTCGCGGACGTCAGCCAAGATTCCAGAATGACTATCTTGACTTACCCCTTTAAAAA
TCTTCCCACTGCATCAAAATGGGCCCTCAGATTTTCCATAAGACCTCTGAGCTGTTCCTCCCAGCTACGAGCTGC
CCCAGCTGTCCAGACCAAAACGAAGAAGACGTTAGCCAAACCCAATATAAGGAATGTTGTGGTGGTGGATGGTGT
TCGCACTCCATTTTTGCTGTCTGGCACTTCATATAAAGACCTGATGCCACATGATTTGGCTAGAGCAGCGCTTAC
GGGTTTGTTGCATCGGACCAGTGTCCCTAAGGAAGTAGTTGATTATATCATCTTTGGTACAGTTATTCAGGAAGT
GAAAACAAGCAATGTGGCTAGAGAGGCTGCCCTTGGAGCTGGCTTCTCTGACAAGACTCCTGCTCACACTGTCAC
CATGGCTTGTATCTCTGCCAACCAAGCCATGACCACAGGTGTTGGCTTGATTGCTTCTGGCCAGTGTGATGTGAT
CGTGGCAGGTGGTGTTGAGTTGATGTCCGATGTCCCTATTCGTCACTCAAGGAAAATGAGAAAACTGATGCTTGA
TCTCAATAAGGCCAAATCTATGGGCCAGCGACTGTCTTTAATCTCTAAATTCCGATTTAATTTCCTAGCACCTGA
GCTCCCTGCGGTTTCTGAGTTCTCCACCAGTGAGACCATGGGCCACTCTGCAGACCGACTGGCCGCTGCCTTTGC
TGTTTCTCGGCTGGAACAGGATGAATATGCACTGCGCTCTCACAGTCTAGCCAAGAAGGCACAGGATGAAGGACT
CCTTTCTGATGTGGTACCCTTCAAAGTACCAGGAAAAGATACAGTTACCAAAGATAATGGCATCCGTCCTTCCTC
ACTGGAGCAGATGGCCAAACTAAAACCTGCATTCATCAAGCCCTACGGCACAGTGACAGCTGCAAATTCTTCTTT
CTTGACTGATGGTGCATCTGCAATGTTAATCATGGCGGAGGAAAAGGCTCTGGCCATGGGTTATAAGCCGAAGGC
ATATTTGAGGGATTTTATGTATGTGTCTCAGGATCCAAAAGATCAACTATTACTTGGACCAACATATGCTACTCC
AAAAGTTCTAGAAAAGGCAGGATTGACCATGAATGATATTGATGCTTTTGAATTTCATGAAGCTTTCTCGGGTCA
GATTTTGGCAAATTTTAAAGCCATGGATTCTGATTGGTTTGCAGAAAACTACATGGGTAGAAAAACCAAGGTTGG
ATTGCCTCCTTTGGAGAAGTTTAATAACTGGGGTGGATCTCTGTCCCTGGGACACCCATTTGGAGCCACTGGCTG
CAGGTTGGTCATGGCTGCTGCCAACAGATTACGGAAAGAAGGAGGCCAGTATGGCTTAGTGGCTGCGTGTGCAGC
TGGAGGGCAGGGCCATGCTATGATAGTGGAAGCTTATCCAAAATAATAGATCCAGAAGAAGTGACCTGAAGTTTC
TGTGCAACACTCACACTAGGCAATGCCATTTCAATGCATTACTAAATGACATTTGTAGTTCCTAGCTCCTCTTAG
GAAAACAGTTCTTGTGGCCTTCTATTAAATAGTTTGCACTTAAGCCTTGCCAGTGTTCTGAGCTTTTCAATAATC
AGTTTACTGCTCTTTCAGGGATTTCTAAGCCACCAGAATCTCACATGAGATGTGTGGGTGGTTGTTTTTGGTCTC
TGTTGTCACTAAAGACTAAATGAGGGTTTGCAGTTGGGAAAGAGGTCAACTGAGATTTGGAAATCATCTTTGTAA
TATTTGCAAATTATACTTGTTCTTATCTGTGTCCTAAAGATGTGTTCTCTATAAAATACAAACCAACGTGCCTAA
TTAATTATGGAAAAATAATTCAGAATCTAAACACCACTGAAAACTTATAAAAAATGTTTAGATACATAAATATGG
TGGTCAGCGTTAATAAAGTGGAGAAATATTGGAAAAAAAAA

FIGURE 712

MTILTYPFKNLPTASKWALRFSIRPLSCSSQLRAAPAVQTKTKKTLAKPNIRNVVVVDGVRTPFLLSGTSYKDLM
PHDLARAALTGLLHRTSVPKEVVDYIIFGTVIQEVKTSNVAREAALGAGFSDKTPAHTVTMACISANQAMTTGVG
LIASGQCDVIVAGGVELMSDVPIRHSRKMRKLMLDLNKAKSMGQRLSLISKFRFNFLAPELPAVSEFSTSETMGH
SADRLAAAFAVSRLEQDEYALRSHSLAKKAQDEGLLSDVVPFKVPGKDTVTKDNGIRPSSLEQMAKLKPAFIKPY
GTVTAANSSFLTDGASAMLIMAEEKALAMGYKPKAYLRDFMYVSQDPKDQLLLGPTYATPKVLEKAGLTMNDIDA
FEFHEAFSGQILANFKAMDSDWFAENYMGRKTKVGLPPLEKFNNWGGSLSLGHPFGATGCRLVMAAANRLRKEGG
QYGLVAACAAGGQGHAMIVEAYPK

FIGURE 713

GGCACGAGGCCACTGCTGTCCTCTTCAGCTCAAG**ATG**GTGGCCTGCCGGGCGATTGGCATCCTCAGCCGCTTTTC
TGCCTTCAGGATCCTCCGCTCCCGAGGTTATATATGCCGCAATTTTACAGGGTCTTCTGCTTTGCTGACCAGAAC
CCATATTAACTATGGAGTCAAAGGGGATGTGGCAGTTGTTCGAATTAACTCTCCCAATTCAAAGGTAAATACACT
GAGTAAAGAGCTACATTCAGAGTTCTCAGAAGTTATGAATGAAATCTGGGCTAGTGATCAAATCAGAAGTGCCGT
CCTTATCTCATCAAAGCCAGGCTGCTTTATTGCAGGTGCTGATATCAACATGTTAGCCGCTTGCAAGACCCTTCA
AGAAGTAACACAGCTATCACAAGAAGCACAGAGAATAGTTGAGAAACTTGAAAAGTCCACAAAGCCTATTGTGGC
TGCCATCAATGGATCCTGCCTGGGAGGAGGACTTGAGGTTGCCATTTCATGCCAATACAGAATAGCAACAAAAGA
CAGAAAAACAGTATTAGGTACCCCTGAAGTTTTGCTGGGGGCCTTACCAGGAGCAGGAGGCACACAAAGGCTGCC
CAAAATGGTGGGTGTGCCTGCTGCTTTGGACATGATGCTGACTGGTAGAAGCATTCGTGCAGACAGGGCAAAGAA
AATGGGACTGGTTGACCAACTGGTGGAACCCCTGGGACCAGGACTAAAACCTCCAGAGGAACGGACAATAGAATA
CCTAGAAGAAGTTGCAATTACTTTTGCCAAAGGACTAGCTGATAAGAAGATCTCTCCAAAGAGAGACAAGGGATT
GGTGGAAAAATTGACAGCGTATGCCATGACTATTCCATTTGTCAGGCAACAGGTTTACAAAAAAGTGGAAGAAAA
AGTGCGAAAGCAGACTAAAGGCCTTTATCCTGCACCTCTGAAAATAATTGATGTGGTAAAGACTGGAATTGAGCA
AGGGAGTGATGCCGGTTATCTCTGTGAATCTCAGAAATTTGGAGAGCTTGTAATGACCAAAGAATCAAAGGCCTT
GATGGGACTCTACCATGGTCAGGTCCTGTGCAAGAAGAATAAATTTGGAGCTCCACAGAAGGATGTTAAGCATCT
GGCTATTCTTGGTGCAGGGCTGATGGGAGCAGGCATCGCCCAAGTCTCCGTGGATAAGGGGCTAAAGACTATACT
TAAAGATGCCACCCTCACTGCGCTAGACCGAGGACAGCAACAAGTGTTCAAAGGATTGAATGACAAAGTGAAGAA
GAAAGCTCTAACATCATTTGAAAGGGATTCCATCTTCAGCAACTTGACTGGGCAGCTTGATTACCAAGGTTTTGA
AAAGGCCGACATGGTGATTGAAGCTGTGTTTGAGGACCTTAGTCTTAAGCACAGAGTGCTAAAGGAAGTAGAAGC
GGTGATTCCAGATCACTGTATCTTTGCCAGTAACACATCTGCTCTCCCAATCAGTGAAATCGCTGCTGTCAGCAA
AAGACCTGAGAAGGTGATTGGCATGCACTACTTCTCTCCCGTGGACAAGATGCAGCTGCTGGAGATTATCACGAC
CGAGAAAACTTCCAAAGACACCAGTGCTTCAGCTGTAGCAGTTGGTCTCAAGCAGGGGAAGGTCATCATTGTGGT
TAAGGATGGACCTGGCTTCTATACTACCAGGTGTCTTGCGCCCATGATGTCTGAAGTCATCCGAATCCTCCAGGA
AGGAGTTGACCCGAAGAAGCTGGATTCCCTGACCACAAGCTTTGGCTTTCCTGTGGGTGCCGCCACACTGGTGGA
TGAAGTTGGTGTGGATGTAGCGAAACATGTGGCGGAAGATCTGGGCAAAGTCTTTGGGGAGCGGTTTGGAGGTGG
AAACCCAGAACTGCTGACACAGATGGTGTCCAAGGGCTTCCTAGGTCGTAAATCTGGGAAGGGCTTTTACATCTA
TCAGGAGGGTGTGAAGAGGAAGGATTTGAATTCTGACATGGATAGTATTTTAGCGAGTCTGAAGCTGCCTCCTAA
GTCTGAAGTCTCATCAGACGAAGACATCCAGTTCCGCCTGGTGACAAGATTTGTGAATGAGGCAGTCATGTGCCT
GCAAGAGGGGATCTTGGCCACACCTGCAGAGGGAGACATCGGAGCCGTCTTTGGGCTTGGCTTCCCGCCTTGTCT
GGGAGGGCCTTTCCGCTTTGTGGATCTGTATGGCGCCCAGAAGATAGTGGACCGGCTCAAGAAATATGAAGCTGC
CTATGGAAAACAGTTCACCCCATGCCAGCTGCTAGCTGACCATGCTAACAGCCCTAACAAGAAGTTCTACCAG**TG**
AGCAGGCCTCATGCCTCGCTCAGTCAGTGCACTAACCCCAGCTGCCGGCAGTGCTGGTTCTCCAACAGAGTGGTG
TCTAGATTTATCAGAGTAACGAGAAGACAAACTCCGGCACTGGGTTTGCTCCCTGATTAAAGTGCCTTCAGCCAA
GACCATCTCTCCCTCCTGGTGAAGTGTGACTTCGAATTAGTTTGCACTTCCTATTGGAAGGTAGAGCCCACTGCT
CATTGTATAAGCCCCGAGGCCTAGAGTGGCAGCCAAGAGCCATCTGAAGCCACCTCTCTGCCTGTTCCTCCCAAG
AGGCCAGGGTGGCCAGGGGTGGTGAGGGCAGTTCTGCACCCAGCCAAACACATAACAATAAAAACCAAACTCTGT
GTCAGCATCTTTGCCCTTCTGGTTTAAACGCCTCCTTCAAAAAGCAATCTGGAAGAAAGCCCTGTGCTTTGGGGG
AGTAAGAATGTGTGTGCAGAATTCTAGGCAGCACCTTAGGGAGGGACTGGGATGAGAGAAAGTGGGACCTGGTGG
GCTCAACCACACACACCTGTCTGTGCAGATGCTTTGCCCAGGCTTCTCACCACGGTGTACCGGGATATTAAACCT
CTTTCCCCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 714

MVACRAIGILSRFSAFRILRSRGYICRNFTGSSALLTRTHINYGVKGDVAVVRINSPNSKVNTLSKELHSEFSEV
MNEIWASDQIRSAVLISSKPGCFIAGADINMLAACKTLQEVTQLSQEAQRIVEKLEKSTKPIVAAINGSCLGGGL
EVAISCQYRIATKDRKTVLGTPEVLLGALPGAGGTQRLPKMVGVPAALDMMLTGRSIRADRAKKMGLVDQLVEPL
GPGLKPPEERTIEYLEEVAITFAKGLADKKISPKRDKGLVEKLTAYAMTIPFVRQQVYKKVEEKVRKQTKGLYPA
PLKIIDVVKTGIEQGSDAGYLCESQKFGELVMTKESKALMGLYHGQVLCKKNKFGAPQKDVKHLAILGAGLMGAG
IAQVSVDKGLKTILKDATLTALDRGQQQVFKGLNDKVKKKALTSFERDSIFSNLTGQLDYQGFEKADMVIEAVFE
DLSLKHRVLKEVEAVIPDHCIFASNTSALPISEIAAVSKRPEKVIGMHYFSPVDKMQLLEIITTEKTSKDTSASA
VAVGLKQGKVIIVVKDGPGFYTTRCLAPMMSEVIRILQEGVDPKKLDSLTTSFGFPVGAATLVDEVGVDVAKHVA
EDLGKVFGERFGGGNPELLTQMVSKGFLGRKSGKGFYIYQEGVKRKDLNSDMDSILASLKLPPKSEVSSDEDIQF
RLVTRFVNEAVMCLQEGILATPAEGDIGAVFGLGFPPCLGGPFRFVDLYGAQKIVDRLKKYEAAYGKQFTPCQLL
ADHANSPNKKFYQ

FIGURE 715

TTCTGTTTTTCTCTCTCATTCTCCAGTGGCGGCGGCGGGGAAGGCGGAGGCAGAGGCAGCAGCAGCCGCGCTGGC
TGCAATGAATGATCCCCCAGCTTGGGGGGAGGACTCCAGGTGAGCCTCTGCCCTCGGGAGGCCCGGGACCCCCGG
CCGCCCACGACCGGCAGCCCACGCTATGGATCCCTAGAGGAAGGAGGAGAAGACAGCTCGCCGCCCACCCCCATC
CCATTTTCCTCTTCCTTTATCTCATTGTTGCCGAAGCTGTTTACGGCAGCGCTCCCTCTGCTCCAGGACTCCCTG
GGGGGGAATGCCAAGACCATCATGGTAGCCACACTGGGGCCAGCTTCTCACAGCTACGATGAGAGCCTCTCCACC
TTGCGCTTTGCCAACCGAGCCAAGAACATCAAGAACAAGCCCCAGGTGAACGAGGACCCCAAGGACACACTGCTG
CGGGAATTCCAAGAGGAGATTGCCCGCCTGAAGGCCCAGCTGGAGAAGAGGGGGATGCTGGGGAAGCGGCCCCGG
AGGAAGAGCAGCCGCAGGAAGAAGGCCGTGTCCGCCCCGCCTGGGTACCCTGAGGGCCCAGTGATTGAGGCCTGG
GTGGCAGAAGAGGAGGATGACAACAACAACAACCACCGCCCGCCCCAGCCCATCCTGGAGTCAGCCTTGGAGAAG
AACATGGAGAATTACCTGCAGGAACAGAAGGAGCGGCTGGAGGAGGAGAAGGCAGCCATCCAGGATGACCGCA

FIGURE 716A

GCTGGAGGTGGCCTCCCCTCCGCCCCAGACAAGAAGAGGCCCTCAGCCCTCCCCCGGTCTCAGAGAGCCCTGAGA
GGAGGCCCAGTCCAGAGCTCTTCCTCCGTTCCCAGTCCACTTCTCTAGGGCCAGTAGCAGACACCAGCCAGTATG
CCGAGGAACCAGGGCTTCTCCGAGCCCGAATACTCGGCCGAGTACTCAGCCGAGTACTCCGTCAGCCTGCCCTCC
GACCCTGACCGCGGGGTGGGCCGGACCCATGAAATCTCGGTCCGGAACTCGGGCTCCTGCCTGTGCCTGCCTCGC
TTCATGCGGCTGACTTTCGTGCCGGAGTCCTTGGAGAACCTCTACCAGACCTACTTCAAAAGGCAGCGCCACGAG
ACCCTGCTGGTGCTGGTGGTCTTTGCAGCCCTCTTTGACTGCTACGTGGTGGTCATGTGTGCTGTGGTCTTCTCC
AGCGACAAGCTGGCTTCCCTCGCCGTGGCTGGAATTGGACTGGTGTTGGACATCATCCTCTTCGTGCTCTGCAAA
AAGGGGCTGCTCCCGGACCGGGTCACCCGCAGAGTGCTGCCCTACGTGCTGTGGCTGCTCATAACCGCCCAGATC
TTCTCCTACCTGGGCCTGAACTTCGCGCGTGCCCACGCGGCTAGTGACACGGTGGGCTGGCAGGTCTTCTTTGTC
TTCTCCTTCTTCATCACGCTGCCCCTCAGCCTCAGCCCCATCGTGATCATCTCCGTGGTCTCCTGTGTGGTGCAC
ACGTTGGTCCTGGGGGTCACCGTGGCCCAGCAGCAGCAGGAGGAGCTCAAGGGGATGCAGCTGCTGCGGGAGATC
CTGGCCAACGTCTTCCTCTACCTGTGCGCCATCGCTGTGGGCATCATGTCCTACTACATGGCTGACCGCAAGCAC
CGCAAGGCCTTCCTGGAGGCCCGCCAGTCGCTGGAGGTGAAGATGAACCTGGAAGAGCAGAGCCAGCAGCAGGAG
AACCTCATGCTTTCCATCCTGCCCAAGCACGTGGCTGACGAGATGCTGAAAGACATGAAGAAAGACGAGAGCCAG
AAGGACCAGCAGCAGTTCAACACCATGTACATGTACCGTCACGAGAACGTCAGCATCCTCTTTGCCGACATCGTG
GGCTTTACCCAGCTGTCTTCTGCCTGCAGTGCCCAGGAGCTTGTGAAGCTGCTCAACGAGCTCTTTGCCCGCTTT
GACAAGCTGGCAGCTAAATACCACCAGCTGCGGATTAAGATCCTGGGCGACTGCTACTACTGCATCTGCGGCTTG
CCCGACTACCGGGAGGACCACGCCGTCTGCTCCATCCTCATGGGGCTGGCCATGGTGGAGGCCATCTCGTATGTG
CGGGAGAAGACCAAGACTGGGGTGGACATGCGTGTGGGGGTGCACACGGGCACCGTGCTGGGGGGCGTCCTGGGC
CAGAAGCGCTGGCAGTACGACGTGTGGTCGACTGATGTCACTGTAGCCAACAAGATGGAGGCCGGCGGCATCCCT
GGGCGCGTGCACATCTCCCAGAGCACCATGGACTGCCTGAAAGGGGAGTTTGATGTGGAGCCAGGCGATGGGGGC
AGCCGCTGTGATTACCTAGAAGAGAAGGGTATTGAAACCTACCTCATCATTGCCTCCAAGCCAGAGGTGAAGAAA
ACAGCCACCCAGAATGGCCTCAATGGCTCGGCCCTGCCCAATGGAGCACCAGCTTCCTCAAAGTCCAGCTCCCCT
GCCCTCATTGAGACCAAGGAGCCCAACGGGAGTGCCCACAGCAGTGGGTCCACGTCGGAGAAGCCCGAGGAGCAG
GATGCCCAGGCCGACAACCCCTCATTCCCCAACCCACGCCGGAGGCTGCGCCTGCAGGACCTGGCTGACCGAGTG
GTGGATGCCTCTGAAGATGAGCACGAGCTCAACCAGCTGCTCAACGAGGCCCTGCTTGAGCGAGAGTCCGCCCAA
GTGTAAAGAAGAGAAACACCTTCCTCTTGTCCATGCGGTTCATGGACCCCGAGATGGAAACCCGCTACTCGGTGG
AGAAGGAGAAGCAGAGTGGGGCTGCCTTCAGCTGCTCCTGCGTCGTCCTGCTCTGCACGGCCCTGGTCGAGATAC
TCATCGACCCCTGGCTAATGACAAACTATGTGACCTTCATGGTGGGGGAGATTCTGCTCCTCATCCTGACCATCT
GCTCCCTGGCTGCCATCTTTCCCCGGGCCTTTCCTAAGAAGCTTGTGGCCTTCTCAACTTGGATTGACCGGACCC
GCTGGGCCAGGAACACCTGGGCCATGCTCGCCATCTTCATCCTGGTGATGGCAAATGTCGTGGACATGCTCAGCT
GTCTCCAGTACTACACGGGACCCAGCAATGCAACGGCAGGGATGGAAACGGAGGGCAGCTGCCTGGAGAACCCCA
AGTATTACAACTATGTGGCCGTGCTGTCCCTCATCGCCACCATCATGCTGGTGCAGGTCAGCCACATGGTGAAGC
TCACGCTCATGCTGCTCGTCGCAGGCGCCGTGGCCACCATCAACCTCTATGCCTGGCGTCCCGTCTTTGATGAAT
ACGACCACAAGCGTTTTCGGGAGCACGACTTACCTATGGTGGCCTTAGAGCAGATGCAAGGATTCAACCCTGGGC
TCAATGGCACTGACAGGCTGCCCCTGGTGCCTTCCAAGTACTCTATGACGGTGATGGTGTTCCTCATGATGCTCA
GCTTCTACTACTTCTCCCGCCACGTAGAAAAACTGGCACGGACACTTTTCTTGTGGAAGATTGAGGTCCACGACC
AGAAGGAACGTGTCTATGAGATGCGACGCTGGAACGAGGCCTTGGTCACCAACATGTTGCCTGAGCACGTGGCAC
GCCATTTCCTGGGGTCCAAGAAGAGAGATGAGGAGCTGTATAGCCAGACGTATGATGAGATTGGAGTCATGTTTG
CCTCCCTGCCCAACTTTGCTGACTTCTACACAGAGGAGAGCATCAACAATGGTGGTATTGAGTGTCTGCGTTTCC
TCAATGAAATCATCTCAGATTTTGACTCTCTCCTGGACAATCCCAAGTTCCGGGTGATCACCAAGATCAAAACCA
TTGGCAGCACGTATATGGCGGCTTCAGGAGTCACCCCCGATGTCAACACCAATGGCTTTGCCAGCTCCAACAAGG
AAGACAAGTCCGAGAGAGAGCGCTGGCAGCACCTGGCTGACCTGGCCGACTTCGCGCTGGCCATGAAGGATACGC
TCACCAACATCAACAACCAGTCCTTCAATAACTTCATGCTGCGCATAGGCATGAACAAAGGCGGGGTTCTGGCTG
GGGTCATCGGAGCCCGGAAACCACACTACGACATCTGGGGCAATACAGTCAATGTAGCCAGCAGGATGGAGTCCA
CGGGGGTCATGGGCAACATTCAGGTATGTCCAGTGGCACAGCTGGCACGTGCTCAGACTCGGCATGAGAACAAAA
CCGGAACAGTGCTTTCCCACGTGCCCCTGCCTCCCACCCTGGCCCTGAACAGTAAGTCCAGAGGCAGAGACGTGG
GGCAAGTGGAAAAGAATCTCTGCAATAGCTAGCCTCAGCACAGGAAGAAACACTTCCACCCATCCACAAAATCTG

FIGURE 716B

GGCTGAAGTTCTAGATGCATATGGCCTACCTTTGGGTATGAACCTTCTAATACCTTGTGATCTGTCTCAGTGGCG
TCTGGCAGAAAAGCTCCACGAAAGGGGCAAAGGACAGAAGAGCAGGCAGTGGCAGTTTCCAGGTAACAGTGCTG
CCACCCAGGTGACCATGGCCATCCTAGGAGAGAAGTCTCTGGATGAGAGGAGGCCCCCAGCCAGTCACTCCAGGG
TTCTCCTTCCCACCCGCTGCTCGCCACGGGTGGAAGGGCTTGGCCC

FIGURE 717

GCCGCGGCACCAGGGCGCGCAGCCGGGCCGGCCCGACCCCACCGGCCATACGGTGGAGCCATCGAAGCCCCCACC
CACAGGCTGACAGAGGCACCGTTCACCAGAGGGCTCAACACCGGGATCTATGTTTAAGTTTTAACTCTCGCCTCC
AAAGACCACGATAATTCCTTCCCCAAAGCCCAGCAGCCCCCCAGCCCCGCGCAGCCCCAGCCTGCCTCCCGGCGC
CCAG**ATG**CCCGCCATGCCCTCCAGCGGCCCCGGGGACACCAGCAGCTCTGCTGCGGAGCGGGAGGAGGACCGAAA
GGACGGAGAGGAGCAGGAGGAGCCGCGTGGCAAGGAGGAGCGCCAAGAGCCCAGCACCACGGCACGGAAGGTGGG
GCGGCCTGGGAGGAAGCGCAAGCACCCCCCGGTGGAAAGCGGTGACACGCCAAAGGACCCTGCGGTGATCTCCAA
GTCCCCATCCATGGCCCAGGACTCAGGCGCCTCAGAGCTATTACCCAATGGGGACTTGGAGAAGCGGAGTGAGCC
CCAGCCAGAGGAGGGGAGCCCTGCTGGGGGGCAGAAGGGCGGGGCCCCAGCAGAGGGAGAGGGTGCAGCTGAGAC
CCTGCCTGAAGCCTCAAGAGCAGTGGAAAATGGCTGCTGCACCCCCAAGGAGGGCCGAGGAGCCCCTGCAGAAGC
GGGCAAAGAACAGAAGGAGACCAACATCGAATCCATGAAAATGGAGGGCTCCCGGGGCCGGCTGCGGGGTGGCTT
GGGCTGGGAGTCCAGCCTCCGTCAGCGGCCCATGCCGAGGCTCACCTTCCAGGCGGGGGACCCCTACTACATCAG
CAAGCGCAAGCGGGACGAGTGGCTGGCACGCTGGAAAAGGGAGGCTGAGAAGAAAGCCAAGGTCATTGCAGGAAT
GAATGCTGTGGAAGAAAACCAGGGGCCCGGGGAGTCTCAGAAGGTGGAGGAGGCCAGCCCTCCTGCTGTGCAGCA
GCCCACTGACCCCGCATCCCCCACTGTGGCTACCACGCCTGAGCCCGTGGGGTCCGATGCTGGGGACAAGAATGC
CACCAAAGCAGGCGATGACGAGCCAGAGTACGAGGACGGCCGGGGCTTTGGCATTGGGGAGCTGGTGTGGGGGAA
ACTGCGGGGCTTCTCCTGGTGGCCAGGCCGCATTGTGTCTTGGTGGATGACGGGCCGGAGCCGAGCAGCTGAAGG
CACCCGCTGGGTCATGTGGTTCGGAGACGGCAAATTCTCAGTGGTGTGTGTTGAGAAGCTGATGCCGCTGAGCTC
GTTTTGCAGTGCGTTCCACCAGGCCACGTACAACAAGCAGCCCATGTACCGCAAAGCCATCTACGAGGTCCTGCA
GGTGGCCAGCAGCCGCGCGGGGAAGCTGTTCCCGGTGTGCCACGACAGCGATGAGAGTGACACTGCCAAGGCCGT
GGAGGTGCAGAACAAGCCCATGATTGAATGGGCCCTGGGGGGCTTCCAGCCTTCTGGCCCTAAGGGCCTGGAGCC
ACCAGAAGAAGAGAAGAATCCCTACAAAGAAGTGTACACGGACATGTGGGTGGAACCTGAGGCAGCTGCCTACGC
ACCACCTCCACCAGCCAAAAAGCCCCGGAAGAGCACAGCGGAGAAGCCCAAGGTCAAGGAGATTATTGATGAGCG
CACAAGAGAGCGGCTGGTGTACGAGGTGCGGCAGAAGTGCCGGAACATTGAGGACATCTGCATCTCCTGTGGGAG
CCTCAATGTTACCCTGGAACACCCCCTCTTCGTTGGAGGAATGTGCCAAAACTGCAAGAACTGCTTTCTGGAGTG
TGCGTACCAGTACGACGACGACGGCTACCAGTCCTACTGCACCATCTGCTGTGGGGGCCGTGAGGTGCTCATGTG
CGGAAACAACAACTGCTGCAGGTGCTTTTGCGTGGAGTGTGTGGACCTCTTGGTGGGGCCGGGGGCTGCCCAGGC
AGCCATTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCACAAGGGTACCTACGGGCTGCTGCGGCGGCGAGA
GGACTGGCCCTCCCGGCTCCAGATGTTCTTCGCTAATAACCACGACCAGGAATTTGACCCTCCAAAGGTTTACCC
ACCTGTCCCAGCTGAGAAGAGGAAGCCCATCCGGGTGCTGTCTCTCTTTGATGGAATCGCTACAGGGCTCCTGGT
GCTGAAGGACTTGGGCATTCAGGTGGACCGCTACATTGCCTCGGAGGTGTGTGAGGACTCCATCACGGTGGGCAT
GGTGCGGCACCAGGGGAAGATCATGTACGTCGGGGACGTCCGCAGCGTCACACAGAAGCATATCCAGGAGTGGGG
CCCATTCGATCTGGTGATTGGGGGCAGTCCCTGCAATGACCTCTCCATCGTCAACCCTGCTCGCAAGGGCCTCTA
CGAGGGCACTGGCCGGCTCTTCTTTGAGTTCTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGGAGATGATCG
CCCCTTCTTCTGGCTCTTTGAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCGCGATTTCTCGA
GTCCAACCCTGTGATGATTGATGCCAAAGAAGTGTCAGCTGCACACAGGGCCCGCTACTTCTGGGGTAACCTTCC
CGGTATGAACAGGCCGTTGGCATCCACTGTGAATGATAAGCTGGAGCTGCAGGAGTGTCTGGAGCATGGCAGGAT
AGCCAAGTTCAGCAAAGTGAGGACCATTACTACGAGGTCAAACTCCATAAAGCAGGGCAAAGACCAGCATTTTCC
TGTCTTCATGAATGAGAAAGAGGACATCTTATGGTGCACTGAAATGGAAAGGGTATTTGGTTTCCCAGTCCACTA
TACTGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGCCGGTCATGGAGCGTGCCAGTCATCCG
CCACCTCTTCGCTCCGCTGAAGGAGTATTTTGCGTGTGTG**TAA**GGGACATGGGGGCAAACTGAGGTAGCGACACA
AAGTT

FIGURE 718

MPAMPSSGPGDTSSSAAEREEDRKDGEEQEEPRGKEERQEPSTTARKVGRPGRKRKHPPVESGDTPKDPAVISKS
PSMAQDSGASELLPNGDLEKRSEPQPEEGSPAGGQKGGAPAEGEGAAETLPEASRAVENGCCTPKEGRGAPAEAG
KEQKETNIESMKMEGSRGRLRGGLGWESSLRQRPMPRLTFQAGDPYYISKRKRDEWLARWKREAEKKAKVIAGMN
AVEENQGPGESQKVEEASPPAVQQPTDPASPTVATTPEPVGSDAGDKNATKAGDDEPEYEDGRGFGIGELVWGKL
RGFSWWPGRIVSWWMTGRSRAAEGTRWVMWFGDGKFSVVCVEKLMPLSSFCSAFHQATYNKQPMYRKAIYEVLQV
ASSRAGKLFPVCHDSDESDTAKAVEVQNKPMIEWALGGFQPSGPKGLEPPEEEKNPYKEVYTDMWVEPEAAAYAP
PPPAKKPRKSTAEKPKVKEIIDERTRERLVYEVRQKCRNIEDICISCGSLNVTLEHPLFVGGMCQNCKNCFLECA
YQYDDDGYQSYCTICCGGREVLMCGNNNCCRCFCVECVDLLVGPGAAQAAIKEDPWNCYMCGHKGTYGLLRRRED
WPSRLQMFFANNHDQEFDPPKVYPPVPAEKRKPIRVLSLFDGIATGLLVLKDLGIQVDRYIASEVCEDSITVGMV
RHQGKIMYVGDVRSVTQKHIQEWGPFDLVIGGSPCNDLSIVNPARKGLYEGTGRLFFEFYRLLHDARPKEGDDRP
FFWLFENVVAMGVSDKRDISRFLESNPVMIDAKEVSAAHRARYFWGNLPGMNRPLASTVNDKLELQECLEHGRIA
KFSKVRTITTRSNSIKQGKDQHFPVFMNEKEDILWCTEMERVFGFPVHYTDVSNMSRLARQRLLGRSWSVPVIRH
LFAPLKEYFACV

FIGURE 719

CTGACCGCCGGGGGGTGCCCCCGGGACGTAGCGCCGCGGAGAGGAAGCGGCAAAGGGGACC**ATG**CGGCGCCTGAC
TCGTCGGCTGGTTCTGCCAGTCTTCGGGGTGCTCTGGATCACGGTGCTGCTGTTCTTCTGGGTAACCAAGAGGAA
GTTGGAGGTGCCGACGGGACCTGAAGTGCAGACCCCTAAGGTTTGGTCCTTGTTTTTCAAGGTGGCTGGGATGAG
CCCTTGGGCGCCTCAGGTGCCTGTATCACCCACTCCTCCCTACCAAAGAGGGCATCTTCCTACAGGAGGACACCT
TGCTGTATGTCATTTCCCATGTCTCTTGCAAGAAGCTCAGTTCCATTTGCAGACTCAGGTCTTTCTTCAAGTCAG
ATGCACACTGCTGGTGTATTGCACGGACCTTCCACCCACTAGCATCATCATCACCTTCCACAACGAGGCCCGCTC
CACGCTGCTCAGGACCATCCGCAGTGTATTAAACCGCACCCCTACGCATCTGATCCGGGAAATCATATTAGTGGA
TGACTTCAGCAATGACCCTGATGACTGTAAACAGCTCATCAAATTGCCCAAGGTGAAATGCTTGCGCAATAATGA
ACGGCAAGGTCTGGTCCGGTCCCGGATTCGGGGCGCTGACATCGCCCAGGGCACCACTCTGACTTTCCTCGACAG
CCACTGTGAGGTGAACAGGGACTGGCTCCAGCCTCTGTTGCACAGGGTCAAAGAGGACTACACGCGGGTGGTGTG
CCCTGTGATCGATATCATTAACCTGGACACCTTCACCTACATCGAGTCTGCCTCGGAGCTCAGAGGGGGGTTTGA
CTGGAGCCTCCACTTCCAGTGGGAGCAGCTCTCCCCAGAGCAGAAGGCTCGGCGCCTGGACCCCACGGAGCCCAT
CAGGACTCCTATCATAGCTGGAGGGCTCTTCGTGATCGACAAAGCTTGGTTTGATTACCTGGGGAAATATGATAT
GGACATGGACATCTGGGGTGGGGAGAACTTTGAAATCTCCTTCCGAGTGTGGATGTGCGGGGGCAGCCTAGAGAT
CGTCCCCTGCAGCCGAGTGGGGCACGTCTTCCGGAAGAAGCACCCCTACGTTTTCCCTGATGGAAATGCCAACAC
GTATATAAAGAACACCAAGCGGACAGCTGAAGTGTGGATGGATGAATACAAGCAATACTATTACGCTGCCCGGCC
ATTCGCCCTGGAGAGGCCCTTCGGGAATGTTGAGAGCAGATTGGACCTGAGGAAGAATCTGCGCTGCCAGAGCTT
CAAGTGGTACCTGGAGAATATCTACCCTGAACTCAGCATCCCCAAGGAGTCCTCCATCCAGAAGGGCAATATCCG
ACAGAGACAGAAGTGCCTGGAATCTCAAAGGCAGAACAACCAAGAAACCCCAAACCTAAAGTTGAGCCCCTGTGC
CAAGGTCAAAGGCGAAGATGCAAAGTCCCAGGTATGGGCCTTCACATACACCCAGCAGATCCTCCAGGAGGAGCT
GTGCCTGTCAGTCATCACCTTGTTCCCTGGCGCCCCAGTGGTTCTTGTCCTTTGCAAGAATGGAGATGACCGACA
GCAATGGACCAAAACTGGTTCCCACATCGAGCACATAGCATCCCACCTCTGCCTCGATACAGATATGTTCGGTGA
TGGCACCGAGAACGGCAAGGAAATCGTCGTCAACCCATGTGAGTCCTCACTCATGAGCCAGCACTGGGACATGGT
GAGCTCT**TGA**GGACCCCTGCCAGAAGCAGCAAGGGCCATGGGGTGGTGCTTCCCTGGACCAGAACAGACTGGAAA
CTGGGCAGCAAGCAGCCTGCAACCACCTCAGACATCCTGGACTGGGAGGTGGAGGCAGAGCCCCCCAGGACAGGA
GCAACTGTCTCAGGGAGGACAGAGGAAAACATCACAAGCCAATGGGGCTCAAAGACAAATCCCACATGTTCTCAA
GGCCGTTAAGTTCCAGTCCTGGCCAGTCATTCCCTGATTGGTATCTGGAGACAGAAACCTAATGGGAAGTGTTTA
TTGTTCCTTTTCCTACAAAGGAAGCAGTCTCTGGAGGCCAGAAAGAAAAGCCTTCTTTTCACTAGGCCAGGACT
ACATTGAGAGATGAAGAATGGAGGTTGTTTCCAAAAGAAATAAAGAGAAACTTAGAAGTTGTCTCTGG

FIGURE 720

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKVWSLFFKVAGMSPWAPQVPVSPTPPYQRGHLP
TGGHLAVCHFPCLLQEAQFHLQTQVFLQVRCTLLVYCTDLPPTSIIITFHNEARSTLLRTIRSVLNRTPTHLIRE
IILVDDFSNDPDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADIAQGTTLTFLDSHCEVNRDWLQPLLHRVKEDY
TRVVCPVIDIINLDTFTYIESASELRGGFDWSLHFQWEQLSPEQKARRLDPTEPIRTPIIAGGLFVIDKAWFDYL
GKYDMDMDIWGGENFEISFRVWMCGGSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKQYY
YAARPFALERPFGNVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLESQRQNNQETPNLK
LSPCAKVKGEDAKSQVWAFTYTQQILQEELCLSVITLFPGAPVVLVLCKNGDDRQQWTKTGSHIEHIASHLCLDT
DMFGDGTENGKEIVVNPCESSLMSQHWDMVSS

FIGURE 721

GGTGTTCACTCAACTTGGATCTGTGCTGAAAAATTGTGACATTTCAGTACATCTGGTAGAGGGTACAGCTTTTAT
CTTGCACATGAATTTTTTGATGTTCTTCCTGTGCATAAATTTCAGAAAACACCACAGGGATGGCGAGAAGTATTT
GTTGACATTGATCCACAGGTTTCTGATAAACTGAGGTTTGTTTTGGCACCTTCTGCCACCCCAGCAGAAGCCTTC
ATACAACATGACGAAACAAGGGATCATGTTGAAGTGTGTCCTGATGCTGGTGTTATCATCGAGGAACTTTCTCAA
CGCATTGCATTAACTGGAGGTGCTGCACTGGTTGCTGATTATGGTCATGATGGAACAAAGACAGATACCTTCAGA
GGGTTTTGCGACCACAAGCTTCATGATGTCTTAATTGCCCCAGGAACAGCAGATCTAACAGCTGATGTGGACTTC
AGTTATTTGCGAAGA**ATG**GCACAGGGAAAAGTAGCCTCTCTGGGCCCAATAAAACAACACACATTTTTAAAAAAT
ATGGGTATTGATGTCCGGCTGAAGGTTCTTTTAGATAAATCAAATGAGCCATCAGTGAGGCAGCAGTTACTTCAA
GGATATGATATGTTAATGAATCCAAAGAAGATGGGAGAGAGATTTAACTTTTTTGCCTTGCTACCTCATCAGAGA
CTTCAAGGTGGAAGATATCAGAGGAATGCACGTCAGTCAAAACCCTTTGCATCCGTTGTAGCTGGGTTTAGTGAA
CTTGCTTGGCAG**TGA**TATTTCAGCTTGGACATTTTACCCTTCAGTCGGCCCAAGAAATCAAAATAAAGGAAACAC
ATTTCATATACTGCAGGTAACAAAAGTCAAAGTATTTTATCTTTTCACAGCAAGAACAGTCCATGTTGTATATAA
TACAACCAACATTATAGAACTTTTAGGGTTGTGACTGGCTTTGGTGCAAATGTGTGCTCAAGCTAATAAGTTATT
GTGAAACTGAGTTTCCTTTAACTTACAAAGCTAGTTGCCATATTTCTATTTTATTTTAAAAAGTAAACATGCGGC
TGGGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGCATATCACCTGAGGTCAGCAGT
TAAAGACCAGCCTGACCAAAATGGAGAAACCCCATCTCTACTAAAAATACAAAACTAGCCGGGTATGGTGGTACA
TGCCTGTAATCCCAGC

FIGURE 722

MAQGKVASLGPIKQHTFLKNMGIDVRLKVLLDKSNEPSVRQQLLQGYDMLMNPKKMGERFNFFALLPHQRLQGGR
YQRNARQSKPFASVVAGFSELAWQ

FIGURE 723

CTTCTCTCGCCAGGCATCCTCGTGGAAGTGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGT
G**ATG**CCCAGGGAAGACAGGGCGACCTGGAAGTCCAACTACTTCCTTAAGATCATCCAACTATTGGATGATTATCC
AAAATGTTTCATCGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCAGATCCGCATGTCCCTTCGCGGGAA
GGTCGTGGTGCTGATGGGCAAGAACACCATGATGCGCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCT
GGAGAAACTGCTGCCTCATATCTGGGGGAATGTGGGCTTTGTGTTCACCAAGGAGGACCTCACTGAGATCAGGGA
CATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCCGTGCTGGTGCCATTGCCCCATGTGAAGTCACTGTGCCAGC
CCAGAACACTGGTCTCGGGCCCGAGAAGACCTCCTTTTTCCAGGCTTTAGGTATCACCACTAAAATCTCCAGGGG
CACCATTGAAATCCTGAGTGATGTGCAGCTGATCAAGACTGGAGACAAAGTGGGAGCCAGCGAAGCCACGCTGCT
GAACATGCTCAACATCTCCCCCTTCTCCTTTGGGCTGGTCATCCAGCAGGTATTCGACAATGGCAGCATCTACAA
CCCTGAAGTGCTTGATAAAACAGAGGAAACTCTGCATTCTCGCTTCCTGGAGGGTGTCCGCAATGTTGCCAGTGT
CTGTCTGCAGACTGGCTACCCAACTGTTGCATCAGTACCCCATTCTATCATCAACGGGTACAAACGAGTCCTGGC
CTTGTCTGTGGAGACGGATTACACCTTCCCACTTGCTGAAAATGTCAAGGCCTTCTTGGCTGATCCATCTGCCTT
TGTGGCTGCTGCCCCTGTGGCTGCTGACACCACAGCTGCTCCTGCTGCTGCTGCAGCCCCAGCTAAGGTTGAAGC
CAAGGAAGAGTCGGAGGAGTCGGACGAGGATATGGGATTTGGTCTCTTTGAC**TAA**TCACCAAAAAGCAACCAACT
TAGCCAGCTTTATTTGCAAAACAAGGAAATAAAGGCTTACTTCTTT

FIGURE 724

MPREDRATWKSNYFLKIIQLLDDYPKCFIVGADNVGSKQMQQIRMSLRGKVVVLMGKNTMMRKAIRGHLENNPAL
EKLLPHIWGNVGFVFTKEDLTEIRDMLLANKVPAAARAGAIAPCEVTVPAQNTGLGPEKTSFFQALGITTKISRG
TIEILSDVQLIKTGDKVGASEATLLNMLNISPFSFGLVIQQVFDNGSIYNPEVLDKTEETLHSRFLEGVRNVASV
CLQTGYPTVASVPHSIINGYKRVLALSVETDYTFPLAENVKAFLADPSAFVAAAPVAADTTAAPAAAAAPAKVEA
KEESEESDEDMGFGLFD

FIGURE 725

GTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCCCAGGGAAGACAGGGCGACCTGGAAGTCCA
ACTACTTCCTTAAGATCATCCAACTATTGGATGATTATCCAAAATGTTTCATCGTGGGAGCAGACAATGTGGGCT
CCAAGCAGATGCAGCAGATCCGCATGTCCCTTCGCGGGAAGGTCGTGGTGCTGATGGGCAAGAACACCATGATGC
GCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATATCTGGGGGAATGTGG
GCTTTGTGTTCACCAAGGAGGACCTCACTGAGATCAGGGACATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCC
GTGCTGGTGCCATTGCCCCATGTGAAGTCACTGTGCCAGCCCAGAACACTGGTCTCGGGCCCGAGAAGACCTCCT
TTTTCCAGGCTTTAGAGTGATGTGCAGCTGATCAAGACTGGAGACAAAGTGGGAGCCAGCGAAGCCACGCTGCTG
AACATGCTCAACATCTCCCCCTTCTCCTTTGGGCTGGTCATCCAGCAGGTATTCGACAATGGCAGCATCTACAAC
CCTGAAGTGCTTGATAAAACAGAGGAAACTCTGCATTCTCGCTTCCTGGAGGGTGTCCGCAATGTTGCCAGTGTC
TGTCTGCAGACTGGCTACCCAACTGTTGCATCAGTACCC

FIGURE 726

CTGCGTGGCAATCCCTGACGCACCGCCGTGATGCCCAGGGAAGACAGGGCGACCTGGAAGTCCAACTACTTCCTT
AAGATCATCCAACTATTGGATGATTATCCAAAATGTTTCATCGTGGGAGCAGACAATGTGGGCTCCAAGCAGATG
CAGCAGATCCGCATGTCCCTTCGCGGGAAGGTCGTGGTGCTGATGGGCAAGAACACCATGATGCGCAAGGCCATC
CGAGGGCACCTGGAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATATCTGGGGGAATGTGGGCTTTGTGTTC
ACCAAGGAGGACCTCACTGAGATCAGGGACATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCCGTGCTGGTGCC
ATTGCCCCATGTGAAGTCACTGTGCCAGCCCAGAACACTGGTCTCGGGCCCGAGAAGACCTCCTTTTTCCAGGCT
TTAGGTATCACCACTAAAATCTCCAGGGGCACCATTGAAATCCTGACAGGTATTCGACAATGGCAGCATCTACAA
CCCTGAAGTGCTTGATAAAACAGAGGAAACTCTGCATTCTCGCTTCCTGGAGGGTGTCCGCAATGTTGCCAGTGT
CTGTCTGCAGACTGGCTACCCAACTGTTGCATCAGTACCCCATTCTATCATCAACGGGTACAAACGAGTCCTGGC

FIGURE 727

CCTCTAGCTTAGCGAGCGCTGGAGTTTGAAGAGCGGGCAGTGGCTGCACACGCCAAACTTTCCCT**ATG**GCTTCGG
TGACCAGGGCCGTGTTTGGAGAGCTGCCCTCGGGAGGAGGGACAGTGGAGAAGTTCCAGCTGCAGTCAGACCTCT
TGAGAGTGGACATCATCTCCTGGGGCTGCACGATCACAGCCCTAGAGGTCAAAGACAGGCAGGGGAGAGCCTCGG
ACGTGGTGCTTGGCTTCGCCGAGTTGGAAGGATACCTCCAAAAGCAGCCATACTTTGGAGCAGTTATTGGGAGGG
TGGCCAACCGAATCGCCAAAGGAACCTTCAAGGTGGATGGGAAGGAGTATCACCTGGCCATTAACAAGGAACCCA
ACAGTCTGCATGGAGGAGTCAGAGGGTTTGATAAAGTGCTCTGGACCCCTCGGGTGCTGTCAAATGGCGTCCAGT
TCTCGCGCATCAGTCCAGATGGTGAAGAAGGCTACCCCGGAGAGTTAAAAGTCTGGGTGACATACACCCTGGATG
GCGGAGAGCTCATAGTCAACTACAGAGCACAAGCCAGTCAGGCCACACCAGTCAACCTGACCAACCATTCTTACT
TCAACCTGGCAGGCCAGGCTTCCCCAAATATAAATGACCATGAAGTCACCATAGAAGCGGATACTTATTTGCCTG
TGGATGAAACCCTGATTCCTACAGGAGAAGTTGCCCCAGTGCAAGGCACTGCATTCGACCTGAGAAAGCCAGTGG
AGCTTGGAAAACACCTGCAGGACTTCCATCTCAATGGTTTGACCACAATTTCTGTCTGAAGGGATCTAAAGAAA
AGCATTTTTGTGCAAGGGTGCATCATGCTGCAAGCGGGCGGTACTAGAAGTATACACCACCCAGCCCGGGGTCC
AGTTTTACACGGGCAACTTCCTGGATGGCACATTAAAGGGCAAGAATGGAGCTGTCTATCCCAAGCACTCCGGTT
TCTGCCTGGAGACTCAGAACTGGCCTGATGCAGTCAATCAGCCCCGCTTCCCTCCTGTGCTGCTGAGGCCTGGTG
AGGAGTATGACCACACCACCTGGTTCAAGTTTTCTGTGGCT**TAA**GGAAGTGTGAAGATATGATCCAGTCCAGGGC
TAGGCTCAGCCACCTGTCTCCTGTCCAGAAAAAAGGTGAAGATTAAGAAGCTTTCAGAATGATTCTATGGATTAA
AATCATACAAATGGTGGCTGTTCTGAGAATCAGTCTGGGTATTGATTTCCTTTTCCAGTGACTGGCTCCAGGCCA
TGTCTAATGACCAGCTCGATTCCCTGTGCAGTTCAGAGAGCAAGTGAACCCAACCAACAATGTCGTCATCTAAGC
CCTGACCCTAGCCAGGGACTCCCATGCTGCTGTTGGCTCCATCTCTCCACACTGCCTCTTTCTTTTCAACTTTTT
GCCCTTCCTTTCTTTAAAGCTATTCTCACATTGCTTTTATTTCCTCCTCCTTCACCTCCAACCACTGTCAGCAGC
ACTCTGGAGTTTTCAAATGTCACATTAGCCTCACCCTGCATGCTAGGAGATGGACCTGTCTCTATACAGCAGTAG
ATGATTGATAAGTGAGGAAACTGAGGCTTACAGAGGTTGAAGACCAACAAGCTAATAAATAAAAAGTTGAGGCCG
GGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGAGGCAGGCGGATCACGAGGTCAGGAGATCGA
GACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACATAAAAAATTAGCTGGGTGTGGTAGCACGCACCCGTAG
TTCCAGCTACTTGGGAGGCTGAAGCAGGAGAATCGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCCGAGATCA
TGCCACTGCACTGGGCAACAGAGCAAAACTCGATCTCAAAAAAAAAAAAAAAAAAAA

FIGURE 728

MASVTRAVFGELPSGGGTVEKFQLQSDLLRVDIISWGCTITALEVKDRQGRASDVVLGFAELEGYLQKQPYFGAV
IGRVANRIAKGTFKVDGKEYHLAINKEPNSLHGGVRGFDKVLWTPRVLSNGVQFSRISPDGEEGYPGELKVWVTY
TLDGGELIVNYRAQASQATPVNLTNHSYFNLAGQASPNINDHEVTIEADTYLPVDETLIPTGEVAPVQGTAFDLR
KPVELGKHLQDFHLNGFDHNFCLKGSKEKHFCARVHHAASGRVLEVYTTQPGVQFYTGNFLDGTLKGKNGAVYPK
HSGFCLETQNWPDAVNQPRFPPVLLRPGEEYDHTTWFKFSVA

FIGURE 729

GACTTCAGGAAAAATCAACCCAGCACCAGCAGCTACCAACCACCATTCCATCTCTTCACTTGAACAGCATTAGTT
AAGTCCAG**<u>ATG</u>**TGGGAACCCTTCTCTTGGAAGAAGTTCCTAATTGTGTCTCAGACCGGTGTAAACAAACCAGCCA
GCCGCCACCTTGCTAAACCTATAAGCTTTTTAAAATCCAATATATTCTGCCAAGAATATGCCTTGATAGTTAGCC
CTCAGCCCATAGGTGTTTTTTGTTTTTTAACAGAATTATATATGTCTGGGGGTGAAAAAACCCTTGCATTCCAAA
GGTCCATACTGGTTACTTGGTTTCATTGCCACCACTTAGTGGATGTTCAGTTTAGAACCATTTTGTCTGCTCCCT
CTGGAAGCCTTGCGCAGAGCTTACTTTGTAATTGTTGGAGAATAACTGCTGAATTTTTAGCTGTTTTGAGT**<u>TGA</u>**T
TCGCACCACTGCACCACAACTCAATATGAAAACTATTTAACTTATTTATTATCTTGTGAAAAGTATACAATGAAA
ATTTTGTTCATACTGTATTTATCAAGTATGATGAAAAGCAATAGATATATATTCTTTTATTATGTTAAATTATGA
TTGCCATTATTAATCGGCAAAATGTGGAGTGTATGTTCTTTTCACAGTAATATATGCCTTTTGTAACTTCACTTG
GTTATTTTATTGTAAATGAGTACAAAATTCTTAATTTAAGAGATTGTATGTAATATTTATTTCATTAATTTCTTT
CCTTGTTTACGTAAATTTTGAAAGATTGCATGATTTCTTGACAGAAATCGATCTTGATGCTGTGGAAGTAGTTTG
AGGAACATCCTATGAGTTTTCTTAGAATGTATAAAGGTTGTAGCCCATCCAACTTCAAAGAAAAAAATGACCACA
TACTTTGCAATCAGGCTGAAATGTGGCATGCTTTTCTAATTCCAACTTTATAAACTAGCAAAAAAGTGTTTGCTT
ATTCCACCAGTTCTACTGTGACATACTCGAGTATAAAGACATGTAGCAATAACGGGGAGTGGGGGGGGAGTCTCA
CAGTGCCTTTGGAAGGGCCCGAACTTGCCTTAAATCTTCCTCAACCAAATAAGTATTTTATTAGTGCTTGAGAGA
ATCTGAATGTAGGATGGGTTCAACTGCACAAAAGGAAAAGATTTTTACCACTTTTTTTATATAGATATAAAGTGA
AGCAACCGCCTTAGTGCTGAAATATGTAGTACATGAATATGCCTTGTTTAATTACAGAAAATTCCTTCCTGGACA
GCAGATGAATGAGCGGTAGCTTTAGTTTGTACGTAGGTACAGTTGGAGCACTATATGTACTCTCTGGACTACTTT
GGACAGAAGTAGGTTTTTGAATGTAACAAGATAAGTCAACTTGAGTTGTAATATATTTTGGGGAATCAGCTCACT
ACAAATTGTGACTGTAAACATTGTACTGTAAATGTTTTGTAGTT

FIGURE 730

MWEPFSWKKFLIVSQTGVNKPASRHLAKPISFLKSNIFCQEYALIVSPQPIGVFCFLTELYMSGGEKTLAFQRSI
LVTWFHCHHLVDVQFRTILSAPSGSLAQSLLCNCWRITAEFLAVLS

FIGURE 731

CCTGATTCTAGGCTGGTCACTACTCCGAGCCTGTGACGTTTGCGGCAGCCAGGCCGTCGACG**ATG**CCCAGTGAAA
CTCTCTGGGAAATTGCAAAAGCTGAAGTGGAAAAAAGGGGAATTAATGGAAGTGAAGGTGATGGAGCTGAAATTG
CAGAAAAATTTGTTTTCTTCATTGGCAGTAAAAATGGGGGAAAGACTACTATTATTCTAAGGTGTCTTGACAGAG
ATGAACCACCAAAACCAACCTTAGCTTTGGAATATACATATGGAAGAAGAGCAAAAGGGCACAACACACCAAAAG
ATATCGCTCACTTTTGGGAACTCGGTGGAGGAACCTCTTTATTGGACTTAATCAGCATACCCATCACAGGTGACA
CCTTACGGACGTTTTCTCTTGTTCTCGTTCTGGATCTTTCAAAACCTAATGATCTCTGGCCCACCATGGAAAATC
TCTTGCAAGCCACAAAAAGCCATGTAGACAAAGTGATAATGAAACTGGGAAAGACAAATGCTAAAGCAGTTTCTG
AAATGAGACAGAAGATCTGGAATAATATGCCGAAGGATCATCCTGATCATGAATTAATTGACCCATTTCCGGTAC
CTCTGGTCATAATTGGAAGTAAATATGATGTTTTTCAGGATTTTGAGTCTGAGAAGAGAAAGGTAATATGCAAGA
CACTTCGATTTGTTGCACATTATTATGGAGCATCATTAATGTTTACCAGTAAATCAGAAGCTCTATTACTAAAAA
TACGTGGAGTTATCAACCAGTTGGCATTTGGCATTGACAAAAGCAAATCAATATGTGTGGATCAGAATAAACCGC
TGTTTATCACAGCAGGATTGGATTCTTTCGGTCAAATAGGATCTCCTCCTGTTCCTGAAAATGACATTGGAAAGC
TTCATGCCCACTCACCTATGGAGTTGTGGAAAAAAGTGTATGAAAAGCTCTTTCCACCAAAGAGTATTAACACGC
TGAAAGATATCAAGGACCCTGCGAGAGATCCTCAGTATGCTGAAAATGAAGTCGATGAGATGAGAATTCAGAAGG
ATCTGGAACTGGAACAGTACAAAAGAAGTTCTTCCAAGTCTTGGAAACAAATCGAGCTTGATTCT**TGA**ACCTATT
TCAATTATTGTATATTTATTTCTTCTTTTCCAAATACAAATAAGATTATACTGTGAATTAACTATTGTGGCAATA
TGTGAAGAAAGTTAAACTGTATAATTTGTTAAAGGACAAGCTGGATTTCTTGGACTAGTGCATCTCCCTGTATAT
CTTGAAGCTTTTTAAAAGGAAAAATTATTGTAGAACCACGTGTAATTTTTTTAAAATAAAAGAATCTTCTACTA
CCTACCTCT

FIGURE 732

MPSETLWEIAKAEVEKRGINGSEGDGAEIAEKFVFFIGSKNGGKTTIILRCLDRDEPPKPTLALEYTYGRRAKGH
NTPKDIAHFWELGGGTSLLDLISIPITGDTLRTFSLVLVLDLSKPNDLWPTMENLLQATKSHVDKVIMKLGKTNA
KAVSEMRQKIWNNMPKDHPDHELIDPFPVPLVIIGSKYDVFQDFESEKRKVICKTLRFVAHYYGASLMFTSKSEA
LLLKIRGVINQLAFGIDKSKSICVDQNKPLFITAGLDSFGQIGSPPVPENDIGKLHAHSPMELWKKVYEKLFPPK
SINTLKDIKDPARDPQYAENEVDEMRIQKDLELEQYKRSSSKSWKQIELDS

FIGURE 733A

ACATGCTCCTCCTGTCCTTCTGGCGGAGCGTGCTTCCCGCTGCGGGGACGTTCGAGCAATGGCAGCCCTGCTGAG
ATCCGCGCGTTGGTTGCTGCGTGCCGGGGCGGCCCCGCGCCTCCCGCTCTCCCTGCGCCTCCTCCCTGGCGGCCC
GGGCCGGCTGCATGCCGCCTCCTATCTGCCCGCCGCTCGCGCCGGGCCCGTGGCCGGAGGACTACTGAGCCCAGC
CAGGCTGTATGCCATTGCTGCCAAAGAAAAAGATATTCAAGAGGAGTCCACTTTTTCTTCTAGGAAGATTTCCAA
TCAGTTTGATTGGGCTCTAATGAGACTAGATCTTTCTGTTCGAAGAACTGGCCGCATTCCAAAGAAGCTTCTACA
AAAAGTTTTTAATGATACCTGCCGCTCAGGTGGCCTAGGTGGTAGTCATGCCTTGCTTCTACTACGTAGTTGTGG
TTCTCTCTTGCCTGAACTAAAGCTTGAAGAGAGAACAGAATTTGCTCATAGGATATGGGACACACTTCAGAAATT
AGGTGCTGTGTATGATGTGAGTCACTATAATGCTTTACTTAAAGTCTATCTTCAAAATGAATATAAATTCTCACC
AACTGATTTCCTGGCAAAAATGGAGGAAGCAAACATTCAACCAAATCGAGTGACATACCAGAGATTGATTGCTTC
TTATTGTAATGTAGGAGATATTGAAGGTGCCAGCAAGATTCTTGGATTTATGAAAACTAAGGATCTCCCAGTTAC
AGAGGCAGTATTCAGTGCCCTTGTGACAGGGCATGCCAGAGCTGGTGATATGGAGAATGCAGAAAACATTCTCAC
AGTGATGAGAGATGCCGGAATTGAGCCTGGTCCAGACACATACCTCGCATTATTGAATGCATATGCTGAGAAGGG
CGACATTGACCATGTTAAGCAGACTCTGGAGAAGGTGGAGAAGTCCGAGCTTCACCTTATGGACCGTGATTTACT
GCAAATTATTTTTAGCTTCAGTAAAGCTGGGTATCCTCAGTATGTCTCAGAAATTTTGGAAAAAGTTACATGTGA
AAGAAGATATATTCCAGATGCAATGAACCTCATTTTACTTTTAGTCACTGAAAAATTGGAAGATGTAGCGTTGCA
AATTTTACTAGCATGCCCCGTATCAAAGGAAGATGGCCCAAGTGTCTTTGGCAGTTTCTTTTTACAACACTGTGT
GACTATGAATACGCCTGTGGAGAAGCTAACAGACTACTGTAAGAAGTTAAAGGAAGTCCAGATGCACTCCTTTCC
TCTGCAGTTCACCCTCCATTGTGCTTTACTCGCCAATAAAACTGATTTGGCAAAAGCCTTAATGAAGGCTGTGAA
GGAGGAAGGTTTTCCTATCAGACCTCACTATTTCTGGCCATTGCTAGTTGGACGTCGGAAGGAAAAAAATGTTCA
AGGTATAATTGAAATCCTCAAAGGAATGCAAGAATTGGGAGTACATCCTGATCAGGAAACATATACAGATTATGT
GATTCCATGCTTTGATAGTGTAAACTCAGCACGAGCCATTTTGCAGGAAAATGGATGTCTGTCTGATAGTGATAT
GTTTTCTCAAGCTGGATTGAGAAGTGAAGCAGCAAATGGGAACTTAGACTTTGTATTATCATTTTTGAAATCAAA
TACATTGCCCATCTCGCTGCAGTCTATAAGAAGTAGCCTACTGCTAGGCTTCAGGAGGTCTATGAATATAAATCT
TTGGAGCGAGATAACAGAATTGTTGTACAAGGATGGACGTTATTGCCAGGAGCCTCGAGGACCGACGGAAGCTGT
TGGCTATTTTCTTTATAACTTGATTGACAGCATGAGTGACTCAGAGGTACAGGCCAAGGAGGAGCATTTGAGACA
ATACTTCCATCAGCTGGAGAAGATGAATGTAAAAATTCCTGAAAATATCTACAGAGGCATTCGTAATCTCCTGGA
AAGCTACCATGTTCCTGAATTGATTAAGGATGCTCACTTGTTGGTTGAGAGTAAGAATTTAGACTTTCAAAAAAC
TGTGCAACTTACATCATCTGAATTGGAGTCCACACTTGAAACACTAAAAGCTGAAAATCAACCTATAAGAGATGT
CCTAAAGCAACTCATATTAGTGCTTTGTTCAGAAGAGAATATGCAAAAAGCCCTTGAATTGAAAGCAAAATATGA
ATCCGACATGGTTACTGGTGGCTATGCAGCTTTAATAAATTTATGCTGTCGACATGATAAAGTAGAAGATGCCTT
GAACTTGAAAGAAGAATTTGACCGCTTAGATTCATCTGCTGTCCTTGACACCGGCAAGTATGTAGGCCTTGTAAG
AGTATTGGCAAAGCATGGCAAGCTCCAAGATGCTATTAACATTCTGAAGGAGATGAAAGAGAAGGATGTTCTTAT
CAAAGATACAACAGCCTTGTCCTTTTTCCACATGCTAAATGGCGCAGCTTTAAGAGGTGAAATTGAAACAGTAAA
ACAGTTGCATGAAGCCATCGTGACTCTAGGGTTAGCAGAACCATCCACCAACATAAGTTTCCCATTGGTCACTGT
ACACTTGGAAAAGGGCGACCTATCTACTGCTCTTGAGGTCGCCATTGACTGCTATGAAAAGTATAAAGTATTACC
AAGGATTCATGATGTCTTGTGTAAACTGGTAGAGAAAGGCGAGACTGATCTAATTCAGAAAGCAATGGACTTTGT
GAGCCAAGAACAAGGTGAAATGGTGATGCTCTATGATCTCTTCTTTGCCTTCCTACAAACAGGAAATTACAAAGA
GGCCAAGAAGATCATTGAGACTCCAGGGATTAGAGCTCGATCTGCAAGGCTTCAGTGGTTTTGTGACAGATGTGT
TGCAAATAATCAGGTTGAAACTCTGGAAAAATTAGTGGAGCTGACACAGAAGCTATTTGAATGTGATAGAGACCA
GATGTACTACAATCTGCTAAAACTGTATAAAATAAACGGTGACTGGCAAAGAGCTGATGCAGTCTGGAATAAAAT
CCAAGAAGAAAATGTTATTCCTCGTGAAAAGACATTAAGATTATTAGCAGAAATCCTTAGAGAGGGTAACCAGGA
AGTTCCGTTTGACGTACCTGAGTTGTGGTATGAAGATGAAAAACATTCCCTGAATTCTTCGTCAGCCTCAACCAC
AGAACCTGATTTCCAGAAAGATATATTGATTGCCTGCCGATTGAACCAAAAAAAAGGGGCATATGATATTTTCCT
GAATGCAAAAGAGCAAAACATTGTGTTTAATGCTGAAACCTACAGCAATCTCATTAAATTACTGATGTCAGAAGA
TTATTTTACACAAGCAATGGAAGTGAAAGCATTCGCGGAGACCCACATCAAGGGCTTCACACTGAACGATGCTGC
CAACAGCCGCCTCATCATAACGCAAGTTAGGCGGGATTATTTGAAAGAGGCTGTGACAACACTGAAAACAGTATT
GGATCAGCAGCAGACCCCTTCTAGGTTAGCAGTGACCCGTGTCATCCAGGCATTGGCCATGAAGGGTGATGTTGA
AAACATAGAAGTAGTTCAGAAGATGTTAAATGGACTCGAAGACTCCATTGGACTTTCAAAAATGGTTTTCATCAA

FIGURE 733B

TAACATTGCTTTGGCTCAAATAAAGAATAATAACATAGATGCCGCAATAGAAAACATTGAAAATATGCTTACTTC
AGAGAATAAAGTCATTGAACCCCAATACTTCGGCTTGGCATACTTATTCAGAAAAGTAATAGAGGAGCAGTTGGA
ACCAGCAGTTGAAAAGAGTAACATCATGGCGGAGAGATTGGCCAATCAGTTTGCAATTTATAAACCTGTCACTGA
TTTTTTCCTTCAACTTGTGGATGCAGGCAAGGTGGATGATGCCAGAGCTCTCCTACAGAGATGTGGTGCAATTGC
TGAACAAACCCCGATTTTGTTGTTGTTCCTCCTTAGGAATTCTAGGAAACAAGGAAAGGCATCAACTGTGAAATC
TGTGTTAGAATTGATTCCTGAATTAAATGAAAAGGAAGAAGCATACAATTCCCTCATGAAAAGCTATGTCTCAGA
GAAAGATGTCACATCTGCTAAAGCACTGTATGAACATTTGACTGCAAAGAATACAAAATTGGATGATCTGTTTCT
AAAGCGTTACGCATCTTTGCTGAAGTATGCTGGAGAGCCTGTCCCTTTCATTGAACCCCCTGAAAGCTTTGAATT
TTATGCACAGCAGCTAAGAAAATTGAGGGAAAACTCTTCTTGAAATAACCAGGCGATACTTTGTTTTGTATATAT
TTGTGATTCTGTGTCTACATGTTATTTTGAAGTATATCTGAGGGAAAAATAAATGAAAATTTTCTTTATGTACTT
ATGTATGTGTGATGCATGTTCAAAGTCTTATTGACCATAACTCTGTGCACTTGGTTATTGGACATTTTTGGAGTT
TTTTTCTCTGGGAAAAATCGATAGTGTTTTCTTCAATGCTGCTGCTGTGTGAAGCCATACTTTTTCAGGATTCTT
CCCCTAATTGGCTCTTTGGTTTCCCTGCTCTGTTTCATTTATTTCATTAAAATGTTATTCCTTTATTTAAGATTC
ACTTATTAGTCTGCTGTTTCTCTGAAAAATTTTAGAGCTAGGTATAGTGACCGTGAACTTTCTAACGCATAATAT
TCTGTGATACAGCCATTCCGTACATGTGTGAAGTCCTGCATAACTTTCGAACTTTGTTAAATGTTGGCACTAGGA
GTCATCAGATCTAGGCTTCATCATTTTCCAGTGAGAAGCAGAGACCCAAAGGGCCTGTTACTTGTGCTTGGTCAG
GGGACTGTCTGTCATGCCTGGAGGCTCTTCGGCACACTTCCCCATCTTTCCCTTCTGCCACTGTGGCTTCAAGCA
CCTCTGTTCATAGAGCGTCTCTGAAATTGAGTCTCGGTCATGACTTATCCCGAAGTAGAGCAATGTGTTTCCTCT
CATTGTAGTTTCAGGACTTTGTCAGTACAAGCTCTGCCCTAGGCTTGTTACTTTATACTCATATCCTGAAAAGAT
GTGATTTCATCTATGAAGGGGTAAAATATTGGTTTGTATTTAATTGTTTGAAATAAAAGTGATCCCTATATTG

FIGURE 734

ATGGGCTCAGGCTACACCAAGGCCGTGTACCGGGTCCGCCTGCCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTG
GACTTTAGCGGCCACGATCTGGGCAGCTGCGTGCGCGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGCTGCGGCACCCCAACGTGCTGCAGCTCTATGGCTACTGC
TACCAGGACAGCGAGGACATCCCAGACACCCTGACCACCATCACGGAGCTGGGCGCCCCTGTAGAAATGATCCAG
CTGCTGCAAACTTCCTGGGAGGATCGATTCCGAATCTGCCTGAGCCTGGGCCGCCTCCTCCACCACCTGGCCCAC
TCCCCACTGGGCTCCGTCACTCTGCTGGACTTCCGCCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATACTCGAGTTTCCGGCC
AGGAACTTCACCCTGCCCTGCTCAGCCCAGGGCTGGTGCGAGGGCATGAACGAGAAGCGGAACCTCTATAATGCC
TACAGGTTTTTCTTCACATACCTCCTGCCTCACAGTGCCCCGCCTTCACTGCGTCCTCTGCTGGACAGCATCGTC
AACGCCACAGGAGAGCTCGCCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAGACAGCACCATCCCC
CAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCCTCCTTTCAGTGTTCAACCTGGCTGAGGCT
GTGGATGTCTGTGAGAGCCATGCCCAGTGTCGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGCAG
CTGGTCTTTTTCAAGACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC
TGA

FIGURE 735

MGSGYTKAVYRVRLPGGAAVALKAVDFSGHDLGSCVREFGVRRGCYRLAAHKLLKEMVLLERLRHPNVLQLYGYC
YQDSEDIPDTLTTITELGAPVEMIQLLQTSWEDRFRICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKV
TDLDDARVEETPCAGSTDCILEFPARNFTLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDSIV
NATGELAWGVDETLAQLEKVLHLYRSGQYLQNSTASSSTEYQCIPDSTIPQEDYRCWPSYHHGSCLLSVFNLAEA
VDVCESHAQCRAFVVTNQTTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

FIGURE 736

GCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAATGTGAGTTTACCA
GCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGT
AAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACT
GTGTTCAATAGTGTGAGAATGTAGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACA
GGAGACTTGGCGGGAGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAGG
GGACACTCCCAGGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCTCAGCATGAGCCAAGACTGGGGTCAGGGA
GCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGGGGCCTTTCTGCCTCATTTGCTTTCAATGAAA
GCCTCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTG
GTTAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAA

FIGURE 737

MWVILYLGRLSLTSRQGTLPGQPRGQGQRCTPQHEPRLGSGSRCGLSQDLGRGWGRGLSASFAFNESLKAAKTRL
SPFLEFEYPESFVLLVG

FIGURE 738A

AGATGACTTTGGGAAATTGCTGCTGGCTGAGGCCCTCCTGGAGCAGTGTTTGAAGGAGAACCATGCCAAAATAAA
AGACTCCATGCCTTTGCTGGAGAAGAATGAGCCGAAGATGAGCGAAGCCAAAAATTATCTAAGCAGTATCCTTAA
CCATGGGAGGCTCTCGCCACAGTACATGTGTGAGGCCATGCTGATCCTGGGCAAACTGCATTACGTGGAGGGCTC
ATACCGAGATGCCATCAGCATGTACGCACGGGCCGGGATTGATGACATGTCCATGGAGAACAAGCCCCTGTATCA
GATGCGGCTGCTGTCGGAGGCTTTTGTCATCAAAGGCCTCTCTCTGGAACGCCTACCCAACTCCATCGCCTCCCG
CTTCCGCCTGACAGAGAGGGAGGAGGAAGTGATCACCTGTTTTGAGAGGGCCTCCTGGATCGCTCAGGTGTTCCT
GCAGGAATTGGAGAAGACCACAAATAACAGCACGTCGAGGCATCTGAAAGGCTGTCACCCGCTTGACTATGAGCT
CACCTACTTCCTGGAAGCTGCCCTCCAGAGCGCCTATGTGAAAAACCTGAAGAAGGGGAACATCGTGAAGGGCAT
GAGAGAGCTCCGGGAGGTGCTGCGGACTGTGGAGACCAAAGCAACTCAGAACTTCAAAGTGATGGCGGCCAAGCA
CCTGGCGGGGGTCCTGCTGCACTCCCTGAGTGAGGAGTGCTACTGGAGCCCCCTGTCCCACCCTCTGCCTGAGTT
CATGGGCAAGGAGGAGAGTTCTTTCGCCACTCAGGCCCTGCGGAAACCTCACCTCTATGAAGGAGACAACCTCTA
CTGCCCCAAGGACAACATCGAGGAAGCCCTCCTGCTCCTCCTCATCAGCGAATCCATGGCAACTCGAGATGTGGT
GCTGAGCCGGGTGCCGGAGCAGGAGGAGGACCGGACAGTGAGCTTGCAGAATGCCGCAGCCATCTATGACCTCCT
GAGCATCACGTTGGGCAGAAGGGGACAGTACGTCATGCTCTCGGAGTGCCTGGAGCGAGCCATGAAGTTTGCGTT
TGGAGAATTTCACCTTTGGTACCAGGTGGCCCTCTCCATGGTGGCTTGTGGGAAGTCAGCCTACGCTGTGTCCCT
GCTGCGGGAGTGTGTGAAGTTGCGGCCCTCGGACCCCACCGTGCCCCTGATGGCCGCGAAGGTCTGCATCGGGTC
CCTTCGCTGGCTAGAGGAAGCAGAGCACTTTGCCATGATGGTGATCAGCCTCGGAGAGGAAGCCGGGGAGTTCCT
CCCCAAGGGCTACCTGGCTCTGGGTCTCACCTATAGCCTGCAGGCCACCGACGCCACCCTGAAGTCCAAGCAAGA
TGAATTGCACCGGAAGGCACTGCAGACGCTGGAGAGGGCTCAGCAGCTGGCGCCCAGTGACCCCCAGGTCATCCT
CTATGTCTCGCTGCAGCTGGCCCTCGTCCGACAGATCTCCAGTGCCATGGAGCAGCTGCAGGAGGCCCTGAAGGT
ACGCAAGGATGATGCCCACGCCCTCCACCTGCTGGCACTGCTCTTCTCTGCCCAGAAGCACCACCAGCATGCCCT
GGATGTTGTCAACATGGCCATCACCGAGCACCCTGAGAACTTCAACCTGATGTTCACCAAGGTGAAGCTGGAGCA
GGTGCTGAAAGGCCCAGAGGAAGCCCTCGTGACCTGCAGACAAGTGCTGAGGCTGTGGCAGACCCTGTACAGCTT
CTCCCAGCTGGGAGGCCTAGAAAAGGATGGCAGCTTCGGTGAGGGCCTCACCATGAAGAAGCAGAGTGGCATGCA
CCTGACTTTGCCTGATGCCCATGATGCAGACTCTGGCTCCCGGCGGGCTTCGTCCATCGCCGCCTCCCGGCTGGA
GGAGGCCATGTCAGAGCTGACTATGCCCTCTTCGGTCCTGAAGCAGGGCCCCATGCAGCTGTGGACCACGCTGGA
ACAGATCTGGCTGCAGGCTGCTGAGCTGTTCATGGAGCAGCAGCACCTCAAGGAAGCAGGTTTCTGCATCCAGGA
GGCGGCGGGCCTCTTCCCCACTTCTCACTCAGTACTCTATATGCGGGGCCGGCTGGCTGAGGTGAAGGGCAACCT
GGAGGAGGCCAAGCAGCTGTACAAGGAGGCGCTCACGGTGAACCCAGATGGCGTGCGCATCATGCATAGCCTGGG
TCTGATGCTGAGTCGGCTGGGCCACAAGAGCTTGGCCCAGAAGGTGCTTCGTGATGCCGTGGAGAGGCAGAGTAC
GTGCCACGAGGCGTGGCAGGGCCTGGGCGAGGTGCTGCAGGCCCAGGGCCAGAACGAGGCTGCCGTTGACTGCTT
CCTCACCGCCCTTGAGCTGGAGGCCAGCAGCCCTGTACTGCCCTTCTCCATCATCCCCAGAGAGCTCTGACGACG
CTGCAGCCGCAGGGAGGGAGGGGCTGGCCAGAGGGAGAGGCAGCAGGGAACGTGGGTCAGGGTGGGGCAACAGTG
GCATCAGGTGCGGGGCCTCAGGGAAATACATCTTTAGTGAACGCCTCTGCAGCTGCAGCCCTCGTTCTCTTGGCT
GGGCCAAGAGGGCCTTCCTGGATTTCTTTGTTGGTGCCTTGGGAAACAGTCTGACTTGAACCCTAAGTGCCTTTG
GAGAGTTTTGTGGTGACCAGACTTGCTCCCCAAGAGCTGGGCAGCGGGGAGCCTCACAGCTGTCCTTCACCCTCA
CCCATGCCTCTGGCTTGGAGTCTGGGTGGGGGTTCTCACTCCCCACTCTCAGCACAGTACAGACTTCTGGATCT
CTCTCAGGTCTTGCCCAGGGCGGTCACAATGTGAAGAAACTGCGGGCAAGTGGGAAGACTATGAGATTTCTGGGT
TCCCTTCTCAGACTTGGAGTTAGTAGATGATTCCTGCATTGCCCCTGCTTGCCCTCTGAGACCAGCTGGGCCCCA
CCTTGCTCTTTCCCCCTGCTACCAAGTGCCTTTGGGGTCTGACCAGGGGTACTGAGCACCGGCCCTAACACTTCC
ATCTCCACCCACCCCATCTCCCTGGCGATGTGCTCCAGCCCAAGCAGCCTCCGTAGGCTTTAGATCCTGTGGTTG
CTAGATCCAGTCCTTTCTAATACCCTGAGTCAACACATTACTCCTGCAGGTCTTAGGCTACAATGCAGGTCCCTT
GAGGGCCACCAACATGGAGGTAGGCAGTTTCTAGGACTGTCCCCAGTACATCTCACCACCCACAGCCCTTTTTTT
GCCTTGATTCGAGCCTCACCCTGGCCTTTTGGCTTCCCCTGCCTGAGAGAGACCTGAGGAGGGGACAGAGCCCAG
CCCCTCTCCTGTGGCTGAGCAGGCCTCTGTGTCCATGACACCTGTCTTCCGGGCCTGGGGGCTGTGGGTGTATGT
CCTCCCTACTGGCTTCCCCGGCCCCTGCTGCATGATGCTCTTGGAACTCTTCTCCAAGGAGTCAGTCCCCCAGGC
CTATCAGGGGATCCTTTTGTATCTGCACTTTGGGTTTTAGTTCAAAGCTCCATCAGGTACAGCTTGCATTTCAG
GATGTGTGGAAAGCTCGGGTGAGGGCTGCCCTGGTTCATCATAGCTCCACCTTCCTCGGAAGGAGTGGGCTGTTG

FIGURE 738B

GAGACCCCCCATCCATGGCACACTAGCTCAGCACTGCATTTCCCGAGATGATTCCCAAGACAGCTGGTGCCTCCT
GGCTTTCCTGTGCCAGGCCAAGGGGCACCACAGAGGACCCTGGATCCTTTGCCTCTTCTTGGTTGAAGGATCTCT
ATGTATGTGTGTATATAAATATAGTTTTTTATCTATATATATAAAATAGAGATCTATTTTTTTTCTGGAATTCTG
TTAGAAAAGTAAAGAAAAAGCAAATGCTGTTGGTTTATCTCAGGGTGCCCAAAGTGGTTATAGTCAATTTTTGGT
ACTAGGAAAGGCACCCAATGCATTTCCTGACTTTTAAGCATTTCCTTGTTGGAAGCAGCAGAGGGCCAGGCCAAG
TTGCTGACAGTGACTTTGCAGGTTGAATAAAGAAACCCTTGGAGGGGAAGCAGGCTTGTCTGAAGCAGCATGTAT
ATTCACTGGGCATGTAGCTCCCACACCAGCCTTGAGCCAGGCCCTGGACAGGAGGGGCTGTTGCAGGATGAGGGA
GGCCAGAGAAGGCATCGAAGCCAAGACCTGGGCCCACCTGGGGAGGGATGTGGGAAAGGAAGGATGGGAGGGAGG
ACCCTCTGGGAAAATGTGGATTTGAGCTGGTGAGAGTGTTGCTAAGGCTGGGCTAAAGCCTGGAGAGGGTAGGAG
GAGGCAAGAGGGGTCCAGGCAGGGCTGATCCTGGCCTCTGACCTGTCCAGGGCGACCCCTGAAGCCCCTGCTGCC
TCTGGGCATTGCTGGGAGAGGCCAAGGCAGGACTCACGTCTGAACAGAGATCCCCTCGGGCATTGCTGATGGGCC
ACCTTCAGCTGCAGGGAAGAAGCCTAGGAGAGGAGGCATGGGAGGGACCTGGGCCTTGTTCAGATTGGCCACCTC
TGCTGAGAAGTCCATACCAGTACACCCCTAATAAGTTATGCCACATACCAACGTACTGTGGATATTATAACCTGC
ATTAAAACAACTCTAAAGAACGCTGCTCATTT

FIGURE 739

MAAKGAHGSYLKVESELERCRAEGHWDRMPELVRQLQTLSMPGGGGNRRGSPSAAFTFPDTDDFGKLLLAEALLE
QCLKENHAKIKDSMPLLEKNEPKMSEAKNYLSSILNHGRLSPQYMCEAMLILGKLHYVEGSYRDAISMYARAGID
DMSMENKPLYQMRLLSEAFVIKGLSLERLPNSIASRFRLTEREEEVITCFERASWIAQVFLQELEKTTNNSTSRH
LKGCHPLDYELTYFLEAALQSAYVKNLKKGNIVKGMRELREVLRTVETKATQNFKVMAAKHLAGVLLHSLSEECY
WSPLSHPLPEFMGKEESSFATQALRKPHLYEGDNLYCPKDNIEEALLLLLISESMATRDVVLSRVPEQEEDRTVS
LQNAAAIYDLLSITLGRRGQYVMLSECLERAMKFAFGEFHLWYQVALSMVACGKSAYAVSLLRECVKLRPSDPTV
PLMAAKVCIGSLRWLEEAEHFAMMVISLGEEAGEFLPKGYLALGLTYSLQATDATLKSKQDELHRKALQTLERAQ
QLAPSDPQVILYVSLQLALVRQISSAMEQLQEALKVRKDDAHALHLLALLFSAQKHHQHALDVVNMAITEHPENF
NLMFTKVKLEQVLKGPEEALVTCRQVLRLWQTLYSFSQLGGLEKDGSFGEGLTMKKQSGMHLTLPDAHDADSGSR
RASSIAASRLEEAMSELTMPSSVLKQGPMQLWTTLEQIWLQAAELFMEQQHLKEAGFCIQEAAGLFPTSHSVLYM
RGRLAEVKGNLEEAKQLYKEALTVNPDGVRIMHSLGLMLSRLGHKSLAQKVLRDAVERQSTCHEAWQGLGEVLQA
QGQNEAAVDCFLTALELEASSPVLPFSIIPREL

FIGURE 740

AGTCCGAGTGGAGAGAGCGAGCTGAGTGGTTGTGTGGTCGCGTCTCGGAAACCGGTAGCGCTTGCAGCATGGCTG
ACCAACTGACTGAAGAGCAGATTGCAGAATTCAAAGAAGCTTTTTCACTATTTGACAAAGATGGTGATGGAACTA
TAACAACAAAGGAATTGGGAACTGTAATGAGATCTCTTGGGCAGAATCCCACAGAAGCAGAGTTACAGGACATGA
TTAATGAAGTAGATGCTGATGGTAATGGCACAATTGACTTCCCTGAATTTCTGACAATGATGGCAAGAAAAATGA
AAGACACAGACAGTGAAGAAGAAATTAGAGAAGCATTCCGTGTGTTTGATAAGGATGGCAATGGCTATATTAGTG
CTGCAGAACTTCGCCATGTGATGACAAACCTTGGAGAGAAGTTAACAGATGAAGAAGTTGATGAAATGATCAGGG
AAGCAGATATTGATGGTGATGGTCAAGTAAACTATGAAGAGTTTGTACAAATGATGACAGCAAAGTGAAGACCTT
GTACAGAATGTGTTAAATTTCTTGTACAAAATTGTTTATTTGCCTTTTCTTTGTTTGTAACTTATCTGTAAAAGG
TTTCTCCCTACTGTCAAAAAAATATGCATGTATAGTAATTAGGACTTCATTCCTCCATGTTTTCTTCCCTTATCT
TACTGTCATTGTCCTAAAACCTTATTTTAGAAAATTGATCAAGTAACATGTTGCATGTGGCTTACTCTGGATATA
TCTAAGCCCTTCTGCACATCTAAACTTAGATGGAGTTGGTCAAATGAGGGAACATCTGGGTTATGCCTTTTTTAA
AGTAGTTTTCTTTAGGAACTGTCAGCATGTTGTTGTTGAAGTGTGGAGTTGTAACTCTGCGTGGACTATGGACAG
TCAACAATATGTACTTAAAAGTTGCACTATTGCAAAACGGGTGTATTATCCAGGTACTCGTACACTATTTTTTTG
TACTGCTGGTCCTGTACCAGAAACATTTTCTTTTATTGTTACTTGCTTTTTAAACTTTGTTTAGCCACTTAAAAT
CTGCTTATGGCACAATTTGCCTCAAAATCCATTCCAAGTTGTATATTTGTTTTCCAATAAAAAAATTACAATTT

FIGURE 741

GGCGGGAAACAGCTTAGTGGGTGTGGGGTCGCGCATTTTCTTCAACCAGGAGGTGAGGAGGTTTCGAC**ATG**GCGG
TGCAGCCGAAGGAGACGCTGCAGTTGGAGAGCGCGGCCGAGGTCGGCTTCGTGCGCTTCTTTCAGGGCATGCCGG
AGAAGCCGACCACCACAGTGCGCCTTTTCGACCGGGGCGACTTCTATACGGCGCACGGCGAGGACGCGCTGCTGG
CCGCCCGGGAGGTGTTCAAGACCCAGGGGGTGATCAAGTACATGGGGCCGGCAGGAGCAAAGAATCTGCAGAGTG
TTGTGCTTAGTAAAATGAATTTTGAATCTTTTGTAAAAGATCTTCTTCTGGTTCGTCAGTATAGAGTTGAAGTTT
ATAAGAATAGAGCTGGAAATAAGGCATCCAAGGAGAATGATTGGTATTTGGCATATAAGGCTTCTCCTGGCAATC
TCTCTCAGTTTGAAGACATTCTCTTTGGTAACAATGATATGTCAGCTTCCATTGGTGTTGTGGGTGTTAAAATGT
CCGCAGTTGATGGCCAGAGACAGGTTGGAGTTGGGTATGTGGATTCCATACAGAGGAAACTAGGACTGTGTGAAT
TCCCTGATAATGATCAGTTCTCCAATCTTGAGGCTCTCCTCATCCAGATTGGACCAAAGGAATGTGTTTTACCCG
GAGGAGAGACTGCTGGAGACATGGGGAAACTGAGACAGATAATTCAAAGAGGAGGAATTCTGATCACAGAAAGAA
AAAAAGCTGACTTTTCCACAAAAGACATTTATCAGGACCTCAACCGGTTGTTGAAAGGCAAAAAGGGAGAGCAGA
TGAATAGTGCTGTATTGCCAGAAATGGAGAATCAGGTTGCAGTTTCATCACTGTCTGCGGTAATCAAGTTTTTAG
AACTCTTATCAGATGATTCCAACTTTGGACAGTTTGAACTGACTACTTTTGACTTCAGCCAGTATATGAAATTGG
ATATTGCAGCAGTCAGAGCCCTTAACCTTTTTCAGGGTTCTGTTGAAGATACCACTGGCTCTCAGTCTCTGGCTG
CCTTGCTGAATAAGTGTAAAACCCCTCAAGGACAAAGACTTGTTAACCAGTGGATTAAGCAGCCTCTCATGGATA
AGAACAGAATAGAGGAGAGATTGAATTTAGTGGAAGCTTTTGTAGAAGATGCAGAATTGAGGCAGACTTTACAAG
AAGATTTACTTCGTCGATTCCCAGATCTTAACCGACTTGCCAAGAAGTTTCAAAGACAAGCAGCAAACTTACAAG
ATTGTTACCGACTCTATCAGGGTATAAATCAACTACCTAATGTTATACAGGCTCTGGAAAAACATGAAGGAAAAC
ACCAGAAATTATTGTTGGCAGTTTTTGTGACTCCTCTTACTGATCTTCGTTCTGACTTCTCCAAGTTTCAGGAAA
TGATAGAAACAACTTTAGATATGGATCAGGTGGAAAACCATGAATTCCTTGTAAAACCTTCATTTGATCCTAATC
TCAGTGAATTAAGAGAAATAATGAATGACTTGGAAAAGAAGATGCAGTCAACATTAATAAGTGCAGCCAGAGATC
TTGGCTTGGACCCTGGCAAACAGATTAAACTGGATTCCAGTGCACAGTTTGGATATTACTTTCGTGTAACCTGTA
AGGAAGAAAAAGTCCTTCGTAACAATAAAAACTTTAGTACTGTAGATATCCAGAAGAATGGTGTTAAATTTACCA
ACAGCAAATTGACTTCTTTAAATGAAGAGTATACCAAAAATAAAACAGAATATGAAGAAGCCCAGGATGCCATTG
TTAAAGAAATTGTCAATATTTCTTCAGGCTATGTAGAACCAATGCAGACACTCAATGATGTGTTAGCTCAGCTAG
ATGCTGTTGTCAGCTTTGCTCACGTGTCAAATGGAGCACCTGTTCCATATGTACGACCAGCCATTTTGGAGAAAG
GACAAGGAAGAATTATATTAAAAGCATCCAGGCATGCTTGTGTTGAAGTTCAAGATGAAATTGCATTTATTCCTA
ATGACGTATACTTTGAAAAAGATAAACAGATGTTCCACATCATTACTGGCCCCAATATGGGAGGTAAATCAACAT
ATATTCGACAAACTGGGGTGATAGTACTCATGGCCCAAATTGGGTGTTTTGTGCCATGTGAGTCAGCAGAAGTGT
CCATTGTGGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACAGTCAATTGAAAGGAGTCTCCACGTTCATGGCTG
AAATGTTGGAAACTGCTTCTATCCTCAGGTCTGCAACCAAAGATTCATTAATAATCATAGATGAATTGGGAAGAG
GAACTTCTACCTACGATGGATTTGGGTTAGCATGGGCTATATCAGAATACATTGCAACAAAGATTGGTGCTTTTT
GCATGTTTGCAACCCATTTTCATGAACTTACTGCCTTGGCCAATCAGATACCAACTGTTAATAATCTACATGTCA
CAGCACTCACCACTGAAGAGACCTTAACTATGCTTTATCAGGTGAAGAAAGGTGTCTGTGATCAAAGTTTTGGGA
TTCATGTTGCAGAGCTTGCTAATTTCCCTAAGCATGTAATAGAGTGTGCTAAACAGAAAGCCCTGGAACTTGAGG
AGTTTCAGTATATTGGAGAATCGCAAGGATATGATATCATGGAACCAGCAGCAAAGAAGTGCTATCTGGAAAGAG
AGCAAGGTGAAAAAATTATTCAGGAGTTCCTGTCCAAGGTGAAACAAATGCCCTTTACTGAAATGTCAGAAGAAA
ACATCACAATAAAGTTAAAACAGCTAAAAGCTGAAGTAATAGCAAAGAATAATAGCTTTGTAAATGAAATCATTT
CACGAATAAAAGTTACTACG**TGA**AAAATCCCAGTAATGGAATGAAGGTAATATTGATAAGCTATTGTCTGTAATA
GTTTTATATTGTTTTATATTAACCCTTTTTCCATAGTGTTAACTGTCAGTGCCCATGGGCTATCAACTTAATAAG
ATATTTAGTAATATTTTACTTTGAGGACATTTTCAAAGATTTTTATTTTGAAAAATGAGAGCTGTAACTGAGGAC
TGTTTGCAATTGACATAGGCAATAATAAGTGATGTGCTGAATTTTATAAATAAAATCATGTAGTTTGTGG

FIGURE 742

MAVQPKETLQLESAAEVGFVRFFQGMPEKPTTTVRLFDRGDFYTAHGEDALLAAREVFKTQGVIKYMGPAGAKNL
QSVVLSKMNFESFVKDLLLVRQYRVEVYKNRAGNKASKENDWYLAYKASPGNLSQFEDILFGNNDMSASIGVVGV
KMSAVDGQRQVGVGYVDSIQRKLGLCEFPDNDQFSNLEALLIQIGPKECVLPGGETAGDMGKLRQIIQRGGILIT
ERKKADFSTKDIYQDLNRLLKGKKGEQMNSAVLPEMENQVAVSSLSAVIKFLELLSDDSNFGQFELTTFDFSQYM
KLDIAAVRALNLFQGSVEDTTGSQSLAALLNKCKTPQGQRLVNQWIKQPLMDKNRIEERLNLVEAFVEDAELRQT
LQEDLLRRFPDLNRLAKKFQRQAANLQDCYRLYQGINQLPNVIQALEKHEGKHQKLLLAVFVTPLTDLRSDFSKF
QEMIETTLDMDQVENHEFLVKPSFDPNLSELREIMNDLEKKMQSTLISAARDLGLDPGKQIKLDSSAQFGYYFRV
TCKEEKVLRNNKNFSTVDIQKNGVKFTNSKLTSLNEEYTKNKTEYEEAQDAIVKEIVNISSGYVEPMQTLNDVLA
QLDAVVSFAHVSNGAPVPYVRPAILEKGQGRIILKASRHACVEVQDEIAFIPNDVYFEKDKQMFHIITGPNMGGK
STYIRQTGVIVLMAQIGCFVPCESAEVSIVDCILARVGAGDSQLKGVSTFMAEMLETASILRSATKDSLIIIDEL
GRGTSTYDGFGLAWAISEYIATKIGAFCMFATHFHELTALANQIPTVNNLHVTALTTEETLTMLYQVKKGVCDQS
FGIHVAELANFPKHVIECAKQKALELEEFQYIGESQGYDIMEPAAKKCYLEREQGEKIIQEFLSKVKQMPFTEMS
EENITIKLKQLKAEVIAKNNSFVNEIISRIKVTT

FIGURE 743

CTTTTGCGGGTGGCGGCGAACGCGGAGAGCACGCCATGAAGGCCTCGGGCACACTACGAGAGTACAAAGTAGTGG
GTCGCTGCCTGCCCACCCCCAAATGCCACACACCACCCCTCTACCGCATGCGAATCTTTGCGCCTAATCATGTCG
TCGCCAAGTCCCGCTTCTGGTACTTCGTATCTCAGTTAAAGAAGATGAAGAAGTCTTCAGGGGAGATTGTCTACT
GTGGGCAGGTGTTTGAGAAGTTCCCCTTGCGGGTGAAGAACTTCGGGATCTGGCTGCGCTATGACTCCCGGAGCG
GCACCCACAACATGTACCGGGAATACCGGGACCTGACCACCGCAGGCGCTGTCACCCGGTGCTACCGAGACATGA
GCGCCCGGCACGGCGGCCGGGCCCACTCCATTCAGATCATGAAGGTGGAGGAGATCGCGGCCAGCAAGTGCCGCC
GGCCGGCTGTCAAGCAGTTCCACGACTCCAAGATCAAGTTCCCGCTGCCCCACCGGGTCCTGCGCCGTCAGCACA
AGCCACGCTTCACCACCAAGAGGCCCAACACCTTCTTCTAGGTGCAGGGCCCTCGCCCGGGTGTGCCCCAAATAA
ACTCAGGAACGCCCC

FIGURE 744A

ATTTCCCGCCAGCAGGAGCCGCGCGGTAGATGCGGTGCTTTTAGGAGCTCCGTCCGACAGAACGGTTGGGCCTTG
CCGGCTGTCGGTATGTCGCGACAGAGCACCCTGTACAGCTTCTTCCCCAAGTCTCCGGCGCTGAGTGATGCCAAC
AAGGCCTCGGCCAGGGCCTCACGCGAAGGCGGCCGTGCCGCCGCTGCCCCCGGGGCCTCTCCTTCCCCAGGCGGG
GATGCGGCCTGGAGCGAGGCTGGGCCTGGGCCCAGGCCCTTGGCGCGATCCGCGTCACCGCCCAAGGCGAAGAAC
CTCAACGGAGGGCTGCGGAGATCGGTAGCGCCTGCTGCCCCCACCAGTTGTGACTTCTCACCAGGAGATTTGGTT
TGGGCCAAGATGGAGGGTTACCCCTGGTGGCCTTGTCTGGTTTACAACCACCCCTTTGATGGAACATTCATCCGC
GAGAAAGGGAAATCAGTCCGTGTTCATGTACAGTTTTTTGATGACAGCCCAACAAGGGGCTGGGTTAGCAAAAGG
CTTTTAAAGCCATATACAGGTTCAAAATCAAAGGAAGCCCAGAAGGGAGGTCATTTTTACAGTGCAAAGCCTGAA
ATACTGAGAGCAATGCAACGTGCAGATGAAGCCTTAAATAAAGACAAGATTAAGAGGCTTGAATTGGCAGTTTGT
GATGAGCCCTCAGAGCCAGAAGAGGAAGAAGAGATGGAGGTAGGCACAACTTACGTAACAGATAAGAGTGAAGAA
GATAATGAAATTGAGAGTGAAGAGGAAGTACAGCCTAAGACACAAGGATCTAGGCGAAGTAGCCGCCAAATAAAA
AAACGAAGGGTCATATCAGATTCTGAGAGTGACATTGGTGGCTCTGATGTGGAATTTAAGCCAGACACTAAGGAG
GAAGGAAGCAGTGATGAAATAAGCAGTGGAGTGGGGGATAGTGAGAGTGAAGGCCTGAACAGCCCTGTCAAAGTT
GCTCGAAAGCGGAAGAGAATGGTGACTGGAAATGGCTCTCTTAAAAGGAAAAGCTCTAGGAAGGAAACGCCCTCA
GCCACCAAACAAGCAACTAGCATTTCATCAGAAACCAAGAATACTTTGAGAGCTTTCTCTGCCCCTCAAAATTCT
GAATCCCAAGCCCACGTTAGTGGAGGTGGTGATGACAGTAGTCGCCCTACTGTTTGGTATCATGAAACTTTAGAA
TGGCTTAAGGAGGAAAAGAGAAGAGATGAGCACAGGAGGAGGCCTGATCACCCCGATTTTGATGCATCTACACTC
TATGTGCCTGAGGATTTCCTCAATTCTTGTACTCCTGGGATGAGGAAGTGGTGGCAGATTAAGTCTCAGAACTTT
GATCTTGTCATCTGTTACAAGGTGGGGAAATTTTATGAGCTGTACCACATGGATGCTCTTATTGGAGTCAGTGAA
CTGGGGCTGGTATTCATGAAAGGCAACTGGGCCCATTCTGGCTTTCCTGAAATTGCATTTGGCCGTTATTCAGAT
TCCCTGGTGCAGAAGGGCTATAAAGTAGCACGAGTGGAACAGACTGAGACTCCAGAAATGATGGAGGCACGATGT
AGAAAGATGGCACATATATCCAAGTATGATAGAGTGGTGAGGAGGGAGATCTGTAGGATCATTACCAAGGGTACA
CAGACTTACAGTGTGCTGGAAGGTGATCCCTCTGAGAACTACAGTAAGTATCTTCTTAGCCTCAAAGAAAAAGAG
GAAGATTCTTCTGGCCATACTCGTGCATATGGTGTGTGCTTTGTTGATACTTCACTGGGAAAGTTTTTCATAGGT
CAGTTTTCAGATGATCGCCATTGTTCGAGATTTAGGACTCTAGTGGCACACTATCCCCCAGTACAAGTTTTATTT
GAAAAAGGAAATCTCTCAAAGGAAACTAAAACAATTCTAAAGAGTTCATTGTCCTGTTCTCTTCAGGAAGGTCTG
ATACCCGGCTCCCAGTTTTGGGATGCATCCAAAACTTTGAGAACTCTCCTTGAGGAAGAATATTTTAGGGAAAAG
CTAAGTGATGGCATTGGGGTGATGTTACCCCAGGTGCTTAAAGGTATGACTTCAGAGTCTGATTCCATTGGGTTG
ACACCAGGAGAGAAAAGTGAATTGGCCCTCTCTGCTCTAGGTGGTTGTGTCTTCTACCTCAAAAAATGCCTTATT
GATCAGGAGCTTTTATCAATGGCTAATTTTGAAGAATATATTCCCTTGGATTCTGACACAGTCAGCACTACAAGA
TCTGGTGCTATCTTCACCAAAGCCTATCAACGAATGGTGCTAGATGCAGTGACATTAAACAACTTGGAGATTTTT
CTGAATGGAACAAATGGTTCTACTGAAGGAACCCTACTAGAGAGGGTTGATACTTGCCATACTCCTTTTGGTAAG
CGGCTCCTAAAGCAATGGCTTTGTGCCCCACTCTGTAACCATTATGCTATTAATGATCGTCTAGATGCCATAGAA
GACCTCATGGTTGTGCCTGACAAAATCTCCGAAGTTGTAGAGCTTCTAAAGAAGCTTCCAGATCTTGAGAGGCTA
CTCAGTAAAATTCATAATGTTGGGTCTCCCCTGAAGAGTCAGAACCACCCAGACAGCAGGGCTATAATGTATGAA
GAAACTACATACAGCAAGAAGAAGATTATTGATTTTCTTTCTGCTCTGGAAGGATTCAAAGTAATGTGTAAAATT
ATAGGGATCATGGAAGAAGTTGCTGATGGTTTTAAGTCTAAAATCCTTAAGCAGGTCATCTCTCTGCAGACAAAA
AATCCTGAAGGTCGTTTTCCTGATTTGACTGTAGAATTGAACCGATGGGATACAGCCTTTGACCATGAAAAGGCT
CGAAAGACTGGACTTATTACTCCCAAAGCAGGCTTTGACTCTGATTATGACCAAGCTCTTGCTGACATAAGAGAA
AATGAACAGAGCCTCCTGGAATACCTAGAGAAACAGCGCAACAGAATTGGCTGTAGGACCATAGTCTATTGGGGG
ATTGGTAGGAACCGTTACCAGCTGGAAATTCCTGAGAATTTCACCACTCGCAATTTGCCAGAAGAATACGAGTTG
AAATCTACCAAGAAGGGCTGTAAACGATACTGGACCAAAACTATTGAAAAGAAGTTGGCTAATCTCATAAATGCT
GAAGAACGGAGGGATGTATCATTGAAGGACTGCATGCGGCGACTGTTCTATAACTTTGATAAAAATTACAAGGAC
TGGCAGTCTGCTGTAGAGTGTATCGCAGTGTTGGATGTTTTACTGTGCCTGGCTAACTATAGTCGAGGGGGTGAT
GGTCCTATGTGTCGCCCAGTAATTCTGTTGCCGGAAGATACCCCCCCCTTCTTAGAGCTTAAAGGATCACGCCAT
CCTTGCATTACGAAGACTTTTTTTGGAGATGATTTTATTCCTAATGACATTCTAATAGGCTGTGAGGAAGAGGAG
CAGGAAAATGGCAAAGCCTATTGTGTGCTTGTTACTGGACCAAATATGGGGGGCAAGTCTACGCTTATGAGACAG
GCTGGCTTATTAGCTGTAATGGCCCAGATGGGTTGTTACGTCCCTGCTGAAGTGTGCAGGCTCACACCAATTGAT

FIGURE 744B

AGAGTGTTTACTAGACTTGGTGCCTCAGACAGAATAATGTCAGGTGAAAGTACATTTTTTGTTGAATTAAGTGAA
ACTGCCAGCATACTCATGCATGCAACAGCACATTCTCTGGTGCTTGTGGATGAATTAGGAAGAGGTACTGCAACA
TTTGATGGGACGGCAATAGCAAATGCAGTTGTTAAAGAACTTGCTGAGACTATAAAATGTCGTACATTATTTTCA
ACTCACTACCATTCATTAGTAGAAGATTATTCTCAAAATGTTGCTGTGCGCCTAGGACATATGGCATGCATGGTA
GAAAATGAATGTGAAGACCCCAGCCAGGAGACTATTACGTTCCTCTATAAATTCATTAAGGGAGCTTGTCCTAAA
AGCTATGGCTTTAATGCAGCAAGGCTTGCTAATCTCCCAGAGGAAGTTATTCAAAAGGGACATAGAAAAGCAAGA
GAATTTGAGAAGATGAATCAGTCACTACGATTATTTCGGGAAGTTTGCCTGGCTAGTGAAAGGTCAACTGTAGAT
GCTGAAGCTGTCCATAAATTGCTGACTTTGATTAAGGAATTATAGACTGACTACATTGGAAGCTTTGAGTTGACT
TCTGACCAAAGGTGGTAAATTCAGACAACATTATGATCTAATAAACTTTATTTTTAAAAATGA

FIGURE 745

MSRQSTLYSFFPKSPALSDANKASARASREGGRAAAAPGASPSPGGDAAWSEAGPGPRPLARSASPPKAKNLNGG
LRRSVAPAAPTSCDFSPGDLVWAKMEGYPWWPCLVYNHPFDGTFIREKGKSVRVHVQFFDDSPTRGWVSKRLLKP
YTGSKSKEAQKGGHFYSAKPEILRAMQRADEALNKDKIKRLELAVCDEPSEPEEEEEMEVGTTYVTDKSEEDNEI
ESEEEVQPKTQGSRRSSRQIKKRRVISDSESDIGGSDVEFKPDTKEEGSSDEISSGVGDSESEGLNSPVKVARKR
KRMVTGNGSLKRKSSRKETPSATKQATSISSETKNTLRAFSAPQNSESQAHVSGGGDDSSRPTVWYHETLEWLKE
EKRRDEHRRRPDHPDFDASTLYVPEDFLNSCTPGMRKWWQIKSQNFDLVICYKVGKFYELYHMDALIGVSELGLV
FMKGNWAHSGFPEIAFGRYSDSLVQKGYKVARVEQTETPEMMEARCRKMAHISKYDRVVRREICRIITKGTQTYS
VLEGDPSENYSKYLLSLKEKEEDSSGHTRAYGVCFVDTSLGKFFIGQFSDDRHCSRFRTLVAHYPPVQVLFEKGN
LSKETKTILKSSLSCSLQEGLIPGSQFWDASKTLRTLLEEEYFREKLSDGIGVMLPQVLKGMTSESDSIGLTPGE
KSELALSALGGCVFYLKKCLIDQELLSMANFEEYIPLDSDTVSTTRSGAIFTKAYQRMVLDAVTLNNLEIFLNGT
NGSTEGTLLERVDTCHTPFGKRLLKQWLCAPLCNHYAINDRLDAIEDLMVVPDKISEVVELLKKLPDLERLLSKI
HNVGSPLKSQNHPDSRAIMYEETTYSKKKIIDFLSALEGFKVMCKIIGIMEEVADGFKSKILKQVISLQTKNPEG
RFPDLTVELNRWDTAFDHEKARKTGLITPKAGFDSDYDQALADIRENEQSLLEYLEKQRNRIGCRTIVYWGIGRN
RYQLEIPENFTTRNLPEEYELKSTKKGCKRYWTKTIEKKLANLINAEERRDVSLKDCMRRLFYNFDKNYKDWQSA
VECIAVLDVLLCLANYSRGGDGPMCRPVILLPEDTPPFLELKGSRHPCITKTFFGDDFIPNDILIGCEEEEQENG
KAYCVLVTGPNMGGKSTLMRQAGLLAVMAQMGCYVPAEVCRLTPIDRVFTRLGASDRIMSGESTFFVELSETASI
LMHATAHSLVLVDELGRGTATFDGTAIANAVVKELAETIKCRTLFSTHYHSLVEDYSQNVAVRLGHMACMVENEC
EDPSQETITFLYKFIKGACPKSYGFNAARLANLPEEVIQKGHRKAREFEKMNQSLRLFREVCLASERSTVDAEAV
HKLLTLIKEL

FIGURE 746A

GTGAGCTGAAGCAGGGCAGGGCATCAACTCACCCAGGAAGTGCAAGGGGTTTGGGGATTTTCCTTTCCTAGCCAA
GGGAAGGCATGACAGACTGTACCTGGAAAAACAGGACACTCTTGCCCAAATACTGCACTTTTTGCACAGTCTTAG
CAACTGGCAGACCAGGAGATTCTCTCCTGTGCCTGATTCATTGGGTCCCACACCCATAGGGCCTTGCTTACTGCC
AGTGCAGCAGTCTGAGATTAACACCCCATCCCCGGGAGAACTCTAAGAAGGAGCTGATGTGGAGGAGCAGCTGAG
ACAGTTCAAG**ATG**ACGACCACAGTAGCCACAGACTATGACAACATTGAGATCCAGCAGCAGTACAGTGATGTCAA
CAACCGCTGGGATGTCGACGACTGGGACAATGAGAACAGCTCTGCGCGGCTTTTTGAGCGGTCCCGCATCAAGGC
TCTGGCAGATGAGCGTGAAGCCGTGCAGAAGAAGACCTTCACCAAGTGGGTCAATTCCCACCTTGCCCGTGTGTC
CTGCCGGATCACAGACCTGTACACTGACCTTCGAGATGGACGGATGCTCATCAAGCTGCTGGAGGTCCTCTCTGG
AGAGAGGCTGCCTAAACCCACCAAGGGACGAATGCGCATCCACTGCTTAGAGAATGTGGACAAGGCCCTTCAGTT
CCTGAAGGAGCAGAGAGTCCATCTTGAGAACATGGGGTCCCATGACATCGTGGATGGAAACCACCGGCTGACCCT
TGGCCTCATCTGGACCATCATCCTGCGCTTCCAGATCCAGGATATCAGTGTGGAAACTGAAGACAACAAAGAGAA
GAAATCTGCCAAGGATGCATTGCTGTTGTGGTGCCAGATGAAGACAGCTGGGTACCCCAATGTCAACATTCACAA
TTTCACCACTAGCTGGAGGGACGGCATGGCCTTCAATGCACTGATACACAAACACCGGCCTGACCTGATAGATTT
TGACAAACTAAAGAAATCTAACGCACACTACAACCTGCAGAATGCATTTAATCTGGCAGAACAGCACCTCGGCCT
CACTAAACTGTTGGACCCCGAAGACATCAGCGTGGACCATCCTGATGAGAAGTCCATAATCACTTATGTGGTGAC
TTATTACCACTACTTCTCTAAGATGAAGGCCTTAGCTGTTGAAGGAAAACGAATTGGAAAGGTGCTTGACAATGC
TATTGAAACAGAAAAAATGATTGAAAAGTATGAATCACTTGCCTCTGACCTTCTGGAATGGATTGAACAAACCAT
CATCATTCTGAACAATCGCAAATTTGCCAATTCACTGGTCGGGGTTCAACAGCAGCTTCAGGCATTCAACACTTA
CCGCACTGTGGAGAAACCACCCAAATTTACTGAGAAGGGGAACTTGGAAGTGCTGCTCTTCACCATTCAGAGCAA
GATGAGGGCCAACAACCAGAAGGTCTACATGCCCCGGGAGGGGAAGCTCATCTCTGACATCAACAAGGCCTGGGA
AAGACTGGAAAAAGCGGAACACGAAAGAGAACTGGCTTTGCGGAATGAGCTCATAAGACAGGAGAAACTGGAACA
GCTCGCCCGCAGATTTGATCGCAAGGCAGCTATGAGGGAGACTTGGCTGAGCGAAAACCAGCGTCTGGTGTCTCA
GGACAACTTTGGGTTTGACCTTCCTGCAGTTGAGGCCGCCACAAAAAAGCACGAGGCCATTGAGACAGACATTGC
CGCATACGAGGAGCGTGTGCAGGCTGTGGTAGCCGTGGCCAGGGAGCTCGAGGCCGAGAATTACCACGACATCAA
GCGCATCACAGCGAGGAAGGACAATGTCATCCGGCTCTGGGAATACCTACTGGAACTGCTCAGGGCCCGGAGACA
GCGGCTCGAGATGAACCTGGGGCTGCAGAAGATATTCCAGGAAATGCTCTACATTATGGACTGGATGGATGAAAT
GAAGGTGCTAGTATTGTCTCAAGACTATGGCAAACACTTACTTGGTGTGGAAGACCTGTTACAGAAGCACACCCT
GGTTGAAGCAGACATTGGCATCCAGGCAGAGCGGGTGAGAGGTGTCAATGCCTCCGCCCAGAAGTTCGCAACAGA
CGGGGAAGGTTACAAGCCCTGTGACCCCCAGGTGATCCGAGACCGCGTGGCCCACATGGAGTTCTGTTATCAAGA
GCTTTGCCAGCTGGCGGCTGAGCGCAGGGCCCGTCTGGAAGAGTCCCGCCGCCTCTGGAAGTTCTTCTGGGAGAT
GGCAGAAGAGGAAGGCTGGATACGGGAGAAGGAGAAGATCCTGTCCTCGGACGATTACGGGAAAGACCTGACCAG
CGTCATGCGCCTGCTCAGCAAGCACCGGGCGTTCGAGGACGAGATGAGCGGCCGCAGTGGCCACTTTGAGCAGGC
CATCAAGGAAGGCGAAGACATGATCGCGGAGGAGCACTTCGGGTCGGAGAAGATCCGTGAGAGGATCATTTACAT
CCGGGAGCAGTGGGCCAACCTAGAGCAGCTCTCGGCCATTCGGAAGAAGCGCCTGGAGGAGGCCTCCCTGCTGCA
CCAGTTCCAGGCAGATGCTGATGACATTGATGCCTGGATGCTGGACATCCTCAAGATTGTCTCCAGCAGCGACGT
GGGCCACGATGAGTATTCCACACAGTCTCTGGTCAAGAAACACAAGGACGTGGCGGAAGAGATCGCCAATTACAG
GCCCACCCTTGACACGCTGCACGAACAAGCCAGCGCCCTCCCCCAGGAGCATGCCGAGTCTCCAGACGTGAGGGG
CAGGCTGTCGGGCATCGAGGAGCGGTATAAGGAGGTGGCAGAGCTGACGCGGCTGCGGAAGCAGGCACTCCAGGA
CACTCTGGCCCTGTACAAGATGTTCAGCGAGGCTGATGCCTGTGAGCTCTGGATCGACGAGAAGGAGCAGTGGCT
CAACAACATGCAGATCCCAGAGAAGCTGGAGGATCTGGAGGTCATCCAGCACAGATTTGAGAGCCTAGAACCAGA
AATGAACAACCAGGCTTCCCGGGTTGCAGTGGTGAACCAGATTGCACGCCAGCTGATGCACAGCGGCCACCCAAG
TGAGAAGGAAATCAAAGCCCAGCAGGACAAACTCAACACAAGGTGGAGCCAGTTCAGAGAACTGGTTGACAGGAA
GAAGGATGCCCTCCTGTCTGCCCTGAGCATCCAGAACTACCACCTCGAGTGCAATGAAACCAAATCCTGGATTCG
GGAAAAGACCAAGGTCATCGAGTCCACCCAGGACCTGGGCAATGACCTGGCTGGCGTCATGGCCCTGCAGCGCAA
GCTGACCGGCATGGAGCGGGACTTGGTGGCCATTGAGGCAAAGCTGAGTGACCTGCAGAAGGAGGCGGAGAAGCT
GGAGTCCGAGCACCCCGACCAGGCCCAGGCCATCCTGTCTCGGCTGGCCGAGATCAGCGACGTGTGGGAGGAGAT
GAAGACCACCCTGAAAAACCGAGAGGCCTCCCTGGGAGAGGCCAGCAAGCTGCAGCAGTTCCTACGGGACTTGGA
CGACTTCCAGTCCTGGCTCTCTAGGACCCAGACAGCGATCGCCTCGGAGGACATGCCAAACACCCTGACCGAGGC

FIGURE 746B

TGAGAAGCTGCTCACGCAGCACGAGAACATCAAGAATGAGATCGACAACTACGAGGAGGACTACCAGAAGATGAG
GGACATGGGCGAGATGGTCACCCAGGGGCAGACCGATGCCCAGTACATGTTTCTGCGGCAGCGGCTGCAGGCCCT
GGACACTGGATGGAACGAGCTCCACAAGATGTGGGAGAACAGACAAAATCTCCTATCCCAGTCACATGCCTACCA
GCAGTTCCTCAGAGACACGAAGCAAGCCGAAGCCTTTCTTAACAACCAGGAGTATGTTCTGGCTCACACTGAAAT
GCCTACCACCTTGGAAGGAGCTGAAGCAGCAATTAAAAAGCAAGAGGACTTCATGACCACCATGGACGCCAATGA
GGAGAAGATCAATGCTGTGGTGGAGACTGGCCGGAGGCTGGTGAGCGATGGGAACATCAACTCAGATCGCATCCA
GGAGAAGGTGGACTCTATTGATGACAGACATAGGAAGAATCGTGAGACAGCCAGTGAACTTTTGATGAGGTTGAA
GGACAACAGGGATCTACAGAAATTCCTGCAAGATTGTCAAGAGCTGTCTCTCTGGATCAATGAGAAGATGCTCAC
AGCCCAGGACATGTCTTACGATGAAGCCAGAAATCTGCACAGTAAATGGTTGAAGCATCAAGCATTTATGGCAGA
ACTTGCATCCAACAAAGAATGGCTTGACAAAATCGAGAAGGAAGGAATGCAGCTCATTTCAGAAAAGCCTGAGAC
GGAAGCTGTGGTGAAGGAGAAACTCACTGGTTTACATAAAATGTGGGAAGTCCTTGAATCCACTACCCAGACAAA
GGCCCAGCGGCTCTTTGATGCAAACAAGGCCGAACTTTTCACCCAGAGCTGTGCAGATCTAGACAAATGGCTGCA
CGGCCTGGAGAGTCAGATTCAGTCTGATGACTATGGCAAACACCTGACCAGTGTCAATATCCTGCTGAAAAAGCA
ACAGATGCTGGAGAATCAGATGGAAGTGCGGAAGAAGGAGATCGAAGAGCTCCAAAGCCAAGCCCAGGCCCTGAG
TCAGGAAGGGAAGAGCACCGACGAGGTAGACAGCAAGCGCCTCACCGTGCAGACCAAGTTCATGGAGTTGCTGGA
GCCCTTGAACGAGAGGAAGCATAACCTGCTGGCCTCCAAAGAGATCCATCAGTTCAACAGGGATGTGGAGGACGA
GATCTTGTGGGTTGGAGAGAGGATGCCTTTGGCAACTTCCACGGATCATGGCCACAACCTCCAGACTGTGCAGCT
GTTAATAAAGAAAAATCAGACCCTCCAGAAAGAAATCCAGGGGCACCAGCCTCGCATTGACGACATCTTTGAGAG
GAGCCAAAACATCGTCACTGACAGCAGCAGCCTCAGCGCTGAGGCCATCAGACAGAGGCTTGCCGACCTGAAGCA
GCTGTGGGGTCTCCTCATTGAGGAGACAGAGAAACGCCACAGGCGGCTGGAGGAGGCGCACAGGGCCCAGCAGTA
CTACTTTGACGCTGCTGAGGCCGAAGCCTGGATGAGCGAGCAGGAGCTGTACATGATGTCAGAGGAGAAGGCCAA
GGATGAGCAGAGTGCTGTCTCCATGTTGAAGAAGCACCAGATCTTAGAACAAGCTGTGGAGGACTATGCAGAGAC
CGTGCATCAGCTCTCCAAGACCAGCCGGGCCCTGGTGGCCGACAGCCATCCTGAAAGTGAGCGCATTAGCATGCG
GCAGTCCAAAGTGGATAAACTGTACGCTGGTCTGAAAGACCTTGCTGAAGAGAGAAGAGGCAAGCTGGATGAGAG
ACACAGGTTATTCCAGCTCAACCGGGAGGTGGACGACCTGGAGCAGTGGATCGCTGAGAGGGAGGTGGTCGCAGG
GTCCCATGAACTGGGACAGGACTATGAGCATGTCACGATGTTACAAGAACGATTCCGGGAGTTTGCCCGAGACAC
CGGGAACATTGGGCAGGAGCGCGTGGACACGGTCAATCACCTGGCAGATGAGCTCATCAACTCTGGACATTCAGA
TGCCGCCACCATCGCTGAATGGAAGGATGGCCTCAATGAAGCCTGGGCCGACCTCCTGGAGCTCATTGACACAAG
AACACAGATTCTTGCCGCTTCCTATGAACTGCACAAGTTTTACCACGATGCCAAGGAGATCTTTGGGCGTATACA
GGACAAACACAAGAAACTCCCTGAGGAGCTTGGGAGAGATCAGAACACAGTGGAGACCTTACAGAGAATGCACAC
TACATTTGAGCATGACATCCAGGCTCTGGGCACACAGGTGAGGCAGCTGCAGGAGGATGCAGCCCGCCTCCAGGC
GGCCTATGCGGGTGACAAGGCCGACGATATCCAGAAGCGCGAGAACGAGGTCCTGGAAGCCTGGAAGTCCCTCCT
GGACGCCTGTGAGAGCCGCAGGGTGCGGCTGGTGGACACAGGGGACAAGTTCCGCTTCTTCAGCATGGTGCGCGA
CCTCATGCTCTGGATGGAGGATGTCATCCGGCAGATCGAGGCCCAGGAGAAGCCAAGGGATGTATCATCTGTTGA
ACTCTTAATGAATAATCATCAAGGCATCAAAGCTGAAATTGATGCACGTAATGACAGTTTCACAACCTGCATTGA
ACTTGGGAAATCCCTGTTGGCGAGAAAACACTATGCATCTGAGGAGATCAAGGAAAAATTACTGCAGTTGACGGA
AAAGAGGAAAGAAATGATCGACAAGTGGGAAGACCGATGGGAATGGTTAAGACTGATTCTGGAGGTCCATCAGTT
CTCAAGAGACGCCAGTGTGGCCGAGGCCTGGCTGCTTGGACAGGAGCCGTACCTATCCAGCCGAGAGATAGGCCA
GAGCGTGGACGAGGTGGAGAAGCTCATCAAGCGCCACGAGGCATTTGAAAAGTCTGCAGCAACCTGGGATGAGAG
GTTCTCTGCCCTGGAAAGGCTGACTACATTGGAGTTACTGGAAGTGCGCAGACAGCAAGAGGAAGAGGAGAGGAA
GAGGCGGCCGCCTTCTCCCGAGCCGAGCACGAAGGTTTCAGAGGAAGCCGAGTCCCAGCAGCAGTGGGATACTTC
AAAAGGAGAACAAGTTTCCCAAAACGGTTTGCCAGCTGAACAGGGATCTCCACGGATGGCAGAAACGGTGGACAC
AAGCGAAATGGTCAACGGCGCTACAGAACAAAGGACGAGCTCTAAAGAGTCCAGCCCCATCCCCTCCCCGACCTC
TGATCGTAAAGCCAAGACTGCCCTCCCAGCCCAGAGTGCCGCCACCTTACCAGCCAGAACCCAGGAGACACCTTC
GGCCCAGATGGAAGGCTTCCTCAATCGGAAACACGAGTGGGAGGCCCACAATAAGAAAGCCTCAAGCAGGTCCTG
GCACAATGTTTATTGTGTCATAAATAACCAAGAAATGGGTTTCTACAAAGATGCAAAGACTGCTGCTTCTGGAAT
TCCCTACCACAGCGAGGTCCCTGTGAGTTTGAAAGAAGCTGTCTGCGAAGTGGCCCTTGATTACAAAAAGAAGAA
ACACGTATTCAAGCTAAGACTAAATGATGGCAATGAGTACCTCTTCCAAGCCAAAGACGATGAGGAAATGAACAC

FIGURE 746C

ATGGATCCAGGCTATCTCTTCCGCCATCTCCTCTGATAAACACGAGGTGTCTGCCAGCACCCAGAGCACGCCAGC
ATCCAGCCGCGCGCAGACCCTCCCCACCAGCGTCGTCACCATCACCAGCGAGTCCAGTCCCGGCAAGCGGGAAAA
GGACAAAGAGAAAGACAAAGAGAAGCGGTTCAGCCTTTTTGGCAAAAAGAAA**TGA**ACTCCTTTCCTTCACCTCCT
GCCCTTCTCTTACCTTTTCAGTGAAATTCCAGCATGCAAGCTCAGAACCAACACATTACTCTCTGTGCCTAATGT
TCCTCAATGTGGTTGATTTATTTTTTTTTTTAATTTATAGAGCATTTCGGGGGGGGTGGGG

FIGURE 747

MTTTVATDYDNIEIQQQYSDVNNRWDVDDWDNENSSARLFERSRIKALADEREAVQKKTFTKWVNSHLARVSCRI
TDLYTDLRDGRMLIKLLEVLSGERLPKPTKGRMRIHCLENVDKALQFLKEQRVHLENMGSHDIVDGNHRLTLGLI
WTIILRFQIQDISVETEDNKEKKSAKDALLLWCQMKTAGYPNVNIHNFTTSWRDGMAFNALIHKHRPDLIDFDKL
KKSNAHYNLQNAFNLAEQHLGLTKLLDPEDISVDHPDEKSIITYVVTYYHYFSKMKALAVEGKRIGKVLDNAIET
EKMIEKYESLASDLLEWIEQTIIILNNRKFANSLVGVQQQLQAFNTYRTVEKPPKFTEKGNLEVLLFTIQSKMRA
NNQKVYMPREGKLISDINKAWERLEKAEHERELALRNELIRQEKLEQLARRFDRKAAMRETWLSENQRLVSQDNF
GFDLPAVEAATKKHEAIETDIAAYEERVQAVVAVARELEAENYHDIKRITARKDNVIRLWEYLLELLRARRQRLE
MNLGLQKIFQEMLYIMDWMDEMKVLVLSQDYGKHLLGVEDLLQKHTLVEADIGIQAERVRGVNASAQKFATDGEG
YKPCDPQVIRDRVAHMEFCYQELCQLAAERRARLEESRRLWKFFWEMAEEEGWIREKEKILSSDDYGKDLTSVMR
LLSKHRAFEDEMSGRSGHFEQAIKEGEDMIAEEHFGSEKIRERIIYIREQWANLEQLSAIRKKRLEEASLLHQFQ
ADADDIDAWMLDILKIVSSSDVGHDEYSTQSLVKKHKDVAEEIANYRPTLDTLHEQASALPQEHAESPDVRGRLS
GIEERYKEVAELTRLRKQALQDTLALYKMFSEADACELWIDEKEQWLNNMQIPEKLEDLEVIQHRFESLEPEMNN
QASRVAVVNQIARQLMHSGHPSEKEIKAQQDKLNTRWSQFRELVDRKKDALLSALSIQNYHLECNETKSWIREKT
KVIESTQDLGNDLAGVMALQRKLTGMERDLVAIEAKLSDLQKEAEKLESEHPDQAQAILSRLAEISDVWEEMKTT
LKNREASLGEASKLQQFLRDLDDFQSWLSRTQTAIASEDMPNTLTEAEKLLTQHENIKNEIDNYEEDYQKMRDMG
EMVTQGQTDAQYMFLRQRLQALDTGWNELHKMWENRQNLLSQSHAYQQFLRDTKQAEAFLNNQEYVLAHTEMPTT
LEGAEAAIKKQEDFMTTMDANEEKINAVVETGRRLVSDGNINSDRIQEKVDSIDDRHRKNRETASELLMRLKDNR
DLQKFLQDCQELSLWINEKMLTAQDMSYDEARNLHSKWLKHQAFMAELASNKEWLDKIEKEGMQLISEKPETEAV
VKEKLTGLHKMWEVLESTTQTKAQRLFDANKAELFTQSCADLDKWLHGLESQIQSDDYGKHLTSVNILLKKQQML
ENQMEVRKKEIEELQSQAQALSQEGKSTDEVDSKRLTVQTKFMELLEPLNERKHNLLASKEIHQFNRDVEDEILW
VGERMPLATSTDHGHNLQTVQLLIKKNQTLQKEIQGHQPRIDDIFERSQNIVTDSSSLSAEAIRQRLADLKQLWG
LLIEETEKRHRRLEEAHRAQQYYFDAAEAEAWMSEQELYMMSEEKAKDEQSAVSMLKKHQILEQAVEDYAETVHQ
LSKTSRALVADSHPESERISMRQSKVDKLYAGLKDLAEERRGKLDERHRLFQLNREVDDLEQWIAEREVVAGSHE
LGQDYEHVTMLQERFREFARDTGNIGQERVDTVNHLADELINSGHSDAATIAEWKDGLNEAWADLLELIDTRTQI
LAASYELHKFYHDAKEIFGRIQDKHKKLPEELGRDQNTVETLQRMHTTFEHDIQALGTQVRQLQEDAARLQAAYA
GDKADDIQKRENEVLEAWKSLLDACESRRVRLVDTGDKFRFFSMVRDLMLWMEDVIRQIEAQEKPRDVSSVELLM
NNHQGIKAEIDARNDSFTTCIELGKSLLARKHYASEEIKEKLLQLTEKRKEMIDKWEDRWEWLRLILEVHQFSRD
ASVAEAWLLGQEPYLSSREIGQSVDEVEKLIKRHEAFEKSAATWDERFSALERLTTLELLEVRRQQEEEERKRRP
PSPEPSTKVSEEAESQQQWDTSKGEQVSQNGLPAEQGSPRMAETVDTSEMVNGATEQRTSSKESSPIPSPTSDRK
AKTALPAQSAATLPARTQETPSAQMEGFLNRKHEWEAHNKKASSRSWHNVYCVINNQEMGFYKDAKTAASGIPYH
SEVPVSLKEAVCEVALDYKKKKHVFKLRLNDGNEYLFQAKDDEEMNTWIQAISSAISSDKHEVSASTQSTPASSR
AQTLPTSVVTITSESSPGKREKDKEKDKEKRFSLFGKKK

FIGURE 748

CACAACCGCCCGCGGCTCTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATCTCCACCCTCCAGC
CATGGAAGACGAGGAGGAAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCT
GGAGAGGAAGCCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTGATGGA
CTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCCCCCGTCGCCCCGGAGCGGCA
GCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCCGCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCC
CTCCAAGCTCCCTGAGGACGACGAGCCTCCGGCCCGG

FIGURE 749

TTCTTCCTTTTCGATCCGCCATCTGCGGTGGAGCCGCCACCAAA**ATG**CAGATTTTCGTGAAAACCCTTACGGGGA
AGACCATCACCCTCGAGGTTGAACCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGATAAGGAAGGAA
TTCCTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGCTGGAAGATGGACGTACTTTGTCTGACTACAATA
TTCAAAAGGAGTCTACTCTTCATCTTGTGTTGAGACTTCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACA
CCACTCCCAAGAAGAATAAGCACAAGAGAAAGAAGGTTAAGCTGGCTGTCCTGAAATATTATAAGGTGGATGAGA
ATGGCAAAATTAGTCGCCTTCGTCGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGCAAGTCACT
TTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACCAGAAGACAAG**TAA**CTGTATGAGT
TAATAAAAGACATGAACTAACAAAAA

FIGURE 750

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRG
GAKKRKKKSYTTPKKNKHKRKKVKLAVLKYYKVDENGKISRLRRECPSDECGAGVFMASHFDRHYCGKCCLTYCF
NKPEDK

FIGURE 751

GGCACGAGCAGAATCCAGGGGCCCGGGGCTGTAGATTCCTTGACAAGGATATCCTAGCGGCGAAACAACACCGTA
CTGGGAGTCAGAACGTCTGGGTTCTAGTCTTGACTGCCATTAACTAGCGGTATGACATTGGAGAAGCTTTTTTGA
CCCTTCTGGATTTCCGTTTCCTTTTCTGTAAAATGAGGAGCTTGGAAGATCCGGAAAATGAGGCCCATAGGAAAC
AAGTGACTTGCTGAGTCCAGATAACACTGACTGTCAGAGAGAAAC**ATG**AACCAGAAGCTACTGAAGTTGGAGAAC
TTGCTACGATTTCACACTATTTATAGGCAACTGCACAGTCTGTGTCAAAGAAGAGCATTAAGACAGTGGAGGCAT
GGGTTTTCATCTGCTTACCCTGTGTGGACAGCTCAACTGTGTGCCTGGCCCTGGCCAACAGATGTGCTCAATGGG
GCTGCTTTATCTCAGTATAGGCTTCTAGTAACAAAAAAGGAAGAAGGACCATGGAAATCTCAGTTATCTTCAACA
AAATCTAAAAAGGTGGTAGAAGTATGGATTGGAATGACTATTGAGGAACTGGCCAGGGCAATGGAAAAAAACACA
GATTATGTATATGAAGCTTTATTGAACACTGATATTGACATAGATTCACTGGAAGCAGACTCACATTTAGATGAA
GTCTGGATCAAAGAAGTGATAACGAAGGCAGGGATGAAGTTAAAGTGGAGTAAATTAAAACAGGACAAAGTCAGA
AAAAATAAAGATGCTGTAAGAAGGCCCCAGGCAGATCCAGCTTTATTAACCCCAAGGTCCCCAGTTGTTACTATA
ATGGGCCATGTTGATCACGGGAAAACGACATTACTTGACAAATTTCGAAAAACTCAAGTGGCAGCAGTGGAAACT
GGAGGCATCACTCAGCACATTGGTGCCTTTCTTGTCTCTCTGCCTTCTGGGGAAAAGATAACTTTTCTTGATACT
CCAGGACATGCTGCTTTCTCAGCAATGAGAGCCAGAGGTGCTCAGGTCACTGACATTGTCGTATTGGTTGTAGCT
GCAGATGATGGAGTGATGAAACAAACTGTAGAATCTATTCAGCATGCCAAAGATGCACAGGTTCCTATTATCCTT
GCCGTAAATAAATGTGACAAAGCTGAGGCTGATCCTGAGAAAGTGAAAAAAGAGCTGCTGGCTTACGATGTGGTA
TGTGAAGATTATGGAGGTGATGTTCAAGCAGTGCCTGTCTCCGCACTTACGGGCGATAATCTGATGGCTTTGGCA
GAAGCAACAGTTGCTCTTGCAGAAATGTTAGAATTGAAAGCAGATCCCAATGGTCCAGTGGAAGGAACAGTAATA
GAGTCTTTCACAGACAAAGGAAGAGGTCTTGTTACTACAGCTATAATTCAAAGAGGAACTTTAAGAAAAGGCTCT
GTTCTGGTTGCTGGAAAATGTTGGGCAAAAGTACGCTTAATGTTTGATGAAAATGGAAAAACAATTGATGAGGCC
TATCCCAGCATGCCAGTGGGAATTACAGGCTGGAGAGACCTTCCTTCTGCAGGAGAAGAAATTCTTGAAGTAGAA
TCTGAGCCAAGGGCACGTGAAGTTGTTGACTGGAGGAAATATGAACAAGAACAGGAGAAAGGTCAGGAGGATCTG
AAAATAATAGAAGAAAAGCGAAAGGAACACAAAGAAGCACATCAGAAAGCCCGTGAGAAGTATGGCCATCTACTG
TGGAAGAAGAGATCAATTCTACGGTTTTTAGAAAGAAAAGAACAAATACCCTTAAAGCCAAAAGAGAAAAGGGAA
AGAGATTCAAATGTACTTTCTGTGATTATTAAAGGTGATGTTGATGGTTCTGTTGAGGCCATTTTGAACATTATA
GATACCTATGATGCTTCACACGAGTGTGAACTAGAATTAGTACATTTTGGAGTGGGTGATATAAGTGCAAATGAT
GTTAACCTTGCTGAAACATTTGATGGTGTTATATATGGCTTTAATGTGAATGCAGGCAATGTTATCCAACAGTCA
GCTGCAAAAAAAGGAGTAAAAATTAAACTTCACAAAATAATTTACCGTCTTGTTGAAGATTTGCAAGAGGAACTG
AGCAGCAGATTACCCTGTGCTGTGGAAGAGCACCCAGTAGGTGAGGCATCTATACTAGCTACCTTCTCTGTAACA
GAAGGGAAGAAAAAAGTTCCTGTGGCTGGCTGCAGAGTCCAAAAGGGACAGTTAGAAAAACAAAAAAAATTTAAA
CTAACCCGTAATGGACATGTAATTTGGAAGGGCTCATTAACCTCATTGAAACACCATAAAGATGACATTTCAATT
GTCAAAACGGGAATGGATTGTGGTCTCAGTTTAGATGAAGACAATATGGAATTTCAAGTGGGAGACAGAATTGTT
TGTTATGAAGAAAAGCAAATTCAAGCCAAGACTTCTTGGGATCCAGGATTT**TAA**AATTACATTAAAAATGTAAAT
AACTCA

FIGURE 752

MNQKLLKLENLLRFHTIYRQLHSLCQRRALRQWRHGFSSAYPVWTAQLCAWPWPTDVLNGAALSQYRLLVTKKEE
GPWKSQLSSTKSKKVVEVWIGMTIEELARAMEKNTDYVYEALLNTDIDIDSLEADSHLDEVWIKEVITKAGMKLK
WSKLKQDKVRKNKDAVRRPQADPALLTPRSPVVTIMGHVDHGKTTLLDKFRKTQVAAVETGGITQHIGAFLVSLP
SGEKITFLDTPGHAAFSAMRARGAQVTDIVVLVVAADDGVMKQTVESIQHAKDAQVPIILAVNKCDKAEADPEKV
KKELLAYDVVCEDYGGDVQAVPVSALTGDNLMALAEATVALAEMLELKADPNGPVEGTVIESFTDKGRGLVTTAI
IQRGTLRKGSVLVAGKCWAKVRLMFDENGKTIDEAYPSMPVGITGWRDLPSAGEEILEVESEPRAREVVDWRKYE
QEQEKGQEDLKIIEEKRKEHKEAHQKAREKYGHLLWKKRSILRFLERKEQIPLKPKEKRERDSNVLSVIIKGDVD
GSVEAILNIIDTYDASHECELELVHFGVGDISANDVNLAETFDGVIYGFNVNAGNVIQQSAAKKGVKIKLHKIIY
RLVEDLQEELSSRLPCAVEEHPVGEASILATFSVTEGKKKVPVAGCRVQKGQLEKQKKFKLTRNGHVIWKGSLTS
LKHHKDDISIVKTGMDCGLSLDEDNMEFQVGDRIVCYEEKQIQAKTSWDPGF

FIGURE 753

GCGTGCCGGGTGTCATGGCGGCCTGCAGGTACTGCTGCTCGTGCCTCCGGCTCCGGCCCCTGAGCGATGGTCCTT
TCCTTCTGCCACGGCGGGATCGGGCACTCACCCAGTTGCAAGTGCGAGCACTATGGAGTAGCGCAGGGTCTCGAG
CTGTGGCCGTGGACTTAGGCAACAGGAAATTAGAAATATCTTCTGGAAAGCTGGCCAGATTTGCAGATGGCTCTG
CTGTAGTACAGTCAGGTGACACTGCAGTAATGGTCACAGCGGTCAGTAAAACAAAACCTTCCCCTTCCCAGTTTA
TGCCTTTGGTGGTTGACTACAGACAAAAAGCTGCTGCAGCAGGTAGAATTCCCACAAACTATCTGAGAAGAGAGA
TTGGTACTTCTGATAAAGAAATTCTAACAAGTCGAATAATAGATCGTTCAATTAGACCGCTCTTTCCAGCTGGCT
ACTTCTATGATACACAGGTTCTGTGTAATCTGTTAGCAGTAGATGGTGTAAATGAGCCTGATGTCCTAGCAATTA
ATGGCGCTTCCGTAGCCCTCTCATTATCAGATATTCCTTGGAATGGACCTGTTGGGGCAGTACGAATAGGAATAA
TTGATGGAGAATATGTTGTTAACCCAACAAGAAAAGAAATGTCTTCTAGTACTTTAAATTTAGTGGTTGCTGGAG
CACCTAAAAGTCAGATTGTCATGTTGGAAGCCTCTGCAGAGAACATTTTACAGCAGGACTTTTGCCATGCTATCA
AAGTGGGAGTGAAATATACCCAACAAATAATTCAGGGCATTCAGCAGTTGGTAAAAGAAACTGGTGTTACCAAGA
GGACACCTCAGAAGTTATTTACCCCTTCGCCAGAGATTGTGAAATATACTCATAAACTTGCTATGGAGAGACTCT
ATGCAGTTTTTACAGATTACGAGCATGACAAAGTTTCCAGAGATGAAGCTGTTAACAAAATAAGATTAGATACGG
AGGAACAACTAAAAGAAAAATTTCCAGAAGCCGATCCATATGAAATAATAGAATCCTTCAATGTTGTTGCAAAGG
AAGTTTTTAGAAGTATTGTTTTGAATGAATACAAAAGGTGCGATGGTCGGGATTTGACTTCACTTAGGAATGTAA
GTTGTGAGGTAGATATGTTTAAAACCCTTCATGGATCAGCATTATTTCAAAGAGGACAAACACAGGTGCTTTGTA
CCGTTACATTTGATTCATTAGAATCTGGTATTAAGTCAGATCAAGTTATAACAGCTATAAATGGGATAAAAGATA
AAAATTTCATGCTGCACTACGAGTTTCCTCCTTATGCAACTAATGAAATTGGCAAAGTCACTGGTTTAAATAGAA
GAGAACTTGGGCATGGTGCTCTTGCTGAGAAAGCTTTGTATCCTGTTATTCCCCGAGATTTTCCTTTCACCATAA
GAGTTACATCTGAAGTCCTAGAGTCAAATGGGTCATCTTCTATGGCATCTGCATGTGGCGGAAGTTTAGCATTAA
TGGATTCAGGGGTTCCAATTTCATCTGCTGTTGCAGGCGTAGCAATAGGATTGGTCACCAAAACCGATCCTGAGA
AGGGTGAAATAGAAGATTATCGTTTGCTGACAGATATTTTGGGAATTGAAGATTACAATGGTGACATGGACTTCA
AAATAGCTGGCACTAATAAAGGAATAACTGCATTACAGGCTGATATTAAATTACCTGGAATACCAATAAAAATTG
TGATGGAGGCTATTCAACAAGCTTCAGTGGCAAAAAAGGAGATATTACAGATCATGAACAAAACTATTTCAAAAC
CTCGAGCATCTAGAAAAGAAAATGGACCTGTTGTAGAAACTGTTCAGGTTCCATTATCAAAACGAGCAAAATTTG
TTGGACCTGGTGGCTATAACTTAAAAAAACTTCAGGCTGAAACAGGTGTAACTATTAGTCAGGTGGATGAAGAAA
CGTTTTCTGTATTTGCACCAACACCCAGTGCTATGCATGAGGCAAGAGACTTCATTACTGAAATCTGCAAGGATG
ATCAGGAGCAGCAATTAGAATTTGGAGCAGTATATACCGCCACAATAACTGAAATCAGAGATACTGGTGTAATGG
TAAAATTATATCCAAATATGACTGCGGTACTGCTTCATAACACACAACTTGATCAACGAAAGATTAAACATCCTA
CTGCCCTAGGATTAGAAGTTGGCCAAGAAATTCAGGTGAAATACTTTGGACGTGACCCAGCCGATGGAAGAATGA
GGCTTTCTCGAAAAGTGCTTCAGTCGCCAGCTACAACCGTGGTCAGAACTTTGAATGACAGAAGTAGTATTGTAA
TGGGAGAACCTATTTCACAGTCATCATCTAATTCTCAGTGATTTTTTTTTTTAAAGAGAATTCTAGAATTCTATT
TTGTCTAGGGTGATGTGCTGTAGAGCAACATTTTAGTAGTATCTTCCATTGTGTAGATTTCTATATAATATAAAT
ACATTTTAATTATTTGTACTAAAATGCTCATTTACATGTGCCATTTTTTTAATTCGAGTAACCCATATTTGTTTA
ATTGTATTTACATTATAAATCAAGAAATATTTATTATTAAAAGTAAGTCATTTATACATCTTAGAAAAAAATTACA
TAGTTTTGTTTTTACAATTCTGAAATATATGAAAAACTTAGATAGAATATGTCATATGTTATTATAACAGATCTC
TTCCTACATCTTATTTTTCTTCTTTGTATACAGTAGTGACAGTTTACCTTCAGTCATCCTACAGGTCACCTCTGT
GCCCAACAACTTTACTTGCCTACAACGGTTCACAAACTGGAACAGGCCATATTCAAAGCCAGTGCCTATTTCTTC
AGAACTGTTAACAGATATAGTGAGTTGAGGGAGCTAATCTGATACACTTTTGATAATATAATGCCTTTCAAATTA
GTTACCAAATCATAAACAGAGTGGAATAAATATAAATGAGATTCTAACTAGGATGAATGTGGTAGTAATGATGTA
TATTTTTCAAATTTACCTAAACAGAAAGATTATTGGCTAAGGCAGGCGGATCATGAGATCAGGAGATCGAGACCA
TCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAGTGCAAAAATTAGCCGGGCGTGGTGGCGCATGCCTGTA
ATCCTAGCTACTCAGGAGGCTGAGGCAGAAGAATCACTTCAACCCAGGAGGTGGAGGTTGTAGTGAGCCGAGATT
GCGCCATTGCACTCCAGCTCAGGCAACAAGAGCAAAACTCCGTCTC

FIGURE 754

MAACRYCCSCLRLRPLSDGPFLLPRRDRALTQLQVRALWSSAGSRAVAVDLGNRKLEISSGKLARFADGSAVVQS
GDTAVMVTAVSKTKPSPSQFMPLVVDYRQKAAAAGRIPTNYLRREIGTSDKEILTSRIIDRSIRPLFPAGYFYDT
QVLCNLLAVDGVNEPDVLAINGASVALSLSDIPWNGPVGAVRIGIIDGEYVVNPTRKEMSSSTLNLVVAGAPKSQ
IVMLEASAENILQQDFCHAIKVGVKYTQQIIQGIQQLVKETGVTKRTPQKLFTPSPEIVKYTHKLAMERLYAVFT
DYEHDKVSRDEAVNKIRLDTEEQLKEKFPEADPYEIIESFNVVAKEVFRSIVLNEYKRCDGRDLTSLRNVSCEVD
MFKTLHGSALFQRGQTQVLCTVTFDSLESGIKSDQVITAINGIKDKNFMLHYEFPPYATNEIGKVTGLNRRELGH
GALAEKALYPVIPRDFPFTIRVTSEVLESNGSSSMASACGGSLALMDSGVPISSAVAGVAIGLVTKTDPEKGEIE
DYRLLTDILGIEDYNGDMDFKIAGTNKGITALQADIKLPGIPIKIVMEAIQQASVAKKEILQIMNKTISKPRASR
KENGPVVETVQVPLSKRAKFVGPGGYNLKKLQAETGVTISQVDEETFSVFAPTPSAMHEARDFITEICKDDQEQQ
LEFGAVYTATITEIRDTGVMVKLYPNMTAVLLHNTQLDQRKIKHPTALGLEVGQEIQVKYFGRDPADGRMRLSRK
VLQSPATTVVRTLNDRSSIVMGEPISQSSSNSQ

FIGURE 755

GACAAG**<u>ATG</u>**GCCACACCGGCGGTACCAGCAAGTGCTCCTCCGGCCACGCCAGCCCCAGTCCCGGCGGCGGTCCCA
GCCTCTGCCCCAGCCTCAGTTCCAGCGCCAACGCCAGCACCGGCTGCGGCTCCGGTTCCCGCTGCGGCTCCAGCC
TCATCCTCAGACCCTGCGGCAGCATCGGCTACAACTGCGGCTCCTGGCCAGACCCCGGCCTCAGCGCAAGCTCCA
GCGCAGACCCCAGCGCCCGCTCTGCCTGGTCCTGCTCTTCCAGGGCCCTTCCCCGGCGGCCGCGTGGTCAGGCTG
CACCCAGTCATTTTGGCCTCCATTGTGGACAGCTACGAGAGACGCAACGAGGGTGCTGCCCGAGTTATCGGGACC
CTGTTGGGAACTGTCGACAAACACTCAGTGGAGGTCACCAATTGCTTTTCAGTGCCGCACAATGAGTCAGAAGAT
GAAGTGGCTGTTGACATGGAATTTGCTAAGAATATGTATGAACTGCATAAAAAAGTTTCTCCAAATGAGCTCATC
CTGGGCTGGTACGCTACAGGCCATGACATCACAGAGCACTCTGTGCTGATCCATGAGTACTACAGCCGAGAGGCC
CCCAACCCCATCCACCTCACTGTGGACACAAGTCTCCAGAACGGCCGCATGAGCATCAAAGCCTATGTCAGCACT
TTAATGGGTGTCCCTGGGAGGACCATGGGAGTGATGTTCACACCTCTGACAGTGAAATACGCATACTATGACACT
GAACGCATCGGAGTTGAGCTGATCATGAAGACCTGCTTTAGCCCCAACAGAGTGATTGGACTCTTAAGTGACTTG
CAGCAAGTAGGAGGGGCATCAGCTCGCATCCAGGATGCCCTGAGTACAGTGTTGCAATATGCAGAGGATGTACTG
TCTGGAAAGGTGTCAGCTGACAATACTGTGGGCCGCTTCCTGATGAGCCTGGTTAACCGAGTACCGAAAATAGTT
CCCGATGACTTTGAGACCATGCTCAACAGCAACATCAATGACCTTTTGATGGTGACCTACCTGGCCAACCTCACA
CAGTCACAGATTGCCCTCAATGAAAAACTTGTAAACCTG**<u>TGA</u>**ATGGACCCCAAGCAGTACACTTGCTGGTCTAGG
TATTAACCCCAGGACTCAGAAGTGAAGGAGAAATGGGTTTTTGTGGTCTTGAGTCACACTGAGATAGTCAGTTG
TGTGTGACTCTAATAAACGGAGCCTACCTTTTGT

FIGURE 756

MATPAVPASAPPATPAPVPAAVPASAPASVPAPTPAPAAAPVPAAAPASSSDPAAASATTAAPGQTPASAQAPAQ
TPAPALPGPALPGPFPGGRVVRLHPVILASIVDSYERRNEGAARVIGTLLGTVDKHSVEVTNCFSVPHNESEDEV
AVDMEFAKNMYELHKKVSPNELILGWYATGHDITEHSVLIHEYYSREAPNPIHLTVDTSLQNGRMSIKAYVSTLM
GVPGRTMGVMFTPLTVKYAYYDTERIGVELIMKTCFSPNRVIGLLSDLQQVGGASARIQDALSTVLQYAEDVLSG
KVSADNTVGRFLMSLVNRVPKIVPDDFETMLNSNINDLLMVTYLANLTQSQIALNEKLVNL

FIGURE 757

GTTGGAGACTCGATTGTTGATGACAGCGGAAGAATGATAACAAA**ATG**CCGGAGCGAGATAGTGAGCCGTTCTCCA
ACCCTTTGGCCCCTGATGGCCACGATGTGGATGATCCTCACTCCTTCCACCAATCAAAACTCACCAATGAAGACT
TCAGGAAACTTCTCATGACCCCCAGGGCTGCACCTACCTCTGCACCACCTTCTAAGTCACGTCACCATGAGATGC
CAAGGGAGTACAATGAGGATGAAGACCCAGCTGCACGAAGGAGGAAAAAGAAAAGTTATTATGCTAAGCTACGCC
AACAAGAAATTGAGAGAGAGAGAGAGCTAGCAGAGAAGTACCGGGGTCGTGCCAAGGAACGGAGAGATGGAGTGA
ACAAAGATTATGAAGAAACCGAGCTTATCAACACCACAGCTAACTACAGGGCTGTTGGCCCCACTACTAAGGCGG
ACAAATCAGCTGCAGAGAAGAGAAGACAGTTGATCCAGGAGTCCAAATTCTTGGGTGGTGACATGGAACACACCC
ATTTGGTGAAAGGCTTGGATTTTGCTCTGCTTCAAAAGGTACGAGCTGAGATTGCCAGCAAAGAGAAAGAGGAAG
AGGAACTGATGGAAAAGCCCCAGAAAGAAACCAAGAAAGATGAGGATCCTGAAAATAAAATTGAATTTAAAACAC
GTCTGGGCCGCAATGTTTACCGAGTGCTTTTTAAGAACAAGCATATAAGCGGAATGAGTTGTTCCTGCCGGGCCG
CATGGCCTATGTGG**TAG**GCCTGGATGATGAGTAAGCTGACACAGATATCCCCACCACTCTTATCCGCAGCAAGGT
TGACTGCCCCACCATGGAGGCCCAGACCATACTGACCACAAATGATATTGTCATTAGCAAGCTTACCCAGTTGCT
TTCATACCTGAGGCAGGGAACCCGTAACAAGAAGCTTAAGAAGAAGGATAAAGGGAAGCTGGAAGAGAAGAAACC
TGCTGAGGCTGACAGGAGTATTTTCGAAGACATTGGGGATTATACACCCTCCACAATCAAGACACCTTGGGACAA
GGAGCGGGAGAGATATCGGGAACGGGAGCGTGATCAGGAGACAGAGACCGTGACCGAGAGCGAGAGCGAGAACGA
GATCAGGAGCGAGAACGAGATCGGGAACGAGAGAGAGAAGAGGAAAAGAAGAGACACAGCTACTTTGAGAAGCCA
AAAGTACATGATGAGTCCGTGGACGTTGACAAAGGACCTGGGTCGGCCAAGGAGTTGATCAAGTCCATCAATGAA
AAGTTTGCTGGGTCTGCTGGCTGGGAAGGCACAGAATCGCTGAAAATTGCAGAAGACAAAAAGCAGCTGAGAGAT
TTCTTTGGCATGTCCAACAGTTATGCAGAGTGCTATCCAGCCACGATGGATGACATGGCTGTGGATAGTGATGAG
GAGGTGGATTATAGCAAAATGGACCAGGGTAACAAGAAGAGAACCTTAAGCCGTTGGGACTTTGATACCCAGGAA
GACTACAGCGAGTATATGAACAACAAAGAGGCTTTGCCCAAGGCTGCATTCCAGTATGGTATCAAAATGTCTGAA
GGGCGGAAAACCAGACGCTTCAAGGAAACCAATGACAAAGCAGCGCTCGATTGCCAGTGGAAGATTAGTGCAATC
ATTGAGAAGAGGAAGAAGATGGAAGCTGATGGGGTTGAAGTCAAAAGACCAAAATACTAA

FIGURE 758

MPERDSEPFSNPLAPDGHDVDDPHSFHQSKLTNEDFRKLLMTPRAAPTSAPPSKSRHHEMPREYNEDEDPAARRR
KKKSYYAKLRQQEIERERELAEKYRGRAKERRDGVNKDYEETELINTTANYRAVGPTTKADKSAAEKRRQLIQES
KFLGGDMEHTHLVKGLDFALLQKVRAEIASKEKEEEELMEKPQKETKKDEDPENKIEFKTRLGRNVYRVLFKNKH
ISGMSCSCRAAWPMW

FIGURE 759

ATGCCCGAGAATGTGGCACCCCGGAGCGGGGCGACTGCCGGGGCTGCCGGCGGCCGCGGGAAAGGCGCCTATCAG
GACCGCGACAAGCCAGCCCAGATCCGCTTCAGCAACATTTCCGCCGCCAAAGCGGTTGCTGATGCTATTAGAACA
AGCCTTGGACCAAAAGGAATGGATAAAATGATTCAAGATGGAAAAGGTGATGTAACCATTACAAATGATGGTGCT
ACCATTCTGAAACAAATGCAAGTATTACATCCAGCAGCCAGAATGCTGGTGGAGCTGTCTAAGGCTCAAGATATA
GAAGCAGGAGATGGCACCACATCAGTAGTCATCATTGCTGGCTCCCTCTTAGATTCTTGTACCAAGCTTCTTCAG
AAAGGGATTCATCCAACCATCATTTCTGAGTCATTCCAGAAGGCCCTGGAAAAGGGCATTGAAATCTTGACTGAC
ATGTCTCGACCTGTGGAACTGAGTGACAGAGAAACTTTGTTAAATAGTGCAACCACTTCACTGAACTCAAAGGTG
GTTTCTCAGTATTCAAGTCTGCTTTCTCCAATGAGTGTAAATGCAGTGATGAAAGTGATTGACCCAGCCACAGCC
ACCAGTGTAGATCTTAGAGATATTAAAATAGTTAAGAAGCTTGGTGGGACAATTGATGACTGTGAGTTGGTGGAA
GGGCTGGTTCTCACCCAAAAAGTGTCAAATTCTGGCATAACCAGAGTTGAAAAGGCCAAGATTGGGCTTATTCAG
TTTTGCTTATCTGCTCCCAAAACAGACATGGATAATCAAATAGTGGTTTCTGACTATGCCCAGATGGACCGAGTG
CTGCGAGAAGAGAGAGCCTATATTTTAAATTTAGTGAAGCAAATTAAAAAAACAGGATGTAATGTCCTTCTCATA
CAGAAATCTATTCTAAGAGATGCTCTTAGTGATCTTGCATTACACTTTCTGAATAAAATGAAGATCATGGTGATT
AAGGATATTGAAAGAGAAGACATTGAATTCATTTGTAAGACAATTGGAACCAAGCCAGTTGCTCATATTGACCAA
TTTACTGCTGACATGCTGGGTTCTGCTGAGTTAGCTGAGGAGGTCAATTTAAATGGTTCTGGCAAACTGCTCAAG
ATTACAGGCTGTGCCAGCCCTGGAAAAACAGTTACAATTGTTGTTCGTGGTTCTAACAAACTGGTGATTGAAGAA
GCTGAGCGCTCCATTCATGATGCCCTATGTGTTATTCGTTGTTTAGTGAAGAAGAGGGCTCTTATTGCAGGAGGT
GGTGCTCCAGAAATAGAGTTGGCCCTAGCATTAACTGAATATTCACGAACACTGAGTGGTATGGAATCCTACTGC
GTTCGTGCTTTTGCAGATGCTATGGAGGTCATTCCATCTACACTAGCTGAAAATGCCGGCCTGAATCCCATTTCT
ACAGTAACAGAACTAAGAAACCGGCATGCCCAGGGAGAAAAAACTGCAGGCATTAATGTCCGAAAGGGTGGTATT
TCCAACATTTTGGAGGAACTGGTTGTCCAGCCTCTGTTGGTATCAGTCAGTGCTCTGACTCTTGCAACTGAAACT
GTTCGGAGCATTCTGAAAATAGATGATGTGGTAAACACTCGA**TAA**TCTGGATAACTGACTAGCACCATTATGATC
ACCAGTATTGTGGCTGGAATGGAAGAAGATCACCTTGGTGTTCCTTGTTTGGAAGATTATTTCCTCTGAATTTCT
GGGCTTGGTCTTCCAGTTGGCATTTGCCTGAAGTTGTATTGAAACAATTTAATGAAAATATTAAATATTTGGTTT
CAAAAGGCAGATTTATCTTCTCCCAACATTCTGTTATTTCTGATACTTTTGAAAAACTAATAAAAACTAATAAAA
GAAGCGTA

FIGURE 760

MPENVAPRSGATAGAAGGRGKGAYQDRDKPAQIRFSNISAAKAVADAIRTSLGPKGMDKMIQDGKGDVTITNDGA
TILKQMQVLHPAARMLVELSKAQDIEAGDGTTSVVIIAGSLLDSCTKLLQKGIHPTIISESFQKALEKGIEILTD
MSRPVELSDRETLLNSATTSLNSKVVSQYSSLLSPMSVNAVMKVIDPATATSVDLRDIKIVKKLGGTIDDCELVE
GLVLTQKVSNSGITRVEKAKIGLIQFCLSAPKTDMDNQIVVSDYAQMDRVLREERAYILNLVKQIKKTGCNVLLI
QKSILRDALSDLALHFLNKMKIMVIKDIEREDIEFICKTIGTKPVAHIDQFTADMLGSAELAEEVNLNGSGKLLK
ITGCASPGKTVTIVVRGSNKLVIEEAERSIHDALCVIRCLVKKRALIAGGGAPEIELALALTEYSRTLSGMESYC
VRAFADAMEVIPSTLAENAGLNPISTVTELRNRHAQGEKTAGINVRKGGISNILEELVVQPLLVSVSALTLATET
VRSILKIDDVVNTR

FIGURE 761A

AGGAAGGAAGGAGCAGTTGGTTCAATCTCTGGTAATCT**ATG**CCAGCAATTATGACAATGTTAGCAGACCATGCAG
CTCGTCAGCTGCTTGATTTCAGCCAAAAACTGGATATCAACTTATTAGATAATGTGGTGAATTGCTTATACCATG
GAGAAGGAGCCCAGCAAAGAATGGCTCAAGAAGTACTGACACATTTAAAGGAGCATCCTGATGCTTGGACAAGAG
TCGACACAATTTTGGAATTTTCTCAGAATATGAATACGAAATACTATGGACTACAAATTTTGGAAAATGTGATAA
AAACAAGGTGGAAGATTCTTCCAAGGAACCAGTGCGAAGGAATAAAAAAATACGTTGTTGGCCTCATTATCAAGA
CGTCATCTGACCCAACTTGTGTAGAGAAAGAAAAGGTGTATATCGGAAAATTAAATATGATCCTTGTTCAGATAC
TGAAACAAGAATGGCCCAAACATTGGCCAACTTTTATCAGTGATATTGTTGGAGCAAGTAGGACCAGCGAAAGTC
TCTGTCAAAATAATATGGTGATTCTTAAACTCTTGAGTGAAGAAGTATTTGATTTCTCTAGTGGACAGATAACCC
AAGTCAAATCTAAGCATTTAAAAGACAGCATGTGCAATGAATTCTCACAGATATTTCAACTGTGTCAGTTTGTAA
TGGAAAATTCTCAAAATGCTCCACTTGTACATGCAACCTTGGAAACATTGCTCAGATTTCTGAACTGGATTCCCC
TGGGATATATTTTTGAGACCAAATTAATCAGCACATTGATTTATAAGTTCCTGAATGTTCCAATGTTTCGAAATG
TCTCTCTGAAGTGCCTCACTGAGATTGCTGGTGTGAGTGTAAGCCAATATGAAGAACAATTTGTAACACTATTTA
CTCTGACAATGATGCAACTAAAGCAGATGCTTCCTTTAAATACCAATATTCGACTTGCGTACTCAAATGGAAAAG
ATGATGAACAGAACTTCATTCAAAATCTCAGTTTGTTTCTCTGCACCTTTCTTAAGGAACATGATCAACTTATAG
AAAAAAGATTAAATCTCAGGGAAACTCTTATGGAGGCCCTTCATTATATGTTGTTGGTATCTGAAGTAGAAGAAA
CTGAAATCTTTAAAATTTGTCTTGAATACTGGAATCATTTGGCTGCTGAACTCTATAGAGAGAGTCCATTCTCTA
CATCTGCCTCTCCGTTGCTTTCTGGAAGTCAACATTTTGATGTTCCTCCCAGGAGACAGCTATATTTGCCCATGT
TATTCAAGGTCCGTTTATTAATGGTTAGTCGAATGGCTAAACCAGAGGAAGTATTGGTTGTAGAGAATGATCAAG
GAGAAGTTGTGAGAGAATTCATGAAGGATACAGATTCCATAAATTTGTATAAGAATATGAGGGAAACATTGGTTT
ATCTTACTCATCTGGATTATGTAGATACAGAAAGAATAATGACAGAGAAGCTTCACAATCAAGTGAATGGTACAG
AGTGGTCATGGAAAAATTTGAATACATTGTGTTGGGCAATAGGCTCCATTAGTGGAGCAATGCATGAAGAGGACG
AAAAACGATTTCTTGTTACTGTTATAAAGGATCTATTAGGATTATGTGAACAGAAAAGAGGCAAAGATAATAAAG
CTATTATTGCATCAAATATCATGTACATAGTAGGTCAATACCCACGTTTTTTGAGAGCTCACTGGAAATTTCTGA
AGACTGTAGTTAACAAGCTGTTCGAATTCATGCATGAGACCCATGATGGAGTCCAGGATATGGCTTGTGATACTT
TCATTAAAATAGCCCAAAAATGCCGCAGGCATTTCGTTCAGGTTCAGGTTGGAGAAGTGATGCCATTTATTGATG
AAATTTTGAACAACATTAACACTATTATTTGTGATCTTCAGCCTCAACAGGTTCATACGTTTTATGAAGCTGTGG
GGTACATGATTGGTGCACAAACAGATCAAACAGTACAAGAGCACTTGATAGAAAAGTACATGTTACTCCCTAATC
AAGTGTGGGATAGTATAATCCAGCAGGCAACCAAAAATGTGGATATACTGAAAGATCCTGAAACAGTCAAGCAGC
TTGGTAGCATTTTGAAAACAAATGTGAGAGCCTGCAAAGCTGTTGGACACCCCTTTGTAATTCAGCTTGGAAGAA
TTTATTTAGATATGCTTAATGTATACAAGTGCCTCAGTGAAAATATTTCTGCAGCTATCCAAGCTAATGGTGAAA
TGGTTACAAAGCAACCATTGATTAGAAGTATGCGAACTGTAAAAAGGGAAACTTTAAAGTTAATATCTGGTTGGG
TGAGCCGATCCAATGATCCACAGATGGTCGCTGAAAATTTTGTTCCCCCTCTGTTGGATGCAGTTCTCATTGATT
ATCAGAGAAATGTCCCAGCTGCTAGAGAACCAGAAGTGCTTAGTACTATGGCCATAATTGTCAACAAGTTAGGGG
GACATATAACAGCTGAAATACCTCAAATATTTGATGCTGTTTTTGAATGCACATTGAATATGATAAATAAGGACT
TTGAAGAATATCCTGAACATAGAACGAACTTTTTCTTACTACTTCAGGCTGTCAATTCTCATTGTTTCCCAGCAT
TCCTTGCTATTCCACCTACACAGTTTAAACTTGTTTTGGATTCCATCATTTGGGCTTTCAAACATACTATGAGGA
ATGTCGCAGATACGGGCTTACAGATACTTTTTACACTCTTACAAAATGTTGCACAAGAAGAAGCTGCAGCTCAGA
GTTTTTATCAAACTTATTTTTGTGATATTCTCCAGCATATCTTTTCTGTTGTGACAGACACTTCACATACTGCTG
GTTTAACAATGCATGCATCAATTCTTGCATATATGTTTAATTTGGTTGAAGAAGGAAAAATAAGTACATCATTAA
ATCCTGGAAATCCAGTTAACAACCAAATCTTTCTTCAGGAATATGTGGCTAATCTCCTTAAGTCGGCCTTCCCTC
ACCTACAAGATGCTCAAGTAAAGCTCTTTGTGACAGGGCTTTTCAGCTTAAATCAAGATATTCCTGCTTTCAAGG
AACATTTAAGAGATTTCCTAGTTCAAATAAAGGAATTTGCAGGTGAAGACACTTCTGATTTGTTTTTGGAAGAGA
GAGAAATAGCCCTACGGCAGGCTGATGAAGAGAAACATAAACGTCAAATGTCTGTCCCTGGCATCTTTAATCCAC
ATGAGATTCCAGAAGAAATGTGTGAT**TAA**AATCCAAATTCATGCTGTTTTTTTTCTCTGCAACTCCGTTAGCAGA
GGAAAACAGCATGTGGGTATTTGTCGACCAAAATGATGCCAATTTGTAAATTAAAATGTCACCTAGTGGCCCTTT
TTCTTATGTGTTTTTTTGTATAAGAAATTTTCTGTGAAATATCCTTCCATTGTTTAAGCTTTTGTTTTGGTCATC
TTTATTTAGTTTGCATGAAGTTGAAAATTAAGGCATTTTTAAAAATTTTACTTCATGCCCATTTTTGTGGCTGGG
CTGGGGGGAGGAGGCAAATTCAATTTGAACATATACTTGTAATTCTAATGCAAAATTATACAATTTTTCCTGTAA

FIGURE 761B

ACAATACCAATTTTTAATTAGGGAGCATTTTCCTTCTAGTCTATTTCAGCCTAGAAGAAAAGATAATGAGTAAAA
CAAATTGCGTTGTTTAAAGGATTATAGTGCTGCATTGTCTGAAGTTAGCACCTCTTGGACTGAATCGTTTGTCTA
GACTACATGTATTACAAAGTCTCTTTGGCAAGATTGCAGCAAGATCATGTGCATATCATCCCATTGTAAAGCGAC
TTCAAAAATATGGGAACACAGTTAGTTATTTTTACACAGTTCTTTTTGTTTTTGTGTGTGTGTGCTGTCGCTTGT
CGACAACAGCTTTTTGTTTTCCTCAATGAGGAGTGTTGCTCATTTGTGAGCCTTCATTAACTCGAAGTGAAATGG
TTAAAAATATTTATCCTGTTAGAATAGGCTGCATCTTTTTAACAACTCATTAAAAAACAAAACAACTCTGGCTTT
TGAGATGACTTATACTAATTTACATTGTTTACCAAGCTGTAGTGCTTTAAGAACACTACTTAAAAAGCAAAATAA
ACTTGGTTTACATTTAAAAAAAA

FIGURE 762

MPAIMTMLADHAARQLLDFSQKLDINLLDNVVNCLYHGEGAQQRMAQEVLTHLKEHPDAWTRVDTILEFSQNMNT
KYYGLQILENVIKTRWKILPRNQCEGIKKYVVGLIIKTSSDPTCVEKEKVYIGKLNMILVQILKQEWPKHWPTFI
SDIVGASRTSESLCQNNMVILKLLSEEVFDFSSGQITQVKSKHLKDSMCNEFSQIFQLCQFVMENSQNAPLVHAT
LETLLRFLNWIPLGYIFETKLISTLIYKFLNVPMFRNVSLKCLTEIAGVSVSQYEEQFVTLFTLTMMQLKQMLPL
NTNIRLAYSNGKDDEQNFIQNLSLFLCTFLKEHDQLIEKRLNLRETLMEALHYMLLVSEVEETEIFKICLEYWNH
LAAELYRESPFSTSASPLLSGSQHFDVPPRRQLYLPMLFKVRLLMVSRMAKPEEVLVVENDQGEVVREFMKDTDS
INLYKNMRETLVYLTHLDYVDTERIMTEKLHNQVNGTEWSWKNLNTLCWAIGSISGAMHEEDEKRFLVTVIKDLL
GLCEQKRGKDNKAIIASNIMYIVGQYPRFLRAHWKFLKTVVNKLFEFMHETHDGVQDMACDTFIKIAQKCRRHFV
QVQVGEVMPFIDEILNNINTIICDLQPQQVHTFYEAVGYMIGAQTDQTVQEHLIEKYMLLPNQVWDSIIQQATKN
VDILKDPETVKQLGSILKTNVRACKAVGHPFVIQLGRIYLDMLNVYKCLSENISAAIQANGEMVTKQPLIRSMRT
VKRETLKLISGWVSRSNDPQMVAENFVPPLLDAVLIDYQRNVPAAREPEVLSTMAIIVNKLGGHITAEIPQIFDA
VFECTLNMINKDFEEYPEHRTNFFLLLQAVNSHCFPAFLAIPPTQFKLVLDSIIWAFKHTMRNVADTGLQILFTL
LQNVAQEEAAAQSFYQTYFCDILQHIFSVVTDTSHTAGLTMHASILAYMFNLVEEGKISTSLNPGNPVNNQIFLQ
EYVANLLKSAFPHLQDAQVKLFVTGLFSLNQDIPAFKEHLRDFLVQIKEFAGEDTSDLFLEEREIALRQADEEKH
KRQMSVPGIFNPHEIPEEMCD

FIGURE 763

GGCGGCGGCAGCAGCTGCTTGGGCGCCGTGCGGTGGTGACTGAGCTACGAGCCTGGCAGCAGGTGTGCGCCGAGC
CCCGGCCTGGCCCGGCCCCCGCGTGCCTCCCAGGCTCCGCACCCCTGATGCTGCGCGGGTGCTGAGCCCACTTCG
GCCAGGACGATGGTTAAGTATTTCCTGGGCCAGAGCGTGCTCCGGAGTTCCTGGGACCAAGTGTTCGCCGCCTTC
TGGCAGCGGTACCCGAATCCCTATAGCAAACATGTCTTGACGGAAGACATAGTACACCGGGAGGTGACCCCTGAC
CAGAAACTGCTGTCCCGGCGACTCCTGACCAAGACCAACAGAATGCCACGCTGGGCCAAGCAACTATTTCCTGCC
AATGTTGCTCACTCGGTGTACATCCTGGAGGACTCTATTGTGGACCCACAGAATCAGACCATGACTACCTTCACC
TGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACGATGTGTTTACTGTGTGAACTCTGACAACAGCGGC
TGGACTGAAATCCGCCGGGAAGCCTGGGTCTCCTCTAGCTTATTTGGTGTCTCCAGAGCTGTCCAGGAATTTGGT
CTTGCCCAGTTCAAAAGCAACGTGACCAAGACTATGAAGGGTTTTGAATATATCTTGACTAAGCTGCAAGGCGAG
GCCCCTTCCAAAACACTTGAGACAGCCAAGGAAGCCAAGGAGAAGGCAGAGGAGACGGCACTGGCAGCTACAGAG
AAGGCCAAGGACCTCGCCAGCAAGGCGGCCACCAAGAAGCAGCAGCAGCAGCAACAGTTTGTGTAGCCAGCCCAC
CACCACCACAGCAACCCAGACAGCTAGGCTTAGCCCCTCTGCCCTCCCTCCATTGTACTTTATCATTAAAAATCA
ACTTCCA

FIGURE 764

CTGACTCTCTGAGGCTCATTTTGCAGTTGTTGAAATTGTCCCCGCAGTTTTCAATCATGTCTGAACCAATCAGAG
TCCTTGTGACTGGAGCAGCTGGTCAAATTGCATATTCACTGCTGTACAGTATTGGAAATGGATCTGTCTTTGGTA
AAGATCAGCCTATAATTCTTGTGCTGTTGGATATCACCCCCATGATGGGTGTCCTGGACGGTGTCCTAATGGAAC
TGCAAGACTGTGCCCTTCCCCTCCTGAAAGATGTCATCGCAACAGATAAAGAAGACGTTGCCTTCAAAGACCTGG
ATGTGGCCATTCTTGTGGGCTCCATGCCAAGAAGGGAAGGCATGGAGAGAAAAGATTTACTGAAAGCAAATGTGA
AAATCTTCAAATCCCAGGGTGCAGCCTTAGATAAATACGCCAAGAAGTCAGTTAAGGTTATTGTTGTGGGTAATC
CAGCCAATACCAACTGCCTGACTGCTTCCAAGTCAGCTCCATCCATCCCCAAGGAGAACTTCAGTTGCTTGACTC
GTTTGGATCACAACCGAGCTAAAGCTCAAATTGCTCTTAAACTTGGTGTGACTGCTAATGATGTAAAGAATGTCA
TTATCTGGGGAAACCATTCCTCGACTCAGTATCCAGATGTCAACCATGCCAAGGTGAAATTGCAAGGAAAGGAAG
TTGGTGTTTATGAAGCTCTGAAAGATGACAGCTGGCTCAAGGGAGAATTTGTCACGACTGTGCAGCAGCGTGGCG
CTGCTGTCATCAAGGCTCGAAAACTATCCAGTGCCATGTCTGCTGCAAAAGCCATCTGTGACCACGTCAGGGACA
TCTGGTTTGGAACCCCAGAGGGAGAGTTTGTGTCCATGGGTGTTATCTCTGATGGCAACTCCTATGGTGTTCCTG
ATGATCTGCTCTACTCATTCCCTGTTGTAATCAAGAATAAGACCTGGAAGTTTGTTGAAGGTCTCCCTATTAATG
ATTTCTCACGTGAGAAGATGGATCTTACTGCAAAGGAACTGACAGAAGAAAAAGAAAGTGCTTTTGAATTTCTTT
CCTCTGCCTGACTAGACAATGATGTTACTAAATGCTTCAAAGCTGAAGAATCTAAATGTCGTCTTTGACTCAAGT
ACCAAATAATAATAATGCTATACTTAAATTACTTGTGAAAAACAACACATTTTAAAGATTACGTGCTTCTTGGTA
CAGGTTTGTGAATGACAGTTTATCGTCATGCTGTTAGTGTGCATTCTAAATAAATATATATTCAAATG

FIGURE 765

MSEPIRVLVTGAAGQIAYSLLYSIGNGSVFGKDQPIILVLLDITPMMGVLDGVLMELQDCALPLLKDVIATDKED
VAFKDLDVAILVGSMPRREGMERKDLLKANVKIFKSQGAALDKYAKKSVKVIVVGNPANTNCLTASKSAPSIPKE
NFSCLTRLDHNRAKAQIALKLGVTANDVKNVIIWGNHSSTQYPDVNHAKVKLQGKEVGVYEALKDDSWLKGEFVT
TVQQRGAAVIKARKLSSAMSAAKAICDHVRDIWFGTPEGEFVSMGVISDGNSYGVPDDLLYSFPVVIKNKTWKFV
EGLPINDFSREKMDLTAKELTEEKESAFEFLSSA

FIGURE 766

TCTTTTAAGTATACTCTCTACTTATTAAAAAAAAAAAAAAAGTCCTTTCCACGCTACCTGCAGAGGGGTCCATACG
GCGTTGTTCTGGATTCCCATCGTAACTTAAAGGGAAACTTTCACAATGTCCGGAGCCCTTGATGTCCTGCAAATG
AAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACTCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAA
CAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAATCTGAAGAGGACCTGGGAGAAGCTTCTGCTG
GCAGCTCGTGCTATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGG
GCCGTGCTAAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTCGCTAAC
CAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTGGTTACTGACCCCAGGGCTGACCACCAGCCTCTCATG
GAGGCATCTTATGTTAACCTACCTACCATTGCGCTGTGTAACACAGATTCTCCTCTGCACTATGTGGACATTGCC
ATCCCATGCAACAACAAGGGAGCTCACTCAGTGGGTTTGATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATG
CGTGGCACCATTTCCTGTGAACACCCATGGGAGGTCATGCCTGATCTGTACTTCTACAGAGATCCTGAAGAGATT
GAAAGAGAAGAGCAGGCTGCTGCTGAAAAGGCAGTGACCAAGGAGGAATTTCAGGGTGAATGGACTGCTCCAGCT
CCTGAGTTCACTGTTACTCAGCCTGAGGTTGCAGACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCCC
TACTGAAGACGGGAGCGCTCAGCCTGCCACGGAAGACTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGT
AGGAGCAACCACTGACTGGTCTTAAGCTGTTCTTGCATAGGCTCTTAAGCAACATGGAAAAATGGTTGATGGAAA
ATAAACATCAGTTTCT

FIGURE 767

MSGALDVLQMKEEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAARAIVAIENPADVS
VISSRNTGQRAVLKFAAATGATPIAGRFTPGTFANQIQAAFREPRLLVVTDPRADHQPLMEASYVNLPTIALCNT
DSPLHYVDIAIPCNNKGAHSVGLMWWMLAREVLRMRGTISCEHPWEVMPDLYFYRDPEEIEREEQAAAEKAVTKE
EFQGEWTAPAPEFTVTQPEVADWSEGVQVPSVPIPY

FIGURE 768

GCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCATCGTAACTTAAAGGGAAACTTTCACA**ATG**TCCGGAGCCC
TTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACTCACTTAGGTGGCACCAATC
TTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAATCTGAAGAGGACCT
GGGAGAAGCTTCTGGCCGCTTCACTCCTGGAACCTTCGCTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCT
TCTTGTGGTTACTGACCCCAGGGCTGACCACCAGCCTCTCATGGAGGCATCTTATGTTAACCTACCTACCATTGC
GCTGTGTAACACAGATTCTCCTCTGCACTATGTGGACATTGCCATCCCATGCAACAACAAGGGAGCTCACTCAGT
GGGTTTGATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTGAACACCCATGGGA
GGTCATGCCTGATCTGTACTTCTACAGAGATCCTGAAGAGATTGAAAGAGAAGAGCAGGCTGCTGCTGAAAAGGC
AGTGACCAAGGAGGAATTTCAGGGTGAATGGACTGCTCCAGCTCCTGAGTTCACTGTTACTCAGCCTGAGGTTGC
AGACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGC

FIGURE 769

MSGALDVLQMKEEDVLKFLAAGTHLGSTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLASLLEPSLTRSRQPSG
SHGFLWLLIPGLTTSLSQRHLKLTYLPLLCVTQILLCAMWTLPSHATARELTQWV

FIGURE 770

GGCCCAGCTGCTGAGAGGAGTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGG
ATCAGAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAAACCCATGTGGGTTGTATTGTTAGAA
GATGGAATTGAATTCTATAAGAAGAAAAGTGACAACAGCCCCAAAGGAATGATCCCGCTGAAAGGGAGCACTCTG
ACTAGCCCTTGTCAAGACTTTGGCAAAAGGATGTTTGTGTTTAAGATCACTACGACCAAACAGCAGGACCACTTC
TTCCAGGCAGCCTTCCTGGAGGAGAGAGATGCCTGGGTTCGGGATATCAAGAAGGCCATTAAATGCATTGAAGGA
GGCCAGAAATTTGCCAGGAAATCTACCAGGAGGTCCATTCGACTGCCAGAAACCATTGACTTAGGTGCCTTATAT
TTGTCCATGAAAGACACTGAAAAAGGAATAAAAGAACTGAATCTAGAGAAGGACAAGAAGATTTTTAATCACTGC
TTCACAGGTAACTGCGTCATTGATTGGCTGGTATCCAACCAGTCTGTTAGGAATCGCCAGGAAGGCCTCATGATT
GCTTCATCGCTGCTCAATGAGGGGTATCTGCAGCCTGCTGGAGACATGTCCAAGAGTGCAGTGGATGGAACTGCT
GAAAACCCTTTCCTGGACAACCCTGATGCCTTCTACTACTTTCCAGACAGTGGGTTCTTCTGTGAAGAGAATTCC
AGTGATGATGATGTGATTCTGAAAGAAGAATTCAGAGGGGTCATTATCAAGCAGGGATGTTTACTGAAGCAGGGG
CATAGAAGGAAAAACTGGAAAGTGAGGAAGTTCATCTTGAGAGAAGACCCTGCCTACCTGCACTACTATGACCCT
GCTGGGGCAGAAGATCCCCTGGGAGCAATTCACTTGAGAGGCTGTGTGGTGACTTCAGTGGAGAGCAACTCAAAT
GGCAGGAAGAGTGAGGAAGAGAACCTTTTTGAGATCATCACAGCAGATGAAGTGCACTATTTCTTGCAAGCAGCC
ACCCCCAAGGAGCGCACAGAGTGGATCAGAGCCATCCAGATGGCCTCCCGAACTGGGAAGTAAAGAGACTCCTGC
ATTCCTCCTCCCCTCCTGAGGGAAGCCCATGGACAAGCTCAGTCCAGGACCTGTCCACTTCTGTGACAAATCAAC
GGGAAACAGCCCAGGGGTGGAAGTTTTCATTTGCAGGGGGGTCTGAATGTAACTCACCATGTGGTGTGCAAGGT
TCCCCTGCATTGTATTGCTCACTGCAGCCCCTCTGCCCCTATCCATGACCCCCAAGCAGATATAACAAGCTGTGC
AGCCTCAGTAGGCTGCTTGCCCTCTCCAGGCCTCAGGGCCTCTTCTGGAAAATGAAGAAATTCAACTAGTAGATT
CCTGAGGTCCCCCTAGCTTAAAAAAAAAAAAAATCTGCCCCATGATTCTAACACTCGCAGTAGTGATAGTGTATC
TAGTTGTTCTGCTGGTGTCCTTCCTTGGCTAAGTCTTGGCCTTCAGTTATCTTCAAATGTACCAGAACCTGAGCC
AACGCCTCCCTGTGAAACTGTTGCTGATCTGTAGTACAGTACCAGGAAGAAACCTCTTTTGTTCTCTTTAGACAT
CTTCTACTTGCTCTTGGCCTTGAGATCGTGTAACAAAATGAAGGAGGGCTCTCTTCTTTCTTCCTCATCCTACTC
AAAAACTTCCCGAGAGCAGTGGTGGTTTTGAGGGTTTTGACTTCTATTACTTTTGGCAGCCTGGAAAGTTGTGTC
TTCTGGGAAAGAGACCTGGGGAGGCCAGGAGTAGCTGAGGGTCCTTTCTGTGCCCTTAAACCGCCCAGAGGAGCC
CTATTCCACTCTGGTTTTAGGCTGATCTGAGAGGGTCTCCCTTTGTTCCTTTCTGGAGCATTTCTCTAACGTTTA
TTACAATTAGGAGGGGGACCCCACATCTGTGAGATTCTGTTTCATTTGAGGTTTACAGAAAAAAAAAAGTGGCCA
GATGTGTTCCCCCCATGGGTGAGAGGCCTGGGCAACTGCCTGGTGAATGTGTCTTGCGGCAGCTGCAGCAAGTGG
AGGGGCTGAACTACTGGCCAGCTCACTGGATGATGGGTTAATACAACAACTGCACTGTAAGGACTCAGAGCCACA
CAGAACTTCTGAGAGGGGCTGTTAGCATTGCGCAGCATCTTCAGTTCTCCAGTAAATGATATTGCGTTCGTGCCT
CAGCTTTAAGCACAAGTAGCAGCAGCTCCTGCTTGAGTTCTGAGGGCATCATGGCCCTATGATTAACCAGAGTGA
TCTAACCTAGACTAAAATTGGGAACTTATTTGCAATTTTTGACCCTGACCACTAACTAGTGATTCTTCTCCAAAA
TTGAGAAAGACAGCACCCATTGAAGCAGATATGTGTGTGAAAGTATATTTTTCAATTCCAGATTTTTAATTTTAA
GGCTCCAGGAAAGAAAGGAGAGTAGAACATTTTTCCTCATTTTATCAAATCCTCTCTTGCCCTCCCTCAATTCCC
CTGTAACATTCCTGAAGCTGTTCCCACTCCCAGATGGTTTTATCAATAGCCTAGAGGTAAAGAACTGTCTTTTTC
TCTGATTCTTTAATAAATTATCTTTATAGAATATGCACAAGTTTTTCTACACTCAGTGTTAAAGTATTTATTAAT
GGGAAGTCAACTTAATGTTTTGAAATAAATATATGACTCTGTTTAAT

FIGURE 771

CTTTCCGGGAGACTGGAGTCGAAGGCCGTGAGGTATTTTTCTAAGXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXAACCCCGGAGGAGGGTGAGGAGCAGAGCTGGCCATAATGGCAGGTGAAGAAATTAATGAAGACTAT
CCAGTAGAAATTCACGAGTATTTGTCAGCGTTTGAGAATTCCATTGGTGCTGTGGATGAGATGCTGAAGACCATG
ATGTCTGTTTCTAGAAATGAGTTGTTGCAGAAGTTGGATCCACTTGAACAAGCAAAAGTGGATTTGGTTTCTGCA
TACACATTAAATTCAATGTTTTGGGTTTATTTGGCAACCCAAGGAGTTAATCCTAAGGAACATCCAGTAAAACAG
GAATTGGAAAGAATCAGAGTATATATGAACAGAGTCAAGGAAATAACAGACAAGAAAAAGGCTGGCAAGCTGGAC
AGAGGTGCAGCTTCAAGATTTGTAAAAAATGCCCTCTGGGAACCAAAATCGAAAAATGCATCAAAAGTTGCCAAT
AAAGGAAAAAGTAAAAGTTAACTTTTTGGTTTTGATGTACACATATTCAAAAAGTACATTAATATGTAAATTCAC
AGTAAATATGTAAAGCTAAATACTTTCCTCTCCAAAGATCATTATCTTTATTGATTAGCACTGAGGATTTTAACA
TTGTGATATATTATATATTTATAATTTACCATCTCTTGATGAGACTCTTATTTCTTTATATAGGTCAGTCTTGCA
AGTACCATTTTATAAGCAGCTGTGAAATTTAAGTGAAATGTTCTTTGTAAACATTTGTACTATTTTAAATGAATA
ATGACCTTATGAAGTATGCTATCTGTAGGCTGAAATTATAGGTACATCTGTTTTCACTATATGATATTAAGAAAG
CGTGAAATGACTTAAATGTTCATTTTTTTCTGTATAGATACTTTATCATGTTTTCATGATTTTAGGAATTACTGC
TTTGTTGATATTCAAAGTGTGAAACTAAAACTTTATGGTTGTACTTTAATTCTTGGCATGTTGCCTCTATGTCCC
ATTTAAAATAAAATACATTCTCATTAACTTTAGATGGGAAATAAGGTTGTATGTTGATGGATGAATTTTGGCATG
ATGACTGTACTCTCAATAAAGGCTGAAAATGTTGT

FIGURE 772

CCTTCACTTCGCCCTCCAGCTGCTGCAGCTGCAGCCCGACCGCGAGCGTGCCAAGCGGCTTCAGCAGCTAGCGGA
GCGGTGGCGGCGGCCCCGCTCAGGAGACCACCAGATTCCCCTCTTCCCGCGGCCTCGCCATGGCGACCCACGGAC
AGACTTGCGCGCGTCCAATGTGTATTCCTCCATCATATGCTGACCTTGGCAAAGCTGCCAGAGATATTTTCAACA
AAGGATTTGGTTTTGGGTTGGTGAAACTGGATGTGAAAACAAAGTCTTGCAGTGGCGTGGAATTTTCAACGTCCG
GTTCATCTAATACAGACACTGGTAAAGTTACTGGGACCCTGGAGACCAAATACAAGTGGTGTGAGTATGGTCTGA
CTTTCACAGAAAAGTGGAACACTGATAACACTCTGGGAACAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTT
TGAAACTGACATTTGATACTACCTTCTCACCAAATCAAAGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGAC
TGGGGACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGA
AGATCTTGACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAGCTAAATA
TCAGTTGGATCCCACTGCTTCCATTTCTGCAAAAGTCAACAACTCTAGCTTAATTGGAGTAGGCTATACTCAGAC
TC

FIGURE 773

AGCTGCTGCAGCTGCAGCCCGACCGCGAGCGTGCCAAGCGGCTTCAGCAGCTAGCGGAGCGGTGGCGGCGGCCCC
GCTCAGGAGACCACCAGATTCCCCTCTTCCCGCGGCCTCGCCATGGCGACCCACGGACAGACTTGCGCGCGTCCA
ATGTGTATTCCTCCATCATATGCTGACCTTGGCAAAGCTGCCAGAGATATTTTCAACAAAGGATTTGGTTTTGGG
TTGGTGAAACTGGATGTGAAAACAAAGTCTTGCAGTGGCGTGGAATTTTCAACGTCCGGTTCATCTAATACAGAC
ACTGGTAAAGTTACTGGGACCCTGGAGACCAAATACAAGTGGTGTGAGTATGGTCTGACTTTCACAGAAAAGTGG
AACACTGATAACACTCTGGGAACAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAAACTGACATTTGAT
ACTACCTTCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTTACAAGAGGGAGTGTATAAACCTTGGT
TGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTGTCTTTGGTTATGAGGGCTGGCTTGCT
GGCTACCAGATGACCTTTGACAGTGCCAAATCAAAGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGGG
GACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGAAGAT
CTTGACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAGCTAAATATCAG
TTGGATCCCACTGCTTCCATTTCTGCAAAAGTCAACAACTCTAGCTTAATTGGAGTAGGCTATACTCAGACTCTG
AGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGGTAGACGGGAAGAGCATTAATGCTGGAGGCCACAAGGTTGGG
CTCGCCCTGGAGTTGGAGGCTTAATCCAGCTGAAAGAAACCTTTGGGAATGGATATCAGAAGATTTGGCCTTAAT
ATATTTCCATTGTGACCAGCAGCAGGCTTTTTTCCCCCAAGAAGATGATCAAAACAAAGGATGATCTCAACAAGA
GCTGTATTTTAAGTATTTAGACAGTTCTTTGTTAGCTGGTTTCTAGTTGAATTGGTTATCTAGTTACCAATGCTG
CAGTCCTGCAGTCACCTATACATTATTTAAATGTATTTAACTGTTAAATGCGCTACCCACCAATAATGAAATAGA
CCTTTATGAAAA

FIGURE 774

MATHGQTCARPMCIPPSYADLGKAARDIFNKGFGFGLVKLDVKTKSCSGVEFSTSGSSNTDTGKVTGTLETKYKW
CEYGLTFTEKWNTDNTLGTEIAIEDQICQGLKLTFDTTFSPNTGKKSGKIKSYKRECINLGCDVDFDFAGPAIHG
SAVFGYEGWLAGYQMTFDSAKSKLTRNNFAVGYRTGDFQLHTNVNDGTEFGGSIYQKVCEDLDTSVNLAWTSGTN
CTRFGIAAKYQLDPTASISAKVNNSSLIGVGYTQTLRPGVKLTLSALVDGKSINAGGHKVGLALELEA

FIGURE 775

ATGGTCTGACTTTCACAGAAAAGTGGAACACTGATAACACTCTGGGAACAGAAATCGCAATTGAAGACCAGATTT
GTCAAGGTTTGAAACTGACATTTGATACTACCTTCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTT
ACAAGAGGGAGTGTATAAACCTTGGTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTG
TCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTTGACAGTGCCAAATCAAAGCTGACAAGGAATA
ACTTTGCAGTGGGCTACAGGACTGGGGACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGAT
CAATTTATCAGAAAGTTTGTGAAGATCTTGACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTC
GTTTTGGCATTGCAGCTAAATATCAGTTGGATCCCACTGCTTCCATTTCTGCTGGTGTGAAGCTTACACTCTCTG
CTCTGGTAGACGGGAAGAGCATTAATGCTGGAGGCCACAAGGTTGGGCTCGCCCTGGAGTTGGAGGCTTAATCCA
GCTGAAAGAAACCTT

FIGURE 776

GAGAAAACGGCCGGGCGGCGGTGGCTGTAGGTTGTGCGGCTGCAGCGGCTCTTCCCTGGGCGGACGATGGACAGC
CAGGGCAGGAAGGTGGTGGTGTGCGACAACGGCACCGGGTTTGTGAAGTGTGGATATGCAGGCTCTAACTTTCCA
GAACACATCTTCCCAGCTTTGGTTGGAAGACCTATTATCAGATCAACCACCAAAGTGGGAAACATTGAAATCAAG
GATCTTATGGTTGGTGATGAGGCAAGTGAATTACGATCAATGTTAGAAGTTAACTACCCTATGGAAAATGGCATA
GTACGAAATTGGGATGACATGAAACACCTGTGGGACTACACATTTGGACCAGAGAAACTTAATATAGATACCAGA
AATTGTAAAATCTTACTCACAGAACCTCCTATGAACCCAACCAAAAACAGAGAGAAGATTGTAGAGGTAATGTTT
GAAACTTACCAGTTTTCCGGTGTATATGTAGCCATCCAGGCAGTTCTGACTTTGTACGCTCAAGGTTTATTGACT
GGTGTAGTGGTAGACTCTGGAGATGGTGTGACTCACATTTGCCCAGTATATGAAGGCTTTTCTCTCCCTCATCTT
ACCAGGAGACTGGATATTGCTGGGAGGGATATAACTAGATATCTTATCAAGCTACTTCTGTTGCGAGGATACGCC
TTCAACCACTCTGCTGATTTTGAAACGGTTCGCATGATTAAAGAAAAACTGTGTTACGTGGGATATAATATTGAG
CAAGAGCAGAAACTGGCCTTAGAAACCACAGTATTAGTTGAATCTTATACACTCCCAGATGGACGTATCATCAAA
GTTGGGGGAGAGAGATTTGAAGCACCAGAAGCTTTATTCAGCCTCACTTGATCAATGTTGAAGGAGTTGGTGTT
GCTGAATTGCTTTTTAACACAATTCAGGCAGCTGACATTGATACCAGATCTGAATTCTACAAACACATTGTGCTT
TCTGGAGGGTCTACTATGTATCCTGGCCTGCCATCACGGTTGGAACGAGAACTTAAACAGCTTTACTTAGAACGA
GTTTTGAAGGGTGATGTGGAAAAACTTTCTAAATTTAAGATCCGCATTGAAGACCCACCCCGCAGAAAGCACATG
GTATTCCTGGGTGGTGCAGTTCTAGCGGATATCATGAAAGACAAAGACAACTTTTGGATGACCCGACAAGAGTAC
CAAGAAAAGGGTGTCCGTGTGCTAGAGAAACTTGGTGTGACTGTTCGATAAACTCCAAAGCTTGTTCCCGTCATA
CCCGTAATGCTTTCTTTTTTCCTTTATTGCCAATCTTTGAACTCATTCAACTCCAGGACATGGAAGAGGCCTCTC
TCTGCCCTTTGACTGGAAAGGTCAAGTTTTATTCTGGTGTCTTGGGGAAGCTTTGTTAAATTTTTGTTAATGTGG
GTAAATCTGAGTTTAATTCAACTGCTTCCCTACATAGACTAGAGGGCTAAGGATTCTGTCTGCTGCTTTGTTTCT
TCTAAGTAGGCATTTAGATCATTCCTATAGGCTTCCTATTTTCACTTTACTGCTCTAATGCTGCTAGTCGTAGTC
TTTAGCACACTAGGTGGTATGCCTTTATTAGCATAAAACAAAAAAAACTTTAACAGGAGCTTTTACATATTACTG
GGATGGGGGGTGGTTCGGGATGGGTGGGCAGCTGCTGAACCCTTTAGGGCATTTCCTCTGTAATGTGGCGCTTTC
AACTGTACTGCTGCAGCTTTAAGTACCTTAAAGCTTCTCCTGTGAACTTCTTAGGGAAATGTTAGGTTCAGAACT
AAAGTGTTTTGGGTGGGTTTTGTTGCGGGGGGGAGGGTAACAATGGGTGGTCTTCTGATTTTTATTTTTGAGGTT
TTGTCAACTGGAGTACGTAGAGGAACTTTATTTACAGTACTTTGATTTGGCAGGTTTCTTCTACTTGTGCTCTG
CCTGGAGCTGTTTCCATATGATATAAAAAGCAAGTGTAGTATTCCATTACTATGTGGCTTAGGGATTTATTTGTT
TTTTAAAATCAACCATGTTAGCTGGGATTAGACTCCCTACAGTCCTTCAATGGAAAAGTAACATTTAAAAATCCT
TTGGGTAATTCGAATTACAGATTTAAAAGAGCTTAAGATCTGGTGTTTTGTTAATGCTTCTGTTTATTCCAGAAG
CATTAAGGTAACCCATTGCCAAGTATCATTCTTGCAAATTATTCTTTTATATAACTGACCAGTGCTTAATAAAAC
AAGCAGGTACTTACAAATAATTACTGGCAGTAGGTTATAATTGGTGGTTTAAAAATAACATTGGAATACAGGACT
TGTTGCCAATTGGGTAATTTTCATTAGTTGTTTTGTTTGTTTTGATTTGAAACCTGGAAATACAGTAAAATTTGA
CTGTTTAAAATGTTGGCCAAAAAAATCAAGATTTAATTTTTTTATTTGTACTGAAAAACTAATCATAACTGTTAA
TTCTCAGCCATCTTTGAAGCTTGAAAGAAGAGTCTTTGGTATTTTGTAAACGTTAGCAGACTTTCCTGCCAGTGT
CAGAAAATCCTATTTATGAATCCTGTCGGTATTCCTTGGTATCTGAAAAAAATACCAAATAGTACCATACATGAG
TTATTTCTAAGTTTGAAAAATAAAAAGAAATTGCATCACACTAATTACAAAATA

FIGURE 777

ATGGAGACACTTGTACAAGTGAATCTCTTTAGAAAGAGAGATTTACGCCAGGTACGTGGAACACAGTCTGAGCAG
CACTGCACACCGTATCAAATCAGGTATCCTGTAGGAAGAGTACCTGGGGATGAAATCAACAAGTTCTTAGTGGAA
TCTTCTCATTTCTTAGAATGTAATGTGGTTGGATGTTTGGAAATTGGTACGAAAGGGGAGAATCCTTTCCCCCAA
TTAGGAAAATGGGGAGTGGGGGCAGAGGAAATGAAGCCCAGGTTCTTCATCGGATGGAAGTTCTCTGGTCAGTGT
ACACAGTTTGCTCTTGAGAGGACTGATGGCCTGGGATATGTTATTGATGGTCCTGAAAGGGATCTGCGTTTGAAT
AGGTCAGAGAAGATGTTCTGGAAGTCTGGAGACTGGGATACGCTCCCTTCCCTACAGGCTCATTCATCCAGCGTT
CTGGCAGTACCCTCTGGTACCGCACAGACTTCAGGGGACCTTGAACAAGCTCCATTTTGTCTCCTGGAAGCTCAT
TCCACCAGGTTTGAGTATGAGCTTCACCACTCGCTCCACCTTCTCCACCAACTACCAGTCCCTGGGCTCTGTCCA
GGTGCCCAGCTAAGACGCTCGGCCAGTCAGCAGCATGACCAGTATCTCTGCAGGGGCTGGGGGCTCTGGTTCCCA
GATCTCCATGTCCCCCTCCACCAGCTTCTGGGGTGGCATGGGGTCTGGGGCCCTGGCCGTGGGGATGGCCAGGGT
TCTGGCAGGATGGAAGACATCCAGAACAAGAAGGAGACCATGCAAAGCCTGAATGACTGCCTGGCCTCCTACCTG
GACAGAGTGAGGAGACTGGATACCAAGAATCGGAAGCTGGAGAGCAAAATCCGGGAGCACCTGGAGAAGAAGGGA
CCCCAAGTCAGAGACTGGAGCCATTACTTCAAGACCGTGGAGGACCTGAGGGCTCAGATCTTCGCAAATACTGTG
GACAATGCCCGCATCGTTCTGCAAGTCGACAATGCCCATCTTGCTGATGACTTTAGAGTCAAGTATGTGACAGAG
CTGGCCATGCGCCAGTCTATGGAGAGCGACATCCATGGGCTCCGCAAGGTCATTGATGACACCAATGTCACTCGG
CTGCAGCTGGAAACAGAGATCGAGGCTCTCAAGGAGGAGCTGCTCTTCATGAAGAAGAACGAAGAAGGGGAAATA
AAAGGCCTACAAGCCCAGATTGCCAGCTCTGGGTTGACTGTGGAGGTAGATATCCCCAAATCTCAGGACCTTGCC
AAGCTCATGGCAGACATCTGGGCCCAATATGATGAGCTGGCTCGGAAGAGCCAAGAGGAGCTGGGCAAGTACTGG
TCTCAGCAGATTGAGGAGAGTATCACAGTAGTCACCATGCAGTCCACCGAGATGGAGCAGTTCAACAGGATCCTG
CTGCACCTGGAGTCAGAGCTGGCACAGACCTGGGCAGAGGGACAGTGCCAGGCCCAGGAGTACGAGGCCCTGCTG
AGCATCAGGGTCAAGCTGGAGGCTGAGATCGCCACCTACCACCACCTGCTGGAAGATACCACCACCGGCCGGATA
GTGGATGGCAAAGTGGGGTCTGAGACCAACAACACCAAAGTTCTGAGACAT**TAA**

FIGURE 778

METLVQVNLFRKRDLRQVRGTQSEQHCTPYQIRYPVGRVPGDEINKFLVESSHFLECNVVGCLEIGTKGENPFPQ
LGKWGVGAEEMKPRFFIGWKFSGQCTQFALERTDGLGYVIDGPERDLRLNRSEKMFWKSGDWDTLPSLQAHSSSV
LAVPSGTAQTSGDLEQAPFCLLEAHSTRFEYELHHSLHLLHQLPVPGLCPGAQLRRSASQQHDQYLCRGWGLWFP
DLHVPLHQLLGWHGVWGPGRGDGQGSGRMEDIQNKKETMQSLNDCLASYLDRVRRLDTKNRKLESKIREHLEKKG
PQVRDWSHYFKTVEDLRAQIFANTVDNARIVLQVDNAHLADDFRVKYVTELAMRQSMESDIHGLRKVIDDTNVTR
LQLETEIEALKEELLFMKKNEEGEIKGLQAQIASSGLTVEVDIPKSQDLAKLMADIWAQYDELARKSQEELGKYW
SQQIEESITVVTMQSTEMEQFNRILLHLESELAQTWAEGQCQAQEYEALLSIRVKLEAEIATYHHLLEDTTTGRI
VDGKVGSETNNTKVLRH

FIGURE 779A

CGGTCCCTCGCCGCGCCGCCCCGAGGGGCACTTCCGGCGGCGGTTCACTTCCTGGTTGGGTGGATGGAGCCGGGC
GGGAGCGCGCGCGGGGGAGGGGCGGCGGGTCAGTCTCCGCCCGGCGCTCCCGGGATCAGCTGGCGGGCGGGCGGG
AGCCGAGCGCGGCCCCGGCTCTCGCTGCAGCGCCGCCTCTTCTCTGCGTCGCAGGCCGGCCCGGCGGCCGTGACA
ATGTCGCGGGGCTGGTAGCAGGGCGCCGGCCGCCGAGCCGTCTCAAGTTTAAACTTACACGAATCGCTTTCTGGA
GGAGGAGGGGACCCGCTGCGCGATTGACACGCATATTCCTATAGGCATCCTCCCTCAGCCCCCACCCCCACGGCC
GGATTCGGGTGGCTCCTCTCCGAGGTGAAATCTGAGAAGAAATCCTTGGATCTCTTTTCTTAAAAAAAAAAAAAA
AAAAAAAAAATCTAGAAACCATCGGTATTTGCTTTGCTGCTCCCTATTCGCAAGATGAAGAAGTTTTTCGACTC
CCGGCGAGAGCAGGGCGGCTCTGGCCTGGGCTCCGGCTCCAGCGGAGGAGGGGGCAGCACCTCGGGCCTGGGCAG
TGGCTACATCGGAAGAGTCTTCGGCATCGGGCGACAGCAGGTCACAGTGGACGAGGTGTTGGCGGAAGGTGGATT
TGCTATTGTATTTCTGGTGAGGACAAGCAATGGGATGAAATGTGCCTTGAAACGCATGTTTGTCAACAATGAGCA
TGATCTCCAGGTGTGCAAGAGAGAAATCCAGATAATGAGGGATCTTTCAGGGCACAAGAATATTGTGGGTTACAT
TGATTCTAGTATCAACAACGTGAGTAGCGGTGATGTATGGGAAGTGCTCATTCTGATGGACTTTTGTAGAGGTGG
CCAGGTGGTAAACCTGATGAACCAGCGCCTGCAAACAGGCTTTACAGAGAATGAAGTGCTCCAGATATTTTGTGA
TACCTGTGAAGCTGTTGCCCGCCTGCATCAGTGCAAAACTCCTATTATCCACCGGGACCTGAAGGTTGAAAACAT
CCTCTTGCATGACCGAGGCCACTATGTCCTGTGTGACTTTGGAAGCGCCACCAACAAATTCCAGAATCCACAAAC
TGAGGGAGTCAATGCAGTAGAAGATGAGATTAAGAAATACACAACGCTGTCCTATCGAGCACCAGAAATGGTCAA
CCTGTACAGTGGCAAAATCATCACTACGAAGGCAGACATTTGGGCTCTTGGATGTTTGTTGTATAAATTATGCTA
CTTCACTTTGCCATTTGGGGAAAGTCAGGTGGCAATTTGTGATGGAAACTTCACAATTCCTGATAATTCTCGATA
TTCTCAAGACATGCACTGCCTAATTAGGTATATGTTGGAACCAGACCCTGACAAAAGGCCGGATATTTACCAGGT
GTCCTACTTCTCATTTAAGCTACTCAAGAAAGAGTGCCCAATTCCAAATGTACAGAACTCTCCCATTCCTGCAAA
GCTTCCTGAACCAGTGAAAGCCAGTGAGGCAGCTGCAAAAAAGACCCAGCCAAAGGCCAGACTGACAGATCCCAT
TCCCACCACAGAGACTTCAATTGCACCCCGCCAGAGGCCTAAAGCTGGGCAGACTCAGCCGAACCCAGGAATCCT
TCCCATCCAGCCAGCGCTGACACCCCGGAAGAGGGCCACTGTTCAGCCCCCACCTCAGGCTGCAGGATCCAGCAA
TCAGCCTGGCCTTTTAGCCAGTGTTCCCCAACCAAAACCCCAAGCCCCACCCAGCCAGCCTCTGCCGCAAACTCA
GGCCAAGCAGCCACAGGCTCCTCCCACTCCACAGCAGACGCCTTCTACTCAGGCCCAGGGTCTGCCCGCTCAGGC
CCAGGCCACACCCCAGCACCAGCAGCAACTCTTCCTCAAGCAGCAACAGCAGCAGCAACAGCCACCGCCAGCACA
GCAGCAGCCGGCAGGCACGTTTTACCAGCAGCAGCAGGCCCAGACTCAGCAGTTTCAGGCAGTACATCCAGCAAC
CCAGAAACCAGCAATTGCTCAGTTCCCTGTGGTGTCCCAAGGAGGCTCTCAACAGCAGCTAATGCAGAATTTCTA
CCAGCAGCAGCAGCAGCAGCAACAACAACAGCAACAGCAACAGCTGGCCACAGCCCTGCATCAACAACAGCTGAT
GACTCAGCAGGCTGCCTTGCAGCAAAAGCCCACTATGGCAGCAGGACAGCAGCCCCAGCCACAGCCAGCTGCAGC
CCCACAGCCAGCCCCTGCCCAGGAGCCAGCGATTCAAGCCCCAGTAAGACAACAGCCAAAGGTTCAGACAACCCC
ACCTCCTGCCGTCCAGGGGCAGAAAGTTGGATCTCTCACTCCACCCTCATCCCCCAAAACCCAACGTGCTGGGCA
CAGGCGTATTCTCAGTGACGTAACCCACAGTGCAGTCTTTGGGGTCCCTGCCAGCAAATCAACCCAGCTGCTCCA
GGCAGCTGCAGCTGAGGCCAGTCTCAATAAGTCCAAGTCTGCAACCACCACTCCATCAGGCTCTCCTCGGACCTC
TCAACAAAACGTTTATAATCCTTCAGAAGGGTCTACGTGGAATCCCTTTGATGACGATAATTTCTCCAAACTCAC
AGCTGAAGAACTGCTAAACAAGGACTTTGCCAAGCTTGGGGAAGGCAAACATCCCGAGAAGCTTGGAGGCTCAGC
TGAGAGTTTGATCCCAGGCTTTCAATCAACCCAAGGTGATGCTTTTGCTACGACCTCATTTTCTGCTGGAACTGC
TGAAAAAAGGAAGGGTGGGCAGACTGTGGACTCTGGCCTCCCGCTTCTAAGCGTGTCTGATCCTTTCATTCCTCT
TCAAGTACCTGATGCACCAGAAAAACTAATTGAGGGACTCAAATCTCCTGACACTTCTCTTCTGCTCCCTGACCT
CTTGCCTATGACAGATCCTTTTGGTAGCACTTCTGATGCTGTAATTGGTAAAGTCATCATCTCTGTTTCTTCAGT
CATGCATGATATGTGTGCCTGTTTCAAGAATGACAAGTACCTAGTTAACCAATCCCTGGGGAATAGCCCTGCCAC
CCCAGAAGCCAAGGCTATTTAATCTCACTTGTATCACTCCAAATGAAGTGTTTTCCTTGCTTTTCGGGGGTACAA
CGTCTATTTTTTGCCTTTCTTGATATCTGGAGATTTCTAGAGTGGATCTCTTATGAATGAGGAGGAATGTGGAAA
GTTTCACATTTAGTTAGAAGAACTTTAAAAAATTGGTTTCTAACTAGACTACCTTTACTGAACTTAATGAAATTT
AGCAGATTCTTCTTTTTTTTTTTTTTGTTTGAGACAGAGTTTCACTCTTGTTGCCTAGGCTGGAGTGCAATGGCA
AGATCTCAGCTCACTGCAACCTCCATCTCCCGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGAGA
TTACAGGCATGCACCACCATGCCTGGCTAATTTTTATATTTTTAGTAGAGATAGGGTTTCTCCATGTTGGTCAGG
CTGGTCTCGAACTCCTGACCTCAGGTGATCCACCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGGGTGAGCC

FIGURE 779B

ACCATGCCCAGCCCAGATTCTTCTTTAGAAGGCCCATGTACATCCAGCTGCAGTGGGACGAGCCTGGGAAGCATA
GGAAGACCCCATCCCTACAAAAAAAATGTTGTTAGTTAGCCAGGTGTGGGGGTGCACACCTGTGCTACCAGCTCT
TTGGGAGGCTGAGACGGAAGATCACTTTGAGCCAGGGGGTTTGAGGCTGCAGTGAGCCCTGATCATGCCACTGCC
CTCCAGCTTAAGTGACAGAGACCCATCTTAAACAAAATTAAAAAATTTAAAAAGGTCCATGTATATACCAAGTAT
CAGTAACTGAGAAAACATTTTGCCCACTGGTTAAGCCCCATAAATAGAATCCAGGGCAGGGGCTTGGTCTGCTTC
CTCTCTCACATTTTCCTATGTTCCAACAGCAAGGCAGGCAAGATTTGCAAAATGTCCAAGGCCCCTGTACTCCAG
GAGGGTCCAATCATGAGGCACCTAATAATGCCTTTGGGCAGAAAGTCCTAGAACTCAGAAGTGCCATGACCTTGC
ATAGGGGTAGGCCTGCAGCTGAGGGGTGTCACGTGGTGCAAAAGGCCTCCCAGCTACATCCTGGGATGGGGTTTG
AGATGGATTAATGGCCTTTGCATGGCACAGAGGATGTTTGCCCCCAGGTTTATCCCTTAATAAAAGTGAAATTAC
CAGAAAAAATTAAGGTGCCTTTCAGCCCATCTCTTCTGACATGGAAGAGGTTTGCTGAGCGGCTTATGTTCTGAA
TTTGTTTATGAGAACTGATCATTAGTGAGACTGGCCACAGTATTTAACCTTGCACATGCATGCTCAGTGAAGCCT
AGACATTCAGAGCAGCAGAAATAAAGTAACTTATTTTTCTTTCCACCTTGCCTGAGACTGGCATTTTAGAGACCT
GTTAAAAGAAAGTCTTCACATGGCTGGGTGCAGTGGCTCACACTTGTAACCACAGGACTTTGGGAGGCCAAGGTG
GGATAGATCGCTTGAGCTCAGGAGCAAGACACCATCTCAAAAAATGAGAATT

FIGURE 780

GCCCCAGGTGCGCTTCCCCTAGAGAGGGATTTTCCGGTCTCGTGGGCAGAGGAACAACCAGGAACTTGGGCTCAG
TCTCCACCCCACAGTGGGGCGGATCCGTCCCGGATAAGACCCGCTGTCTGGCCCTGAGTAGGGTGTGACCTCCGC
AGCCGCAGAGGAGGAGCGCAGCCCGGCCTCGAAGAACTTCTGCTTGGGTGGCTGAACTCTGATCTTGACCTAGAG
TCATGGCCATGGCAACCAAAGGAGGTACTGTCAAAGCTGCTTCAGGATTCAATGCCATGGAAGATGCCCAGACCC
TGAGGAAGGCCATGAAAGGGCTCGGCACCGATGAAGACGCCATTATTAGCGTCCTTGCCTACCGCAACACCGCCC
AGCGCCAGGAGATCAGGACAGCCTACAAGAGCACCATCGGCAGGGACTTGATAGACGACCTGAAGTCAGAACTGA
GTGGCAACTTCGAGCAGGTGATTGTGGGGATGATGACGCCCACGGTGCTGTATGACGTGCAAGAGCTGCGAAGGG
CCATGAAGGGAGCCGGCACTGATGAGGGCTGCCTAATTGAGATCCTGGCCTCCCGGACCCCTGAGGAGATCCGGC
GCATAAGCCAAACCTACCAGCAGCAATATGGACGGAGCCTTGAAGATGACATTCGCTCTGACACATCGTTCATGT
TCCAGCGAGTGCTGGTGTCTCTGTCAGCTGGTGGGAGGGATGAAGGAAATTATCTGGACGATGCTCTCGTGAGAC
AGGATGCCCAGGACCTGTATGAGGCTGGAGAGAAGAAATGGGGGACAGATGAGGTGAAATTTCTAACTGTTCTCT
GTTCCCGGAACCGAAATCACCTGTTGCATGTGTTTGATGAATACAAAAGGATATCACAGAAGGATATTGAACAGA
GTATTAAATCTGAAACATCTGGTAGCTTTGAAGATGCTCTGCTGGCTATAGTAAAGTGCATGAGGAACAAATCTG
CATATTTTGCTGAAAAGCTCTATAAATCGATGAAGGGCTTGGGCACCGATGATAACACCCTCATCAGAGTGATGG
TTTCTCGAGCAGAAATTGACATGTTGGATATCCGGGCACACTTCAAGAGACTCTATGGAAAGTCTCTGTACTCGT
TCATCAAGGGTGACACATCTGGAGACTACAGGAAAGTACTGCTTGTTCTCTGTGGAGGAGATGATTAAAATAAAA
ATCCCAGAAGGACAGGAGGATTCTCAACACTTTGAATTTTTTAACTTCATTTTTCTACACTGCTATTATCATTA
TCTCAGAATGCTTATTTCCAATTAAAACGCCTACAGCTGCCTCCTAGAATATAGACTGTCTGTATTATTATTCAC
CTATAATTAGTCATTATGATGCTTTAAAGCTGTACTTGCATTTCAAAGCTTATAAGATATAAATGGAGATTTTAA
AGTAGAAATAAATATGTATTCCATGTTTTTAAAAGATTACTTTCTACTTTGTGTTTCACAGACATTGAATATATT
AAATTATTCCATATTTTCTTTTCAGTGAAAAATTTTTTAAATGGAAGACTGTTCTAAAATCACTTTTTTCCCTAA
TCCAATTTTTAGAGTGGCTAGTAGTTTCTTCATTTGAAATTGTAAGCATCCGGTCAGTAAGAATGCCCATCCAGT
TTTCTATATTTCATAGTCAAAGCCTTGAAAGCATCTACAAATCTCTTTTTTTAGGTTTTGTCCATAGCATCAGTT
GATCCTTACTAAGTTTTTCATGGGAGACTTCCTTCATCACATCTTATGTTGAAATCACTTTCTGTAGTCAAAGTA
TACCAAAACCAATTTATCTGAACTAAATTCTAAAGTATGGTTATACAAACCATATACATCTGGTTACCAAACATA
AATGCTGAACATTCCATATTATTATAGTTAATGTCTTAATCCAGCTTGCAAGTGAATGGAAAAAAAAATAAGCTT
CAAACTAGGTATTCTGGGAATGATGTAATGCTCTGAATTTAGTATGATATAAAGAAAACTTTTTTGTGCTAAAAA
TACTTTTTAAAATCAATTTTGTTGATTGTAGTAATTTCTATTTGCACTGTGCCTTTCAACTCCAGAAACATTCTG
AAGATGTACTTGGATTTAATTAAAAAGTTCACTTTGT

FIGURE 781

MAMATKGGTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAYRNTAQRQEIRTAYKSTIGRDLIDDLKSELS
GNFEQVIVGMMTPTVLYDVQELRRAMKGAGTDEGCLIEILASRTPEEIRRISQTYQQQYGRSLEDDIRSDTSFMF
QRVLVSLSAGGRDEGNYLDDALVRQDAQDLYEAGEKKWGTDEVKFLTVLCSRNRNHLLHVFDEYKRISQKDIEQS
IKSETSGSFEDALLAIVKCMRNKSAYFAEKLYKSMKGLGTDDNTLIRVMVSRAEIDMLDIRAHFKRLYGKSLYSF
IKGDTSGDYRKVLLVLCGGDD

FIGURE 782

CGCCACCGCCGCGCCCTCGCCCACCCGCCCGCCCGCCGCTCCCGGCCCCGCTCGCCCCCTCCGCCGCCGCCGCCC
GCCCCTGCGACTACGCTGCGGCCTCCCGCCCGCTCCCGCTCGCTCCCGCGGCCCTCGCTCGCCTCGCGCCGGCAG
TTTTGGGCCTACACCTCCCCTCCCCCCGCCAGCCGCCAAAGACTTGACCACGTAACGAGCCCAACTCCCCCGAAC
GCCGCCCGCCGCTCGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCATTCGGCTTCTTA
TGCACGGAAAGGAAGTAGGAAGCATCATTGGGAAGAAAGGGGAGTCGGTTAAGAGGATCCGCGAGGAGAGTGGCG
CGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCTTTA
AGGCTTTCGCTATGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTACCGCGGCCAGCA
GGCCCCCGGTCACCCTGAGGCTGGTGGTGCCGGCCACCCAGTGCGGCTCCCTGATTGGGAAAGGCGGGTGTAAGA
TCAAAGAGATCCGCGAGAGTACGGGGGCGCAGGTCCAGGTGGCGGGGGATATGCTGCCCAACTCCACCGAGCGGG
CCATCACCATCGCTGGCGTGCCGCAGTCTGTCACCGAGTGTGTCAAGCAGATTTGCCTGGTCATGCTGGAGACGC
TCTCCCAGTCTCCGCAAGGGAGAGTCATGACCATTCCGTACCAGCCCATGCCGGCCAGCTCCCCAGTCATCTGCG
CGGGCGGCCAAGATCGGTGCAGCGACGCTGCGGGCTACCCCCATGCCACCCATGACCTGGAGGGACCACCTCTAG
ATGCCTACTCGATTCAAGGACAACACACCATTTCTCCGCTCGATCTGGCCAAGCTGAACCAGGTGGCAAGACAAC
AGTCTCACTTTGCCATGATGCACGGCGGGACCGGATTCGCCGGAATTGACTCCAGCTCTCCAGAGGTGAAAGGCT
ATTGGGCAAGTTTGGATGCATCTACTCAAACCACCCATGAACTCACCATTCCAAATAACTTAATTGGCTGCATAA
TCGGGCGCCAAGGCGCCAACATTAATGAGATCCGCCAGATGTCCGGGGCCCAGATCAAAATTGCCAACCCAGTGG
AAGGCTCCTCTGGTAGGCAGGTTACTATCACTGGCTCTGCTGCCAGTATTAGTCTGGCCCAGTATCTAATCAATG
CCAGGCTTTCCTCTGAGAAGGGCATGGGGTGCAGCTAGAACAGTGTAGGTTCCCTCAATAACCCCTTTCTGCTGT
TCTCCCATGATCCAACTGTGTAATTTCTGGTCAGTGATTCCAGGTTTTAAATAATTTGTAAGTGTTCAGTTTCTA
CACAACTTTATCATCCGCTAAGAATTTAAAAATCACATTCTCTGTTCAGCTGTTAATGCTGGGATCCATATTTAG
TTTTATAAGCTTTTCCCTGTTTTTAGTTTTGTTTTGGGTTTTTTGGCTCATGAATTTTATTTCTGTTTGTCGATA
AGAAATGTAAGAGTGGAATGTTAATAAATTTCAGTTTAGTTCTGTAATGTCAAGAATTTAAGAATTAAAAAACGG
ATTGGTTAAAAAATGCTTCATATTTGAAAAAGCTGGGAATTGCTGTCTT

FIGURE 783

CCAAGCTGAACCAGGTGGCAAGACAACAGTCTCACTTTGCCATGATGCACGGCGGGACCGGATTCGCCGGAATTG
ACTCCAGCTCTCCAGAGGTGAAAGGCTATTGGGCAAGTTTGGATGCATCTACTCAAACCACCCATGAACTCACCA
TTCCAAATAACTTAATTGGCTGCATAATCGGGCGCCAAGGCGCCAACATTAATGAGATCCGCCAGATGTCCGGGG
CCCAGATCAAAATTGCCAACCCAGTGGAAGGCTCCTCTGGTAGGCAGGTTACTATCACTGGCTCTGCTGCCAGTA
TTAGTCTGGCCCAGTATCTAATCAATGCCAGGCTTTCCTCTGAGAAGGGCATGGGGTGCAGCTAGAACAGTGTAG
GTTCCCTCAATAACCCCTTTCTGCTGTTCTCCCATGATCCAACTGTGTAATTTCTGGTCAGTGATTCCAGGTTTT
AAATAATTTGTAAGTGTTCAGTTTCTACACAACTTTATCATCCGCTAAGAATTTAAGCTTTTCCCTGTTTTTAGT
TTTGTTTTGGGTTTTTTGGCTCATGAATTTTA

FIGURE 784

CGCAGAGCTCGCGCGTCGGTGTGGTTACAGCCGGCAGCCACGGCACCTCCTTCCGGCCGACTAGTCTCCAGGTCC
CGCGGTCTGGCCCCTGGTCACCCGGCGCTGTCCCTCGTTCCTTGAAGATCTCCAGTGCTACCTTTTGTTGAACAT
CTCGAATACACCAAACCTTCTAGCTGCTAATACTCAGATTTATGGACAAGAAGTTATCATTGAAATTAAATGGTG
GCAGACATGTCCAAGGAATATTGCGGGGATTTGATCCCTTTATGAACCTTGTGATAGATGAATGTGTGGAGATGG
CGACTAGTGGACAACAGAACAATATTGGAATGGTGGTAATACGAGGAAATAGTATCATCATGTTAGAAGCCTTGG
AACGAGTATAAATAATGGCTGTTCAGCAGAGAAACCCATGTCCTCTCTCCATAGGGCCTGTTTTACTATGATGTA
AAAATTAGGTCATGTACATTTTCATATTAGACTTTTTGTTAAATAAACTTTTGTAATAGTCAAAAATGCTTTCTC
AGATGTTCTGAATATAGAATATCAGCTCTCATTCCAGTTTTTTCTAACATGAATTTTCCTGGTTGACATTGATTT
CAAAGGGTTTTATGCATTAAAGTGAAAGAATCTTATTAAATGTGAAACATGGCAAGGATTCCTTCTGTCCATCAT
CTTTCAACACTGAACAGATAAAGAAGTTACAAACATGAGTGAGTTTCTTCTAAAACACTAATTTTC

FIGURE 785

GTACGCCGATTCCATATGGGCGCCGGCGCGGAGCGCCGCGGGGCAGCGCGGGGTCGCC**ATG**GCTGAGCTGCAGCA
GCTCCGGGTGCAGGAGGCGATGGAGTCCATGGTGAAGAGTCTGGAAAGAGAGAACATCCGGAAGATGCAGGGTCT
CATGTTCCGGTGCAGCGCCAGCTGTTGTGAGGACAGCCAGGCCTCCATGAAGCAGGTGCACCAGTGCATCGAGCG
CTGCCATGTGCCTCTGGCTCAAGCCCAGGCTTTGGTCACCAGTGAGCTGGAGAAGTTCCAGGACCGCCTGGCCCG
GTGCACCATGCATTGCAATGACAAAGCCAAAGATTCAATAGATGCTGGGAGTAAGGAGCTTCAGGTGAAGCAGCA
GCTGGACAGTTGTGTGACCAAGTGTGTGGATGACCACATGCACCTCATCCCAACTATGACCAAGAAGATGAAGGA
GGCTCTCTTATCAATTGGAAAA**TAA**AGTATTTGCCAGTGGCCATCAGGCTGAGGGCAAGAATATATTTTTTATA
AGGAATTGGGAATTTTAGTCTTTTAAGCAAAGTTTACGAATGAAGAAATGAAGGATGGCCACAAGCGTAAGGCAT
ATGTCACTTGCCTCTGGACACTGGTTATTTTATGTTTCAGTCCCTAAAAAATGAAATGGAAAAAAGTGGTGCTAA
ATCGAGTCAGAGATATTACAGGAGAGTTTTAGAGCTTATTATTTCCTGTGGCCAGTGCTTGTCCTGGCAGTAAGG
CTCTCCCCTGTAACAAGCCAGAGCCCTCCAAGGTACCAGACTCTTCTTACTACACAGGTACTAACAGGCTGGCAG
GTTAGAGTTGGTGGAGTCTGAGGAGAGATATTTTCTCTTTGTTGCCAACATCCTGTTTACCAAAAGTGTCACCCC
ACCATCTTCCATAAGCTGTGAAACAAAATCAATGAGGTCACTAACTTAGAAGGGAAAGAAAGTTTTCTGGGTCTT
TGTTTTCTTGATTTGGGGTAATTTATACAAGGGCATACAAGTTGATTTTAAGATGTGGAACTGGGAGGTAGACTA
GTTTGGATAAGAACTTTGAAATGTTCCTTGTGGATCCCCATTTCTGGTCATCAAGATGTGGATGTACATTTCTTA
AAATTATTACATGCTGCATCTTTCAGCCTGGAGACTGTGCAGAAACATGAGAGGTGATGACACACTAATTATGGG
AAGCAGAATTACTGGCTGATGGCCCCTGAGGCTGTGTGTAACAAAATGACAGGACAATCTTGCAGTAACACTTTC
CCCTTGAAGAGAAGGGGGTTTTGATTGTGATATATACTAGTATCTAGGAATGAACAGTAAAAGAGGAGCAGTTGG
CTACTTGATTACAACAGAGTAAATGAAGTACTGGATTTGGGAAAACCTGGTTTTATTAGAACATATGGAATGAAA
GCCTACACCTAGCATTGCCTACTTAGCCCCCTGAATTAACAGAGCCCAATTGAGACAAACCCCTGGCAACAGGAA
ATTCAAGGGAGAAAAAGTAAGCAACTTGGGCTAGGATGAGCTGACTCCCTTAGAGCAAAGGAGAGACAGCCCCCA
TTACCAAATACCATTTTTGCCTGGGGCTTGTGCAGCTGGCAGTGTTCCTGCCCCAGCATGGCACCTTATTGTTTT
GATAGCAACTTCGTTGAATTTTCACCAACTTATTACTTGAAATTATAATATAGCCTGTCCGTTTGCTGTTTCCAG
GCTGTGATATATTTTCCTAGTGGTTTGACTTTAAAAATAAATAAGGTTTAATTTTCTCCCC

FIGURE 786

MAELQQLRVQEAMESMVKSLERENIRKMQGLMFRCSASCCEDSQASMKQVHQCIERCHVPLAQAQALVTSELEKF
QDRLARCTMHCNDKAKDSIDAGSKELQVKQQLDSCVTKCVDDHMHLIPTMTKKMKEALLSIGK

FIGURE 787A

CAGACCCGCCCGTGGCTGCAGCAGTGGTGTCCCATTTTAATGACTGCCCAGATTCCCACACTCAGTTCTGCTTCC
ATGGAACCTGCAGGTTTTTGGTGCAGGAGGACAAGCCAGCATGTGTCTGCCATTCTGGGTACGTTGGTGCACGCT
GTGAGCATGCGGACCTCCTGGCCGTGGTGGCTGCCAGCCAGAAGAAGCAGGCCATCACCGCCTTGGTGGTGGTCT
CCATCGTGGCCCTGGCTGTCCTTATCATCACATGTGTGCTGATACACTGCTGCCAGGTCCGAAAACACTGTGAGT
GGTGCCGGGCCCTCATCTGCCGGCACGAGAAGCCCAGCGCCCTCCTGAAGGGAAGAACCGCTTGCTGCCACTCAG
AAACAGTGGTCTGAAGAGCCCAGAGGAGGAGTTTGGCCAGGTGGACTGTGGCAGATCAATAAAGAAAGGCTTCTT
CAGGACAGCACTGCCAGAGATGCCTGGGTGTGCCACAGACCTTCCTACTTGGCCTGTAATCACCTGTGCAGCCTT
TTGTGGGCCTTCAAAACTCTGTCAAGAACTCCGTCTGCTTGGGGTTATTCAGTGTGACCTAGAGAAGAAATCAGC
GGACCACGATTTCAAGACTTGTTAAAAAAGAACTGCAAAGAGACGGACTCCTGTTCACCTAGGTGAGGTGTGTGC
AGCAGTTGGTGTCTGAGTCCACATGTGTGCAGTTGTCTTCTGCCAGCCATGGATTCCAGGCTATATATTTCTTTT
TAATGGGCCACCTCCCCACAACAGAATTCTGCCCAACACAGGAGATTTCTATAGTTATTGTTTTCTGTCATTTGC
CTACTGGGGAAGAAAGTGAAGGAGGGGAAACTGTTTAATATCACATGAAGACCCTAGCTTTAAGAGAAGCTGTAT
CCTCTAACCACGAGACCCTCAACCAGCCCAACATCTTCCATGGACACATGACATTGAAGACCATCCCAAGCTATC
GCCACCCTTGGAGATGATGTCTTATTTATTAGATGGATAATGGTTTATTTTTAATCTCTTAAGTCAATGTAAAA
AGTATAAAACCCCTTCAGACTTCTACATTAATGATGTATGTGTTGCTGACTGAAAAGCTATACTGATTAGAAATG
TCTGGCCTCTTCAAGACAGCTAAGGCTTGGGAAAAGTCTTCCAGGGTGCGGAGATGGAACCAGAGGCTGGGTTAC
TGGTAGGAATAAAGGTAGGGGTTCAGAAATGGTGCCATTGAAGCCACAAAGCCGGTAAATGCCTCAATACGTTCT
GGGAGAAAACTTAGCAAATCCATCAGCAGGGATCTGTCCCCTCTGTTGGGGAGAGAGGAAGAGTGTGTGTGTCTA
CACAGGATAAACCCAATACATATTGTACTGCTCAGTGATTAAATGGGTTCACTTCCTCGTGAGCCCTCGGTAAGT
ATGTTTAGAAATAGAACATTAGCCACGAGCCATAGGCATTTCAGGCCAAATCCATGAAAGGGGGACCAGTCATTT
ATTTTCCATTTTGTTGCTTGGTTGGTTTGTTGCTTTATTTTTAAAAGGAGAAGTTTAACTTTGCTATTTATTTTC
GAGCACTAGGAAAACTATTCCAGTAATTTTTTTTTCCTCATTTCCATTCAGGATGCCGGCTTTATTAACAAAAAC
TCTAACAAGTCACCTCCACTATGTGGGTCTTCCTTTCCCCTCAAGAGAAGGAGCAATTGTTCCCCTGAGCATCTG
GGTCCATCTGACCCATGGGGCCTGCCTGTGAGAAACAGTGGGTCCCTTCAAATACATAGTGGATAGCTCATCCCT
AGGAATTTTCATTAAAATTTGGAAACAGAGTAATGAAGAAATAATATATAAACTCCTTATGTGAGGAAATGCTAC
TAATATCTGAAAAGTGAAAGATTTCTATGTATTAACTCTTAAGTGCACCTAGCTTATTACATCGTGAAAGGTACA
TTTAAAATATGTTAAATTGGCTTGAAATTTTCAGAGAATTTTGTCTTCCCCTAATTCTTCTTCCTTGGTCTGGAA
GAACAATTTCTATGAATTTTCTCTTTATTTTTTTTTATAATTCAGACAATTCTATGACCCGTGTCTTCATTTTTG
GCACTCTTATTTAACAATGCCACACCTGAAGCACTTGGATCTGTTCAGAGCTGACCCCCTAGCAACGTAGTTGAC
ACAGCTCCAGGTTTTTAAATTACTAAAATAAGTTCAAGTTTACATCCCTTGGGCCAGATATGTGGGTTGAGGCTT
GACTGTAGCATCCTGCTTAGAGACCAATCAACGGACACTGGTTTTTAGACCTCTATCAATCAGTAGTTAGCATCC
AAGAGACTTTGCAGAGGCGTAGGAATGAGGCTGGACAGATGGCGGAAGCAGAGGTTCCCTGCGAAGACTTGAGAT
TTAGTGTCTGTGAATGTTCTAGTTCCTAGGTCCAGCAAGTCACACCTGCCAGTGCCCTCATCCTTATGCCTGTAA
CACACATGCAGTGAGAGGCCTCACATATACGCCTCCCTAGAAGTGCCTTCCAAGTCAGTCCTTTGGAAACCAGCA
GGTCTGAAAAAGAGGCTGCATCAATGCAAGCCTGGTTGGACCATTGTCCATGCCTCAGGATAGAACAGCCTGGCT
TATTTGGGGATTTTTCTTCTAGAAATCAAATGACTGATAAGCATTGGATCCCTCTGCCATTTAATGGCAATGGTA
GTCTTTGGTTAGCTGCAAAAATACTCCATTTCAAGTTAAAAATGCATCTTCTAATCCATCTCTGCAAGCTCCCTG
TGTTTCCTTGCCCTTTAGAAAATGAATTGTTCACTACAATTAGAGAATCATTTAACATCCTGACCTGGTAAGCTG
CCACACACCTGGCAGTGGGGAGCATCGCTGTTTCCAATGGCTCAGGAGACAATGAAAAGCCCCCATTTAAAAAAA
TAACAAACATTTTTTAAAAGGCCTCCAATACTCTTATGGAGCCTGGATTTTTCCCACTGCTCTACAGGCTGTGAC
TTTTTTTAAGCATCCTGACAGGAAATGTTTTCTTCTACATGGAAAGATAGACAGCAGCCAACCCTGATCTGGAAG
ACAGGGCCCCGGCTGGACACACGTGGAACCAAGCCAGGGATGGGCTGGCCATTGTGTCCCCGCAGGAGAGATGGG
CAGAATGGCCCTAGAGTTCTTTTCCCTGAGAAAGGAGAAAAAGATGGGATTGCCACTCACCCACCCACACTGGTA
AGGGAGGAGAATTTGTGCTTCTGGAGCTTCTCAAGGGATTGTGTTTTGCAGGTACAGAAAACTGCCTGTTATCTT
CAAGCCAGGTTTTCGAGGGCACATGGGTCACCAGTTGCTTTTTCAGTCAATTTGGCCGGGATGGACTAATGAGGC
TCTAACACTGCTCAGGAGACCCCTGCCCTCTAGTTGGTTCTGGGCTTTGATCTCTTCCAACCTGCCCAGTCACAG
AAGGAGGAATGACTCAAATGCCCAAAACCAAGAACACATTGCAGAAGTAAGACAAACATGTATATTTTTAAATGT
TCTAACATAAGACCTGTTCTCTCTAGCCATTGATTTACCAGGCTTTCTGAAAGATCTAGTGGTTCACACAGAGAG

FIGURE 787B

AGAGAGAGTACTGAAAAAGCAACTCCTCTTCTTAGTCTTAATAATTTACTAAAATGGTCAACTTTTCATTATCTT
TATTATAATAAACCTGATGCTTTTTTTTAGAACTCCTTACTCTGATGTCTGTATATGTTGCACTGAAAAGGTTAA
TATTTAATGTTTTAATTTATTTTGTGTGGTAAGTTAATTTTGATTTCTGTAATGTGTTAATGTGATTAGCAGTTA
TTTTCCTTAATATCTGAATTATACTTAAAGAGTAGTGAGCAATATAAGACGCAATTGTGTTTTTCAGTAATGTGC
ATTGTTATTGAGTTGTACTGTACCTTATTTGGAAGGATGAAGGAATGAATCTTTTTTTCCT

FIGURE 788A

ATTTCCTCCCAGCCTCGTGCGGGAAATGGCTTTAATTCTGACGGCAGGGCTGTGAGGGACTAGCGGGAACCCGAG
CCTTTTGTCAAGGAACTGCGGCGTCGGTGGCCAGTCATCCCCGCCGCCGCGGAGCCGCTGCACTGCTGGGGGATC
TCCCAGCAGCTCTGACGAGCGCGGGCTGCAGCATGGGCAGAAAACGCTGCCCTGCAGATTAGCTGGGTGGATTTT
TTAAGCGCACCCCACCCCCCAAACCCATAAAATAACAAAACCAACCCGCAGTGGCCGACCGGAGATAGCTAAGAT
GCCGCGCAGGAGTTTCCACCTGGATGTTTGAGGTTGTGTAGATGTGGCCGGCACCCTTGAGAGTGGAGCTAGGGG
GTGCAGACTGAGCAGTGAACAGAAGGAGCCTTGGACAGGGCTGGGCCAGCCTCCCGAGTTCCAGGAGCGAATTGC
AAACCCACCGGGAAAATGAGCGAAGAGACGGTCCCCGAGGCTGCCTCGCCGCCGCCCCCGCAGGGGCAGCCTTAC
TTTGACCGCTTCTCAGAGGACGACCCCGAGTACATGCGCCTTCGCAACCGGGCGGCGGACCTGCGGCAGGACTTC
AACCTGATGGAGCAGAAGAAGCGCGTCACCATGATCCTGCAGAGTCCCTCTTTCAGGGAGGAGCTGGAAGGCCTC
ATCCAGGAGCAGATGAAGAAGGGGAACAACTCCTCCAACATCTGGGCCCTGCGACAGATCGCGGACTTCATGGCC
AGCACCTCCCACGCAGTCTTCCCGACATCTTCCATGAATGTCTCCATGATGACGCCTATCAATGACCTCCACACA
GCTGACTCCCTGAACCTGGCCAAAGGGGAGCGGCTCATGCGGTGCAAGATCAGCAGTGTCTACCGACTCCTGGAC
CTCTATGGCTGGGCCCAGCTGAGTGACACCTATGTCACGTTGAGAGTCAGCAAGGAGCAGGACCACTTCCTGATC
AGCCCTAAGGGAGTTTCTTGCAGTGAAGTCACAGCGTCCAGCCTGATCAAGGTGAACATTCTGGGAGAGGTGGTG
GAGAAGGGCAGCAGCTGCTTCCCAGTGGACACCACAGGCTTCTGTCTGCACTCGGCCATCTATGCAGCGAGGCCC
GACGTGCGCTGCATCATCCACCTGCACACACCGGCCACAGCAGCGGTGTCGGCCATGAAGTGGGGCCTCCTGCCT
GTCTCCCACAATGCCCTGCTGGTGGGGGACATGGCCTATTATGACTTCAATGGGGAAATGGAGCAGGAAGCCGAT
CGGATCAACCTGCAGAAGTGCCTTGGACCCACCTGCAAGATCCTGGTGCTAAGAAACCATGGAGTGGTTGCTCTG
GGTGACACGGTAGAGGAGGCATTTTACAAGATCTTCCACCTGCAGGCTGCATGTGAGATACAGGTGTCGGCTCTG
TCCAGTGCCGGGGGAGTGGAGAACCTCATCCTCCTGGAGCAGGAGAAGCACCGGCCCCATGAGGTGGGCTCCGTG
CAGTGGGCCGGGAGCACCTTTGGGCCTATGCAGAAGAGTCGGCTGGGGGAGCATGAGTTTGAGGCCCTCATGAGG
ATGCTGGACAACCTGGGCTACAGAACAGGTTACACGTATCGCCACCCCTTTGTTCAAGAGAAAACCAAACACAAA
AGTGAGGTGGAGATTCCAGCCACGGTCACAGCCTTCGTGTTTGAGGAGGACGGTGCCCCGGTGCCCGCCCTGCGA
CAGCATGCCCAGAAGCAGCAGAAGGAGAAGACCCGCTGGCTCAATACGCCCAACACCTACCTGCGGGTCAATGTG
GCCGATGAGGTCCAGAGGAGCATGGGCAGCCCCCGACCCAAGACCACGTGGATGAAGGCTGACGAGGTGGAGAAA
TCCAGCAGTGGCATGCCGATTCGCATCGAAAACCCAAACCAATTTGTGCCTCTCTATACTGACCCCCAGGAAGTA
CTGGAGATGAGGAACAAGATTCGAGAACAAAACCGACAAGATGTGAAGTCAGCGGGGCCTCAGTCCCAGCTCCTG
GCGAGCGTCATTGCCGAGAAGAGCCGAAGCCCGTCTACAGAGAGCCAGCTGATGTCCAAGGGAGACGAGGATACC
AAAGACGATTCAGAGGAGACGGTGCCCAACCCCTTCAGCCAACTCACTGACCAGGAGTTGGAGGAGTACAAGAAA
GAGGTGGAGAGGAAGAAACTAGAACTTGATGGAGAGAAAGAAACTGCCCCAGAAGAGCCTGGCTCACCTGCAAAG
TCTGCACCTGCTTCTCCAGTGCAGAGCCCAGCGAAGGAGGCAGAGACAAAGAGCCCTTTAGTCTCTCCTTCCAAG
TCTTTAGAGGAAGGTACTAAGAAGACAGAAACAAGCAAAGCCGCCACCACAGAGCCCGAAACAACCCAGCCGGAA
GGGGTGGTGGTCAACGGGAGGGAGGAGGAGCAGACGGCAGAGGAAATCCTCAGCAAAGGCCTGAGCCAGATGACC
ACCAGTGCTGACACGGATGTTGATACCTCTAAGGACAAAACCGAGTCGGTCACCAGCGGCCCCATGTCCCCAGAG
GGCTCACCTTCCAAGTCTCCCTCAAAGAAGAAAAAGAAATTCCGAACCCCCTCCTTCCTGAAAAAGAGCAAAAAG
AAGGAGAAAGTGGAGTCCTGATTCATGACACCCTTGGGCTCCCTCCTGCCTCCTCTCTCTCCTCCCCTTCCCTTC
TCCCATCTCTGTCCCTGCAAGCACAGGGCTAAGGAGGGATAGAGTAGGACCCTGGACCACATTCGGAAGGGGAAC
TTAGAGATCACCCGACCAACCCTTCGTTTTACAGTTGCCCAAGAGAAATCAGGTGACTTGCCCAAGGTCACACAG
CTAGTTAGCGGCAGAGCCTGCACTCGAATTCAGGTCTCCTGACTTCCAGTCCAGTGCTCCTTCTACTACACAACA
CTGCCTAGTTGTGGGCTGCCTTTGTTTGGATGCTGTCCACCAATCTGAGCCTAGGGCAAGAAGGCCAGAAATGGG
CCGTGAGCTCTCACAGGCTCAGACTAAATCAGAGGTCAAGGCTTCCCCTGAGTAAGGTCCATTTCTTCCCAGGAA
TCCAATCTCCTGTGGATGGAGCTATCTCTACATTTAAAAATCTCTTCTCTTTTCCACTTTGGGTCCCTGCCCTGC
TGCTCAAAGTGACTAGCCAAATTGACCCCTCCAACAGAAAGTAATCTTTGTTCCCAAGGGCTGATGGCTTAGCTT
GTACTACCCCAAACATTAACCCTGAGCTTTCTTCATGGAACCTCTTGAATGATGGATGGAAGAGCTATAAGAGGT
GGTAGGCATAGGGGCAAGCCATGTAAGCTGAGGATTGGGGATGGTTTCATCAACATAAGAGGCCAGGAACTTGAC
CCCTTTGAATTGTGCATCTCAGGCACTTCAAAACTAAAACCAAATTTAGCATAGGAAAAAGTTGTTTAATGCTCA
GGGCAGAAATTTGGGGAAGTTGAAATCCTCTGTTGGCTTTGGGTTGTATAAGGAGGATCAAAACAACAGAGGAAA
TGCTGACTTTCTAGCTTTGCATGACACCTGGAGCAATGCACTGTACCTGCCTCACTCCTGTCCAGTGGTCAGGTT

FIGURE 788B

TCCCCTGACCTTCCCTCACCCCCAGAAACACTTGCTTACAGACCGAAACTGGCATCTTACTCTTGGCACCTTGAC
TTGCACCCTCTGAGGTTCCAACTCAGTCATTCTTTGTCCAGCAGAGGAGAATCAGAAATGAGCCCTTCAGGATTA
ATCCTCTTGCACCAGCTCTCAGAGAAATGCTGGGTATCCCTGTCCTTGTCCCTATCTGTCCATCCTGGGGCCTGG
TAATGGCCACAGTTATTGTTTTAAATGCCAACACTGTCTTCTCATGTTCTTCCGTGGGGCATTGATTAATGAGCA
TTTGTTGGCTCCTAAAAATTAGACAATCCATTCTCTTG

FIGURE 789

GGCACGAGGCGGAGAACAGGAGC<u>ATG</u>GAGGGCGGGCTGGGGCGTGCTGTGTGCTTGCTGACCGGGGCCTCCCGCG
GCTTCGGCCGGACGCTGGCCCCGCTCCTGGCCTCGCTGCTGTCGCCCGGCTCCGTGCTTGTCCTTAGCGCCCGCA
ACGACGAGGCACTGCGCCAGCTGGAGGCCGAGCTGGGCGCCGAGCGGTCTGGCCTGCGCGTGGTGCGGGTGCCCG
CCGACCTGGGCGCCGAGGCCGGCTTGCAGCAGCTGCTCGGCGCCCTGCGCGAGCTCCCCCGGCCCAAGGGGCTGC
AGCGACTGCTGCTTATCAACAACGCGGGCTCTCTTGGGGATGTGTCCAAAGGCTTCGTGGACCTGAGTGACTCCA
CTCAAGTGAACAACTACTGGGCACTGAACTTGACCTCCATGCTCTGCCTGACTTCCAGCGTCCTGAAGGCCTTCC
CGGACAGTCCTGGCCTCAACAGAACCGTGGTTAACATCTCGTCCCTCTGTGCCCTGCAACCTTTCAAAGGCTGGG
CGCTGTACTGTGCAGGAAAGGCTGCTCGTGATATGCTGTTCCAGGTCCTGGCGCTGGAGGAACCTAATGTGAGGG
TGCTGAACTATGCCCCAGGTCCTCTGGACACAGACATGCAGCAGTTGGCCCGGGAGACCTCCGTGGACCCAGACA
TGCGAAAAGGGCTGCAGGAGCTGAAGGCAAAGGGGAAGCTGGTGGATTGCAAGGTGTCAGCCCAGAAACTGCTGA
GCTTACTGGAAAAGGACGAGTTCAAGTCTGGAGCCCACGTGGACTTCTATGACAAA<u>TAA</u>GCCCATGTTTTTGGCT
TCCTGAACCTTTTTGCCCCCACTTTTAGACATACCCCAGAGCCCTGTGGCTCCCCACACCCTGCCATAGGGGCAG
TCCTGCCTTACACATAGAAGCATTCATGCCTGCTGCCCTGCCCTCAGGCACAGCCAGCTGTGAGCTCCCAGGTCA
TTGGCCTTACCAGTTGTCAGGAGTCTGTGCTGTGCACCCTGGGTTATAAGGAGGCTTAGGAGAGAGGTTATGGGT
ATTGGTGTCTCTATCCCCAGGAATAGAACTTAAGGGGTGGGAAGAACAGGAAAAGAAGCTGGAACACAGAAGAGA
GGAGGTTGTGTCTCTTGCTCATAGCAAGCCTGTGGGTAGAGGAAAGAGTGATCTGGTGTCGAATAGGAGGACCCA
TGTAGATTCGCAGATGGCCTGGATGGGAGGAAGGGCAGACGGTACATGTCCCAGCCCACATAGATGCCCCTTGCT
GAGGGTAGCAGGACCTTCTGTTGAACTTTGTGTCCTCACTCTGATGTCTCCTTCCTTCAGAATCTACCACCCCTC
CCCCAGGCTGGGAGAAGGGGCTCCTGGGTGTCTGTATACACGCCAAAGGCAGATACAAATAAAATACAGATTGTC
CTTTAAAAAAAAAAAAAAAAAA

FIGURE 790

MEGGLGRAVCLLTGASRGFGRTLAPLLASLLSPGSVLVLSARNDEALRQLEAELGAERSGLRVVRVPADLGAEAG
LQQLLGALRELPRPKGLQRLLLINNAGSLGDVSKGFVDLSDSTQVNNYWALNLTSMLCLTSSVLKAFPDSPGLNR
TVVNISSLCALQPFKGWALYCAGKAARDMLFQVLALEEPNVRVLNYAPGPLDTDMQQLARETSVDPDMRKGLQEL
KAKGKLVDCKVSAQKLLSLLEKDEFKSGAHVDFYDK

FIGURE 791

GGAGCATGGAGGGCGGGCTGGGGCGTGCTGTGTGCTTGCTGACCGGGGCCTCCCGCGGCTTCGGCCGGACGCTGG
CCCCGCTCCTGGCCTCGCTGCTGTCGCCCGGCTCCGTGCTTGTCCTTAGCGCCCGCAACGACGAGGCACTGCGCC
AGCTGGAGGCCGAGCTGGGCGCCGAGCGGTCTGGCCTGCGCGTGGTGCGGGTGCCCGCCGACCTGGGCGCCGAGG
CCGGCTTGCAGCAGCTGCTCGGCGCCCTGCGCGAGCTCCCCCGGCCCAAGGGGCTGCAGCGACTGCTGCTTATCA
ACAACGCGGGTAAGACCCCGGGGCTGGAGCGGACTCCCCATGTGAGCGCCCACTTCCTCCACCGCTGGGGAATTT
AAGGGCTACTCCTAGGGGTCAGATAGGACGCCTAGAAATCTAAAGCCCTAGTTGTTCCAGCTTGAGTAGCAAGTG
GAGGCGAGGTGTACAGGAAGACTCGGTGCCGTCGGGACAACAGTCTGCCCCCACTTCCTGGAAAATTGGCCAGCC
GGGTTTTCCAAAGCGCCTGTAGAACTTTCCCGAGCCCCTTGCTCTGCGCCCTCTGGCGGAGGCCTGAGTCAGGGC
TTGGAGTCTCCAAACAAGTAAACTCTCTGCTTCTCCAAAGGACCGCTAGAGCTTTCCTTCAGCCCCACGGCAAGG
GCTCTCTTGGGGATGTGTCCAAAGGCTTCGTGGACCTGAGTGACTCCACTCAAGTGAACAACTACTGGGCACTGA
ACTTGACCTCCATG

FIGURE 792

GTTCCAAGGTTTGCGGCCCGGTCTCGGAGAAGAGGGGAGAGTGGAGGGCCGCTGAATAAGCTTCCAAA**ATG**ATGC
CCACACCAGTTATCCTATTGAAAGAGGGGACTGATAGCTCCCAAGGCATCCCCCAGCTTGTGAGTAACATCAGTG
CCTGCCAGGTGATTGCTGAGGCTGTAAGAACTACCCTGGGTCCCCGTGGCATGGACAAGCTTATTGTAGATGGCA
GAGGCAAAGCAACAATTTCTAATGATGGGGCCACAATTCTGAAACTTCTTGATGTTGTCCATCCTGCAGCAAAGA
CTTTGGTAGACATTGCCAAATCCCAAGATGCTGAGGTGGGTGATGGCACCACCTCAGTGACCTTGCTGGCTGCAG
AGTTTCTGAAGCAGGTGAAACCCTATGTGGAGGAAGGTTTACACCCCCAGATCATCATTCGAGCTTTCCGCACAG
CCACCCAGCTGGCAGTTAACAAGATCAAAGAGATTGCTGTGACCGTGAAGAAGGCAGATAAAGTGGAGCAGAGGA
AGCTGCTGGAAAAGTGTGCCATGACCGCTCTGAGCTCCAAGCTGATCTCCCAGCAGAAAGCTTTCTTTGCTAAGA
TGGTGGTGGATGCAGTGATGATGCTCGATGATTTGCTGCAGCTTAAAATGATTGGAATCAAGAAGGTACAGGGTG
GAGCCCTCGAGGATTCTCAGCTGGTAGCTGGTGTTGCATTCAAGAAGACTTTCTCTTACGCTGGGTTTGAAATGC
AACCCAAAAAGTACCACAATCCCAAGATTGCCCTTTTGAATGTCGAGCTCGAGTTGAAAGCTGAGAAAGACAATG
CTGAGATAAGAGTCCACACAGTTGAGGATTATCAGGCAATTGTTGATGCTGAGTGGAACATTCTCTATGACAAGT
TAGAGAAGATCCATCATTCTGGAGCCAAAGTTGTCTTGTCCAAACTCCCCATTGGGGATGTGGCCACCCAGTACT
TTGCTGACAGGGACATGTTCTGTGCTGGCCGAGTACCTGAGGAGGATCTGAAGAGGACAATGATGGCCTGTGGAG
GCTCAATCCAGACCAGTGTGAATGCTCTGTCAGCAGATGTGCTGGGTCGATGCCAGGTGTTTGAAGAGACCCAGA
TTGGAGGCGAGAGGTACAATTTTTTTACTGGCTGCCCCAAGGCCAAGACATGCACCTTCATTCTCCGTGGCGGCG
CCGAGCAGTTTATGGAGGAGACAGAGCGGTCCCTGCATGATGCCATCATGATCGTCAGGAGGGCCATCAAGAATG
ATTCAGTGGTGGCTGGTGGCGGGGCCATTGAGATGGAACTCTCCAAGTACCTGCGGGATTACTCAAGGACTATTC
CAGGAAAACAGCAGCTGTTGATTGGGGCTTATGCCAAGGCCTTGGAGATTATCCCACGCCAGCTGTGTGACAATG
CTGGCTTTGATGCCACAAACATTCTCAACAAGCTGCGGGCTCGGCATGCCCAGGGGGGTACATGGTATGGAGTAG
ACATCAACAACGAGGACATTGCTGACAACTTTGAAGCTTTCGTGTGGGAGCCAGCTATGGTGCGGATCAATGCGC
TGACAGCAGCCTCTGAGGCTGCGTGCCTGATCGTGTCTGTAGATGAAACCATCAAGAACCCCCGCTCGACTGTGG
ATGCTCCCACAGCAGCAGGCCGGGGCCGTGGTCGTGGCCGCCCCCAC**TGA**GAGGCACCCCACCCATCACATGGCT
GGCTGGCTGCTGGGTGCACTTACCCTCCTTGGCTTGGTTACTTCATTTTACAAGGAAGGGGTAGTAATTGGCCCA
CTCTCTTCTTACTGGAGGCTATTTAAATAAAATGTAAGACTTCAAAAAAAAAAAAAAAAAAA

FIGURE 793

MMPTPVILLKEGTDSSQGIPQLVSNISACQVIAEAVRTTLGPRGMDKLIVDGRGKATISNDGATILKLLDVVHPA
AKTLVDIAKSQDAEVGDGTTSVTLLAAEFLKQVKPYVEEGLHPQIIIRAFRTATQLAVNKIKEIAVTVKKADKVE
QRKLLEKCAMTALSSKLISQQKAFFAKMVVDAVMMLDDLLQLKMIGIKKVQGGALEDSQLVAGVAFKKTFSYAGF
EMQPKKYHNPKIALLNVELELKAEKDNAEIRVHTVEDYQAIVDAEWNILYDKLEKIHHSGAKVVLSKLPIGDVAT
QYFADRDMFCAGRVPEEDLKRTMMACGGSIQTSVNALSADVLGRCQVFEETQIGGERYNFFTGCPKAKTCTFILR
GGAEQFMEETERSLHDAIMIVRRAIKNDSVVAGGGAIEMELSKYLRDYSRTIPGKQQLLIGAYAKALEIIPRQLC
DNAGFDATNILNKLRARHAQGGTWYGVDINNEDIADNFEAFVWEPAMVRINALTAASEAACLIVSVDETIKNPRS
TVDAPTAAGRGRGRGRPH

FIGURE 794

ATATAACCGCGTGGCCCGCGCGCGCGCTTCCCTCCCGGCGCAGTCACCGGCGCGGTCTATGGCTGCGACTTCTCT
A**ATG**TCTGCTTTGGCTGCCCGGCTGCTGCAGCCCGCGCACAGCTGCTCCCTTCGCCTTCGCCCTTTCCACCTCGC
GGCAGTTCGAAATGAAGCTGTTGTCATTTCTGGAAGGAAACTGGCCCAGCAGATCAAGCAGGAAGTGCGGCAGGA
GGTAGAAGAGTGGGTGGCCTCAGGCAACAAACGGCCACACCTGAGTGTGATCCTGGTTGGCGAGAATCCTGCAAG
TCACTCCTATGTCCTCAACAAAACCAGGGCAGCTGCAGTTGTGGGAATCAACAGTGAGACAATTATGAAACCAGC
TTCAATTTCAGAGGAAGAATTGTTGAATTTAATCAATAAACTGAATAATGATGATAATGTAGATGGCCTCCTTGT
TCAGTTGCCTCTTCCAGAGCATATTGATGAGAGAAGGATCTGCAATGCTGTTTCTCCAGACAAGGATGTTGATGG
CTTTCATGTAATTAATGTAGGACGAATGTGTTTGGATCAGTATTCCATGTTACCGGCTACTCCATGGGGTGTGTG
GGAAATAATCAAGCGAACTGGCATTCCAACCCTAGGGAAGAATGTGGTTGTGGCTGGAAGGTCAAAAAACGTTGG
AATGCCCATTGCAATGTTACTGCACACAGATGGGGCGCATGAACGTCCCGGAGGTGATGCCACTGTTACAATATC
TCATCGATATACTCCCAAAGAGCAGTTGAAGAAACATACAATTCTTGCAGATATTGTAATATCTGCTGCAGGTAT
TCCAAATCTGATCACAGCAGATATGATCAAGGAAGGAGCAGCAGTCATTGATGTGGGAATAAATAGAGTTCACGA
TCCTGTAACTGCCAAACCCAAGTTGGTTGGAGATGTGGATTTTGAAGGAGTCAGACAAAAAGCTGGGTATATCAC
TCCAGTTCCTGGAGGTGTTGGCCCCATGACAGTGGCAATGCTAATGAAGAATACCATTATTGCTGCAAAAAAGGT
GCTGAGGCTTGAAGAGCGAGAAGTGCTGAAGTCTAAAGAGCTTGGGGTAGCCACTAAT**TAA**CTACTGTGTCTTCT
GTGTCACAAACAGCACTCCAGGCCAGCTCAAGAAGCAAAGCAGGCCAATAGAAATGCAATATTTTTAATTTATTC
TACTGAAATGGTTTAAAATGATGCCTTGTATTTATTGAAAGCTTAAATGGGTGGGTGTTTCTGCACATACCTCTG
CAGTACCTCACCAGGGAGCATTCCAGTATCATGCAGGGTCCTGTGATCTAGCCAGGAGCAGCCATTAACCTAGTG
ATTAATATGGGAGACATTACCATATGGAGGATGGATGCTTCACTTTGTCAAGCACCTCAGTTACACATTCGCCTT
TTCTAGGATTGCATTTCCCAAGTGCTATTGCAATAACAGTTGATACTCATTTAGGTACCAGACCTTTTGAGTTC
AACTGATCAAACCAAAGGAAAAGTGTTGCTAGAGAAAATTGGGGAAAAGGTGAAAAAGAAAAAATGGTAGTAATT
GAGCAGAAAAAAATTAATTTATATATGTATTGATTGGCAACCAGATTTATCTAAGTAGAACTGAATTGGCTAGGA
AAAAAGAAAAACTGCATGTTAATCATTTTCCTAAGCTGTCCTTTTGAGGCTTAGTCAGTTTATTGGGAAAATGTT
TAGGATTATTCCTTGCTATTAGTACTCATTTTATGTATGTTACCCTTCAGTAAGTTCTCCCCATTTTAGTTTTCT
AGGACTGAAAGGATTCTTTTCTACATTATACATGTGTGTTGTCATATTTGGCTTTTGCTATATACTTTAACTTCA
TTGTTAAATTTTTGTATTGTATAGTTTCTTTGGTGTATCTTAAAACCTATTTTTGAAAAACAAACTTGGCTTGAT
AATCATTTGGGCAGCTTGGGTAAGTACGCAACTTACTTTTCCACCAAAGAACTGTCAGCAGCTGCCTGCTTTTCT
GTGATGTATGTATCCTGTTGACTTTTCCAGAAATTTTTTAAGAGTTTGAGTTACTATTGAATTTAATCAGACTTT
CTGATTAAAGGGTTTTCTTTCTTTTTTAATAAAACACATCTGTCTGGTATGGTA

FIGURE 795

MSALAARLLQPAHSCSLRLRPFHLAAVRNEAVVISGRKLAQQIKQEVRQEVEEWVASGNKRPHLSVILVGENPAS
HSYVLNKTRAAAVVGINSETIMKPASISEEELLNLINKLNNDDNVDGLLVQLPLPEHIDERRICNAVSPDKDVDG
FHVINVGRMCLDQYSMLPATPWGVWEIIKRTGIPTLGKNVVVAGRSKNVGMPIAMLLHTDGAHERPGGDATVTIS
HRYTPKEQLKKHTILADIVISAAGIPNLITADMIKEGAAVIDVGINRVHDPVTAKPKLVGDVDFEGVRQKAGYIT
PVPGGVGPMTVAMLMKNTIIAAKKVLRLEEREVLKSKELGVATN

FIGURE 796

GGAAAATTTGTCACAGCAGCCAGAGGGGTTTAACAGGAGTGCAGAGGGATAAGGGCAGCTTCTGCCCTCTGCCCA
AGAGCTGGCCACCTCTTTAAAGACTGAGGGAACAGTGGGAGGAGGAACTGTGGGACAGTGTGGTACCTATCTGTC
CCCCCTCTGGAGGGGTTGACAAGGGAAAGGGCACCGGGGGGCACAGAG**ATG**CAGGACAGATTGCACATCCTGGAG
GACCTGAATATGCTCTACATTCGGCAGATGGCACTCAGCCTGGAGGACACGGAGTTGCAGAGGAAGCTAGACCAT
GAGATCCGGATGAGGGAAGGGGCCTGTAAGCTGCTGGCAGCCTGCTCCCAGCGAGAGCAGGCTCTGGAGGCCACC
AAGAGCCTGCTAGTGTGCAACAGCCGCATCCTCAGCTACATGGGCGAGCTGCAGCGGCGCAAGGAGGCGCAGGTG
CTGGGGAAGACAAGCCGGCGGCCTTCTGACAGTGGCCCGCCCGCTGAGCGCTCCCCCTGCCGCGGCCGGGTCTGC
ATCTCTGACCTCCGGATTCCACTCATGTGGAAGGACACAGAATATTTCAAGAACAAAGGTGACTTGCACCGCTGG
GCTGTGTTCCTGCTGCTGCAGCTGGGGGAACACATCCAGGACACAGAGATGATCCTAGTGGACAGGACCCTCACA
GACATCTCCTTTCAGAGCAATGTGCTCTTCGCTGAGGCGGGGCCAGACTTTGAACTGCGGTTAGAGCTGTATGGG
GCCTGTGTGGAAGAAGAGGGGGCCCTGACTGGCGGCCCCAAGAGGCTTGCCACCAAACTCAGCAGCTCCCTGGGC
CGCTCCTCAGGGAGGCGTGTCCGGGCATCGCTGGACAGTGCTGGGGGTTCAGGGAGCAGTCCCATCTTGCTCCCC
ACCCCAGTTGTTGGTGGTCCTCGTTACCACCTCTTGGCTCACACCACACTCACCCTGGCAGCAGTGCAAGATGGA
TTCCGCACACATGACCTCACCCTTGCCAGTCATGAGGAGAACCCTGCCTGGCTGCCCCTTTATGGTAGCGTGTGT
TGCCGTCTGGCAGCTCAGCCTCTCTGCATGACTCAGCCCACTGCAAGTGGTACCCTCAGGGTGCAGCAAGCTGGG
GAGATGCAGAACTGGGCACAAGTGCATGGAGTTCTGAAAGGCACAAACCTCTTCTGTTACCGGCAACCTGAGGAT
GCAGACACTGGGGAAGAGCCGCTGCTTACTATTGCTGTCAACAAGGAGACTCGAGTCCGGGCAGGGGAGCTGGAC
CAGGCTCTAGGACGGCCCTTCACCCTAAGCATCAGTAACCAGTATGGGGATGATGAGGTGACACACACCCTTCAG
ACAGAAAGTCGGGAAGCACTGCAGAGCTGGATGGAGGCTCTGTGGCAGCTTTTCTTTGACATGAGCCAATGGAAG
CAGTGCTGTGATGAAATCATGAAAATTGAAACTCCTGCTCCCCGGAAACCACCCCAAGCACTGGCAAAGCAGGGG
TCCTTGTACCATGAGATGGCTATTGAGCCGCTGGATGACATCGCAGCGGTGACAGACATCCTGACCCAGCGGGAG
GGCGCAAGGCTGGAGACACCCCCACCCTGGCTGGCAATGTTTACAGACCAGCCTGCCCTGCCTAACCCCTGCTCG
CCTGCCTCAGTGGCCCCAGCCCCAGACTGGACCCACCCCCTGCCCTGGGGGAGACCCCGAACCTTTTCCCTGGAT
GCTGTCCCCCCAGACCACTCCCCTAGGGCTCGCTCGGTTGCCCCCCTCCCACCTCAGCGATCCCCACGGACCAGA
GGCCTCTGCAGCAAAGGCCAACCTCGCACTTGGCTCCAGTCACCAGTG**TGA**GAGAGAAAGGTGCTGGCATAGGAT
CTGCCCAGAAGAGAAAATGACCCATGCGCAGTTGGGCTCTGGATACGGCGCTGTCTATAGCAAGTTGGCCAGTCT
GGCCTCCTGTTCCTCTGCTGGACCTGGGGTAGGCTGCAGGGGTGGGCAGAAGCCCCTCTTAAATTGTGGTTGCCA
TGGTACCGAGGGACTCATTCCTGGGGCTCGCTGGGACCTCCCTAAACCCTTCCTGGAAGAAAACTGGAACCAACT
CTGCCCTACCTCCCTGCACTAACCAGCTTTGAGGATGGCACTGAAGAACCCTTGGAGCAAACATACCTCCCTTGT
GACTCCCACATCAACCATTAAAGTTATTTAACAGCAAAAAAAAAAAAAAA

FIGURE 797

MQDRLHILEDLNMLYIRQMALSLEDTELQRKLDHEIRMREGACKLLAACSQREQALEATKSLLVCNSRILSYMGE
LQRRKEAQVLGKTSRRPSDSGPPAERSPCRGRVCISDLRIPLMWKDTEYFKNKGDLHRWAVFLLLQLGEHIQDTE
MILVDRTLTDISFQSNVLFAEAGPDFELRLELYGACVEEEGALTGGPKRLATKLSSSLGRSSGRRVRASLDSAGG
SGSSPILLPTPVVGGPRYHLLAHTTLTLAAVQDGFRTHDLTLASHEENPAWLPLYGSVCCRLAAQPLCMTQPTAS
GTLRVQQAGEMQNWAQVHGVLKGTNLFCYRQPEDADTGEEPLLTIAVNKETRVRAGELDQALGRPFTLSISNQYG
DDEVTHTLQTESREALQSWMEALWQLFFDMSQWKQCCDEIMKIETPAPRKPPQALAKQGSLYHEMAIEPLDDIAA
VTDILTQREGARLETPPPWLAMFTDQPALPNPCSPASVAPAPDWTHPLPWGRPRTFSLDAVPPDHSPRARSVAPL
PPQRSPRTRGLCSKGQPRTWLQSPV

FIGURE 798

GACTACGTGGGTCTGGAGCTGACTGCCGTCCTGACACGTCCTAGAGCTGCAAGTCCTGCCAGAGAGCCACCATGA
CCTCTCAGCCTCTCAGGCTAGCAGAAGAGTATGGCCCAAGTCCTGGGGAGTCTGAACTGGCTGTGAACCCCTTTG
ATGGGCTTCCCTTCTCTTCCCGCTACTATGAGCTGCTGAAGCAGCGCCAAGCCTTGCCCATCTGGGCTGCTCGCT
TTACCTTCTTGGAGCAGTTGGAGAGTAACCCCACTGGAGTGGTGCTGGTGTCTGGGGAGCCTGGTTCTGGCAAGA
GCACCCAGATCCCTCAGTGGTGTGCAGAGTTTGCGCTGGCCAGAGGGTTCCAGAAAGGACAGGTTACTGTTACTC
AGCCCTACCCTCTTGCAGCCCGGGAGCCTGGCTCTGCGGGTTGCTGATGAG<u>ATG</u>GACCTGACCCTGGGTCATGAG
GTTGGATCCAGCATCCCCCAGGAGGACTGCACGGGGCCCAACACCCTGCTCAGGTTCTGCTGGGACAGGCTGCTT
CTGCAGGAGGTGGCCTCGACCCGAGGCACTGGAGCCTGGGGCGTGCTGGTACTAGATGAGGCTCAGGAGCGGTCG
GTGGCATCAGATTCACTCCAGGGGCTACTGCAAGATGCCAGGCTGGAAAAACTTCCGGGGGACCTCAGAGTGGTT
GTGGTTACTGACCCAGCCCTTGAACCTAAGCTCCGAGCTTTCTGGGGCAATCCTCCTATTGTGCATATACCCAGA
GAGCCTGGTGAGAGACCTTCCCCCATCTACTGGGACACCATCCCACCTGATCGGGTGGAAGCTGCCTGCCAAGCA
GTGCTTGAATTGTGTCGGAAGGAGCTTCCAGGAGATGTGCTAGTGTTCCTGCCCAGTGAGGAGGAAATTTCCCTG
TGCTGTGAATCCTTGTCCAGGGAGGTAGAGTCCTTGCTTCTCCAAGGGCTTCCACCACGAGTACTGCCCCTTCAC
CCAGACTGTGGACGAGCCGTTCAGGCTGTGTATGAGGACATGGATGCCCGAAAGGTTGTGGTCACTCACTGGCTG
GCTGACTTCTCCTTCTCCCTCCCTTCCATCCAACATGTCATCGACTCAGGACTGGAGCTCCGAAGTGTTTACAAT
CCTAGGATCCGAGCAGAATTCCAAGTGTTGAGGCCAATCAGCAAGTGTCAGGCAGAGGCAAGACGATTGCGAGCA
AGAGGGTTCCCACCAGGATCCTGCCTCTGCCTGTATCCTAAGTCCTTCTTAGAACTAGAAGCTCCACCATTGCCA
CAACCCAGGGTGTGTGAGGAGAATCTGAGCTCCCTGGTGTTACTACTAAAAAGGAGACAGATTGCAGAGCCAGGG
GAGTGTCACTTCCTGGACCAGCCTGCTCCAGAAGCACTGATGCAAGCCCTGGAAGATTTAGACTATCTGGCAGCC
CTGGATGATGATGGGGACCTGTCAGATCTGGGTGTCATACTATCAGAATTCCCTCTGGCCCCTGAGCTGGCCAAA
GCCCTGCTGGCCTCATGCGAGTTTGACTGTGTGGACGAGATGCTCACCCTGGCTGCCATGCTCACAGCTGCCCCT
GGGTTTACCCGTCCTCCACTCAGTGCAGAAGAAGCTGCCCTGCGTCGGGCCCTGGAACACACGGATGGTGACCAC
AGTTCTCTGATCCAGGTGTATGAAGCCTTTATACAAAGTGGAGCAGATGAGGCTTGGTGCCAGGCTCGAGGTCTG
AATTGGGCAGCATTGTGCCAAGCCCATAAACTTCGGGGAGAACTCCTAGAACTCATGCAACGAATTGAACTTCCC
TTGTCCCTACCAGCCTTTGGCTCTGAGCAGAATCGCAGAGACCTTCAGAAAGCACTGGTGTCAGAATACTTTCTC
AAGGTGGCCAGAGACACAGACGGGACTGGAAATTACCTTCTCCTAACCCATAAGCATGTGGCCCAGCTCTCCTCA
TACTGCTGCTACCGAAGCCGCAGAGCTCCTGCCAGACCCCCACCATGGGTGCTCTACCACAATTTCACCATATCC
AAAGACAACTGCCTCTCCATTGTTTCTGAGATTCAACCACAGATGCTGGTGGAATTGGCCCCTCCATACTTCCTG
AGTAACTTGCCTCCCAGTGAGAGCAGAGACCTTCTGAACCAGCTAAGGGAAGGAATGGCAGATTCTACAGCAGGG
AGCAAATCATCCTCAGCCCAGGAGTTCAGAGATCCCTGTGTCCTGCAG<u>TGA</u>CCTGCCTGCCTATGGAATGGAGCT
GGGTTCATCTCATCACATTAGATTATCCCTCAGGGTGACACCAAAGCACCCAGACAGATTTAGAAGCCCAAAGTT
TAGGGTCAAATGTAAACCCTGGAACCTGAGTCCCAAGAAATGGTAGACTGGGAATGGAAAGAATGGGGTAAACCA
CAGTCTACATAGGGAAGGACTCTTTCCTTAGCCTTCTCTTATTGATTGGAGAGGGACTGACATGCTCCTCATTCT
CTTAACTTTGCCAAACCCATTCTTGTACTCCCTTGTGATCTATAAAAGATTTTTCTATGATGCCAAAAAAAAAAA
AAAAAAAAA

FIGURE 799

MDLTLGHEVGSSIPQEDCTGPNTLLRFCWDRLLLQEVASTRGTGAWGVLVLDEAQERSVASDSLQGLLQDARLEK
LPGDLRVVVVTDPALEPKLRAFWGNPPIVHIPREPGERPSPIYWDTIPPDRVEAACQAVLELCRKELPGDVLVFL
PSEEEISLCCESLSREVESLLLQGLPPRVLPLHPDCGRAVQAVYEDMDARKVVVTHWLADFSFSLPSIQHVIDSG
LELRSVYNPRIRAEFQVLRPISKCQAEARRLRARGFPPGSCLCLYPKSFLELEAPPLPQPRVCEENLSSLVLLLK
RRQIAEPGECHFLDQPAPEALMQALEDLDYLAALDDDGDLSDLGVILSEFPLAPELAKALLASCEFDCVDEMLTL
AAMLTAAPGFTRPPLSAEEAALRRALEHTDGDHSSLIQVYEAFIQSGADEAWCQARGLNWAALCQAHKLRGELLE
LMQRIELPLSLPAFGSEQNRRDLQKALVSEYFLKVARDTDGTGNYLLLTHKHVAQLSSYCCYRSRRAPARPPPWV
LYHNFTISKDNCLSIVSEIQPQMLVELAPPYFLSNLPPSESRDLLNQLREGMADSTAGSKSSSAQEFRDPCVLQ

FIGURE 800

CGAAAATGGCGGCGGCGGCGACGGCCGGGCGCTCCTGAAGCAGCAGTTATGGAGCTTCCCTCAGGGCCGGGGCCG
GAGCGGCTCTTTGACTCGCACCGGCTTCCGGGTGACTGCTTCCTACTGCTCGTGCTGCTGCTCTACGCGCCAGTC
GGGTTCTGCCTCCTCGTCCTGCGCCTCTTTCTCGGGATCCACGTCTTCCTGGTCAGCTGCGCGCTGCCAGACAGC
GTCCTTCGCAGATTCGTAGTGCGGACCATGTGTGCGGTGCTAGGGCTCGTGGCCCGGCAGGAGGACTCCGGACTC
CGGGATCACAGTGTCAGGGTCCTCATTTCCAACCATGTGACACCTTTCGACCACAACATAGTCAATTTGCTTACC
ACCTGTAGCACCCCTCTACTCAATAGTCCCCCCAGCTTTGTGTGCTGGTCTCGGGGCTTCATGGAGATGAATGGG
CGGGGGGAGTTGGTGGAGTCACTCAAGAGATTCTGTGCTTCCACGAGGCTTCCCCCCACTCCTCTGCTGCTATTC
CCTGAGGAAGAGGCCACCAATGGCCGGGAGGGGCTCCTGCGCTTCAGTTCCTGGCCATTTTCTATCCAAGATGTG
GTACAACCTCTTACCCTGCAAGTTCAGAGACCCCTGGTCTCTGTGACGGTGTCAGATGCCTCCTGGGTCTCAGAA
CTGCTGTGGTCACTTTTCGTCCCTTTCACGGTGTATCAAGTAAGGTGGCTTCGTCCTGTTCATCGCCAACTAGGG
GAAGCGAATGAGGAGTTTGCACTCCGTGTACAACAGCTGGTGGCCAAGGAATTGGGCCAGACAGGGACACGGCTC
ACTCCAGCTGACAAAGCAGAGCACATGAAGCGACAAAGACACCCCAGATTGCGCCCCCAGTCAGCCCAGTCTTCT
TTCCCTCCCTCCCCTGGTCCTTCTCCTGATGTGCAACTGGCAACTCTGGCTCAGAGAGTCAAGGAAGTTTTGCCC
CATGTGCCATTGGGTGTCATCCAGAGAGACCTGGCCAAGACTGGCTGTGTAGACTTGACTATCACTAATCTGCTT
GAGGGGGCCGTAGCTTTCATGCCTGAAGACATCACCAAGGGAACTCAGTCCCTACCCACAGCCTCTGCCTCCAAG
TTTCCCAGCTCTGGCCCGGTGACCCCTCAGCCAACAGCCCTAACATTTGCCAAGTCTTCCTGGGCCCGGCAGGAG
AGCCTGCAGGAGCGCAAGCAAGCACTATATGAATACGCAAGAAGGAGATTCACAGAGAGACGAGCCCAGGAGGCT
GACTGAGCTCAAAGGAACAGGATGGCACCCAGAGCCGCAGGACGGAGACTGGGGGCAGCCCTCACCCAACTCACA
ACAGGCTGGATGGGTGGGTGGTAAAAAGGGAAGGATGAGGCTCCCCCAATGTCACATTAAATTCATGGTTTTCAT
TC

FIGURE 801

CGTGGATCCCGAGAAAGAGGCGCAGGACGAGGAGGCAGAACCCGACTGGCGCGTAGAGCAGCAGCACGAGCAGTA
GGAAGCAGTCACCCGGAAGCCTGGGGGCGAGAGGCGAAGTGGTCAGGCGCCGAAGGCCGAGAGCACGCGGGGATC
GGTCTCTTCCCGCCGGGTCTCTTACCGGTGCGAGTCAAAGAGCCGCTCCGGCCCCGGCCCTGAGGGAAGCTCCAT
AACTGCTGCTTCAGGAGCGCCCGGCCGTCGCCGCCGCCGCCATTTTCGCGCCCGGCCGCAGGGGCTCTTGGGAAG
GCGGAGTCTTTGGGCATCCGCCCGGGGTGAGGGGACCCGAAGTCCTGAGGCGCGCCGGAAGGGCTAGCGGTCCCA
GCATACCCCGCGGCCCCTTGGGCCGTCTCACAACTCGCGTCCGGCGGAGACCACAATTCCCGGCATTCGTGGGGC
AGGGAGGAGTCGGCCTCCCGGAATCCTGGTCCCGGCGTGCACTTCTGAAGGACTTCAGGTACCGGCGTGCCCCGC
GTCCTACTGTCCGCCTGCTCGCGTCCTGGGTGCCGCCTCTGAGTAGGGCGGGCGAGGAGGCAGCCAAGGCGGAGC
TG<u>ATG</u>GCTGCGCCGAGGGCGGGGCGGGGTGCAGGCTGGAGCCTTCGGGCATGGCGGGCTTTGGGGGGCATTCGCT
GGGGGAGGAGACCCCGTTTGACCCCTGACCTCCGGGCCCTGCTGACGTCAGGAACTTCTGACCCCCGGGCCCGAG
TGACTTATGGGACCCCCAGTCTCTGGGCCCGGTTGTCTGTTGGGGTCACTGAACCCCGAGCATGCCTGACGTCTG
GGACCCCGGGTCCCCGGGCACAACTGACTGCGGTGACCCCAGATACCAGGACCCGGGAGGCCTCAGAGAACTCTG
GAACCCGTTCGCGCGCGTGGCTGGCGGTGGCGCTGGGCGCTGGGGGGGCAGTGCTGTTGTTGTTGTGGGGCGGGG
GTCGGGGTCCTCCGGCCGTCCTCGCCGCCGTCCCTAGCCCGCCGCCCGCTTCTCCCCGGAGTCAGTACAACTTCA
TCGCAGATGTGGTGGAGAAGACAGCACCTGCCGTGGTCTATATCGAGATCCTGGACCGGCACCCTTTCTTGGGCC
GCGAGGTCCCTATCTCGAACGGCTCAGGATTCGTGGTGGCTGCCGATGGGCTCATTGTCACCAACGCCCATGTGG
TGGCTGATCGGCGCAGAGTCCGTGTGAGACTGCTAAGCGGCGACACGTATGAGGCCGTGGTCACAGCTGTGGATC
CCGTGGCAGACATCGCAACGCTGAGGATTCAGACTAAGGAGCCTCTCCCCACGCTGCCTCTGGGACGCTCAGCTG
ATGTCCGGCAAGGGGAGTTTGTTGTTGCCATGGGAAGTCCCTTTGCACTGCAGAACACGATCACATCCGGCATTG
TTAGCTCTGCTCAGCGTCCAGCCAGAGACCTGGGACTCCCCCAAACCAATGTGGAATACATTCAAACTGATGCAG
CTATTGATTTTGGAAACTCTGGAGGTCCCCTGGTTAACCTGGATGGGGAGGTGATTGGAGTGAACACCATGAAGG
TCACAGCTGGAATCTCCTTTGCCATCCCTTCTGATCGTCTTCGAGAGTTTCTGCATCGTGGGGAAAAGAAGAATT
CCTCCTCCGGAATCAGTGGGTCCCAGCGGCGCTACATTGGGGTGATGATGCTGACCCTGAGTCCCAGCATCCTTG
CTGAACTACAGCTTCGAGAACCAAGCTTTCCCGATGTTCAGCATGGTGTACTCATCCATAAAGTCATCCTGGGCT
CCCCTGCACACCGGGCTGGTCTGCGGCCTGGTGATGTGATTTTGGCCATTGGGGAGCAGATGGTACAAAATGCTG
AAGATGTTTATGAAGCTGTTCGAACCCAATCCCAGTTGGCAGTGCAGATCCGGCGGGGACGAGAAACACTGACCT
TATATGTGACCCCTGAGGTCACAGAA<u>TGA</u>ATAGATCACCAAGAGTATGAGGCTCCTGCTCTGATTTCCTCCTTGC
CTTTCTGGCTGAGGTTCTGAGGGCACCGAGACAGAGGGTTAAATGAACCAGTGGGGGCAGGTCCCTCCAACCACC
AGCACTGACTCCTGGGCTCTGAAGAATCACAGAAACACTTTTTATATAAAATAAAATTATACCTAGCAACATATT
ATAGTAAAAAATGAGGTGGGAGGGCTGGATCTTTTCCCCCACCAAAAGGCTAGAGGTAAAGCTGTATCCCCCTAA
ACTTAGGGGAGATACTGGAGCTGACCATCCTGACCTCCTATTAAAGAAAATGAGCTGCTGAAAAAAAAAAAAAAA
A

FIGURE 802

MAAPRAGRGAGWSLRAWRALGGIRWGRRPRLTPDLRALLTSGTSDPRARVTYGTPSLWARLSVGVTEPRACLTSG
TPGPRAQLTAVTPDTRTREASENSGTRSRAWLAVALGAGGAVLLLLWGGGRGPPAVLAAVPSPPPASPRSQYNFI
ADVVEKTAPAVVYIEILDRHPFLGREVPISNGSGFVVAADGLIVTNAHVVADRRRVRVRLLSGDTYEAVVTAVDP
VADIATLRIQTKEPLPTLPLGRSADVRQGEFVVAMGSPFALQNTITSGIVSSAQRPARDLGLPQTNVEYIQTDAA
IDFGNSGGPLVNLDGEVIGVNTMKVTAGISFAIPSDRLREFLHRGEKKNSSSGISGSQRRYIGVMMLTLSPSILA
ELQLREPSFPDVQHGVLIHKVILGSPAHRAGLRPGDVILAIGEQMVQNAEDVYEAVRTQSQLAVQIRRGRETLTL
YVTPEVTE

FIGURE 803

GCAACGCGAGTGGGAGCACCAGGATCTCGGGCTCGGAACGAGACTGCACGGATTGTTTTAAGAAA<u>**ATG**</u>GCAGACA
AACCAGACATGGGGGAAATCGCCAGCTTCGATAAGGCCAAGCTGAAGAAAACGGAGACGCAGGAGAAGAACACCC
TGCCGACCAAAGAGACCATTGAGCAGGAGAAGCGGAGTGAAATTTCC<u>**TAA**</u>GATCCTGGAGGATTTCCTACCCCCG
TCCTCTTCGAGACCCCAGTCGTGATGTGGAGGAAGAGCCACCTGCAAGATGGACACGAGCCACAAGCTGCACTGT
GAACCTGGGCACTCCGCGCCGATGCCACCGGCCTGTGGGTCTCTGAAGGGACCCCCCCCCAATCGGACTGCCAAA
TTCTCCGGTTTGCCCCGGGATATTATAGAAAATTATTTGTATGAATAATGAAAATAAAACACACCTCGTGGCATG
GCA

FIGURE 804

MADKPDMGEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSEIS

FIGURE 805

CACCAAATGGCGGATGACGCCGGTGCAGCGGGGGGGCCCAGAGCCCTGGTGGCCATGGGATAGGGAACCGCGGTG
GCTTCCACGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGGAGTGGACGGGGCCGTGCCGAGGCCGCGG
AGCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCTGTCACCAAGCTGGGCCGCTTGGTCAAGGACATGAA
GATCAAGTCCCTGGAGGAGATCTATCTCTTCTCCCTGCCCATTAAGGAATCTGAGATCATTGATTTCTTCCTGGG
GGACTCTCTCAAGGATGAGGTTTTGAAGATTATGCCGGTGCAGAAGCAGACCCGTGCCGGCCAGCGCACCAGGTT
CAAGGTGACAGGCCGCTGCGGCTCTGTGCTGGTGCGCCTCATCCCTGCACCCAGGGGCACTGGCATCGTCTCCGC
ACCTGTGCCCAAGAAGCTGCTCATGATGGCTGGTATCGATGACTGCTACACCTCAGCCCGGGGCTGCACTGCCAC
CCTGGGCAACTTCGCCAAGGCCACCTTTGATGCCATCTCTAAGACCTACAGCTACCTGACCCCCGACCTCTGGAA
GGAGACTGTATTTACCAAGTCTCCCTATCAGGAATTCACTGACCACCTCGTCAAGACCCACACCAGAGTCTCGGT
GCAGCGGACCCAGGCTTCAGATGTGGCTACAACATAGGGTTTTTATACAAGAAAAATAAAGTGAATTAAGCCTG

FIGURE 806

CGCAGGCTGGAAGGAAGACGAACCTACGAAGCAGAGATCTGAAGACAGC<u>ATG</u>TACACAGCCATTCCCCAGAGTGG
CTCTCCATTCCCAGGCTCAGTGCAGGATCCAGGCCTGCATGTGTGGCGGGTGGAGAAGCTGAAGCCGGTGCCTGT
GGCGCAAGAGAACCAGGGCGTCTTCTTCTCGGGGGACTCCTACCTAGTGCTGCACAATGGCCCAGAAGAGGTTTC
CCATCTGCACCTGTGGATAGGCCAGCAGTCATCCCGGGATGAGCAGGGGGCCTGTGCCGTGCTGGCTGTGCACCT
CAACACGCTGCTGGGAGAGCGGCCTGTGCAGCACCGCGAGGTGCAGGGCAATGAGTCTGACCTCTTCATGAGCTA
CTTCCCACGGGGCCTCAAGTACCAGGAAGGTGGTGTGGAGTCAGCATTTCACAAGACCTCCACAGGAGCCCCAGC
TGCCATCAAGAAACTCTACCAGGTGAAGGGGAAGAAGAACATCCGTGCCACCGAGCGGGCACTGAACTGGGACAG
CTTCAACACTGGGGACTGCTTCATCCTGGACCTGGGCCAGAACATCTTCGCCTGGTGTGGTGGAAAGTCCAACAT
CCTGGAACGCAACAAGGCGAGGGACCTGGCCCTGGCCATCCGGGACAGTGAGCGACAGGGCAAGGCCCAGGTGGA
GATTGTCACTGATGGGGAGGAGCCTGCTGAGATGATCCAGGTCCTGGGCCCCAAGCCTGCTCTGAAGGAGGGCAA
CCCTGAGGAAGACCTCACAGCTGACAAGGCAAATGCCCAGGCCGCAGCTCTGTATAAGGTCTCTGATGCCACTGG
ACAGATGAACCTGACCAAGGTGGCTGACTCCAGCCCCTTTGCCCTTGAACTGCTGATATCTGATGACTGCTTTGT
GCTGGACAACGGGCTCTGTGGCAAGATCTATATCTGGAAGGGGCGAAAAGCGAATGAGAAGGAGCGGCAGGCAGC
CCTGCAGGTGGCCGAGGGCTTCATCTCGCGCATGCAGTACGCCCCGAACACTCAGGTGGAGATTCTGCCTCAGGG
CCGTGAGAGTCCCATCTTCAAGCAATTTTTCAAGGACTGGAAA<u>TGA</u>GGGTGGGCGTCTTCCTGCCCCATGCTCCC
CTGCCCCCCACCACCTGCCTGCTTGCTTCTCTGGCTGCCTGGTCAGTGCAGAGGTGCCCCCTGCAGATGTTCAAT
AAAGGAGACAAGTGCTTTCCC

FIGURE 807

MYTAIPQSGSPFPGSVQDPGLHVWRVEKLKPVPVAQENQGVFFSGDSYLVLHNGPEEVSHLHLWIGQQSSRDEQG
ACAVLAVHLNTLLGERPVQHREVQGNESDLFMSYFPRGLKYQEGGVESAFHKTSTGAPAAIKKLYQVKGKKNIRA
TERALNWDSFNTGDCFILDLGQNIFAWCGGKSNILERNKARDLALAIRDSERQGKAQVEIVTDGEEPAEMIQVLG
PKPALKEGNPEEDLTADKANAQAAALYKVSDATGQMNLTKVADSSPFALELLISDDCFVLDNGLCGKIYIWKGRK
ANEKERQAALQVAEGFISRMQYAPNTQVEILPQGRESPIFKQFFKDWK

FIGURE 808

GGCACGAGGCGCCCGCCTGCTACGAGTAGAACGCTGTCCGCAGCTTGCGCATTTCGCAGCCGCTGCCGCCTCGCC
GCTGCTCCTTCGTAAGGCCACTTCCGCACACCGACACCAAC**ATG**AACGGACAGCTCAACGGCTTCCACGAGGCGT
TCATCGAGGAGGGCACATTCCTTTTCACCTCAGAGTCGGTCGGGGAAGGCCACCCAGATAAGATTTGTGACCAAA
TCAGTGATGCTGTCCTTGATGCCCACCTTCAGCAGGATCCTGATGCCAAAGTAGCTTGTGAAACTGTTGCTAAAA
CTGGAATGATCCTTCTTGCTGGGGAAATTACATCCAGAGCTGCTGTTGACTACCAGAAAGTGGTTCGTGAAGCTG
TTAAACACATTGGATATGATGATTCTTCCAAAGGTTTTGACTACAAGACTTGTAACGTGCTGGTAGCCTTGGAGC
AACAGTCACCAGATATTGCTCAAGGTGTTCATCTTGACAGAAATGAAGAAGACATTGGTGCTGGAGACCAGGGCT
TAATGTTTGGCTATGCCACTGATGAAACTGAGGAGTGTATGCCTTTAACCATTGTCTTGGCACACAAGCTAAATG
CCAAACTGGCAGAACTACGCCGTAATGGCACTTTGCCTTGGTTACGCCCTGATTCTAAAACTCAAGTTACTGTGC
AGTATATGCAGGATCGAGGTGCTGTGCTTCCCATCAGAGTCCACACAATTGTTATATCTGTTCAGCATGATGAAG
AGGTTTGTCTTGATGAAATGAGGGATGCCCTAAAGGAGAAAGTCATCAAAGCAGTTGTGCCTGCGAAATACCTTG
ATGAGGATACAATCTACCACCTACAGCCAAGTGGCAGATTTGTTATTGGTGGGCCTCAGGGTGATGCTGGTTTGA
CTGGACGCAAAATCATTGTGGACACTTATGGCGGTTGGGGTGCTCATGGAGGAGGTGCCTTTTCAGGAAAGGATT
ATACCAAGGTCGACCGTTCAGCTGCTTATGCTGCTCGTTGGGTGGCAAAATCCCTTGTTAAAGGAGGTCTGTGCC
GGAGGGTTCTTGTTCAGGTCTCTTATGCTATTGGAGTTTCTCATCCATTATCTATCTCCATTTTCCATTATGGTA
CCTCTCAGAAGAGTGAGAGAGAGCTATTAGAGATTGTGAAGAAGAATTTCGATCTCCGCCCTGGGGTCATTGTCA
GGGATCTGGATCTGAAGAAGCCAATTTATCAGAGGACTGCAGCCTATGGCCACTTTGGTAGGGACAGCTTCCCAT
GGGAAGTGCCCAAAAAGCTTAAATAT**TGA**AAGTGTTAGCCTTTTTCCCCAGACTTGTTGGCGTAGGCTACAGAG
AAGCCTTCAAGCTCTGAGGGAAAGGGCCCTCCTTCCTAAATTTCCTGTCCTCTTTCAGCTCCTGACCAGTTGCA
GTCACTCTAGTCAATGACATGAATTTTAGCTTTTGTGGGGGACTGTAAGTTGGGCTTGCTATTCTGTCCCTAGGT
GTTTTGTTCACCATTATAATGAATTTAGTGAGCATAGGTGATCCATGTAACTGCCTAGAAACAACACTGTAGTAA
ATAATGCTTTGAAATTGAACCTTTGTGCCCTATCACCCAACGCTCCAAAGTCATAATTGCATTGACTTTCCCCAC
CAGATGCTGAAAATGTCCTTGTGATGTGCACGTAAAGTACTTGTAGTTCCACTTATAGCCTCTGTCTGGCAATGC
CACAGCCCTGTCAGCATGAATTTGTAATGTCTTGAGCTCTATTATGAATGTGAAGCCTTCCCCTTATCCTCCCTG
TAACTTGATCCATTTCTAATTATGTAGCTCTTTGTCAGGGAGTGTTCCCTATCCAATCAATCTTGCATGTAACGC
AAGTTCCCAGTTGGAGCTCCAGCCTGACATCAAAAAAGGCAGTTACCATTAAACCATCTCCCTGGTGCTTATGCT
CTTAATTGCCACCTCTAACAGCACCAAATCAAAATCTCTCCACTTTCAGCTGTCTTTTGGAGGACGTACGTAATA
AGGTTTTAATTTAGTAAACCAATCCTATGCATGGTTTCAGCACTAGCCAAACCTCACCAACTCCTAGTTCTAGAA
AAACAGGCACTTGGCAGCCTTGTGATGTCATACAGAGAAGTCACAGGGCAGTACCTGAGGGTCTGTAGGTTGCAC
ACTTTGGTACCAGATAACTTTTTTTTTTCTTTATAAGAAAGCCTGAGTACTCCACACTGCACAATAACTCCTCCC
AGGGTTTTAACTTTGTTTTATTTTCAAAACCAGGTCCAATGAGCTTTCTGAACAGCTGGTGTAGCTACAGAGAAA
CCAGCTTCCTTCAGAGAGCAGTGCTTTTGGCGGGGAGGAGGAAATCCCTTCATACTTGAACGTTTTCTAATTGCT
TATTTATTGTATTCTGGGGTATGGCGTAAGTACAGAGAAGCCATCACCTCAGATGGCAGCTTTTAAAAGATTTTT
TTTTTTTCTCTCAACACCATGATTCCTTTAACAACATGTTTCCAGCATTCCCAGGTAGGCCAAGGTGTCCTACAG
AAAAACCTTGGGTTAGACCTACAGGGGGTCTGGCTGGTGTTAACAGAAGGGAGGGCAGAGCTGGTGCGGCTGGCC
ATGGAGAAAGCTGACTTGGCTGGTGTGGTACAGAGAAGCCAGCTTGTTTACATGCTTATTCCATGACTGCTTGCC
CTAAGCAGAAAGTGCCTTTCAGGATCTATTTTTGGAGGTTTATTACGTATGTCTGGTTCTCAATTCCAACAGTTT
AATGAAGATCTAAATAAAATGCTAGGTTCTACCTTAAAAAAAAAAAAAAAAAA

FIGURE 809

MNGQLNGFHEAFIEEGTFLFTSESVGEGHPDKICDQISDAVLDAHLQQDPDAKVACETVAKTGMILLAGEITSRA
AVDYQKVVREAVKHIGYDDSSKGFDYKTCNVLVALEQQSPDIAQGVHLDRNEEDIGAGDQGLMFGYATDETEECM
PLTIVLAHKLNAKLAELRRNGTLPWLRPDSKTQVTVQYMQDRGAVLPIRVHTIVISVQHDEEVCLDEMRDALKEK
VIKAVVPAKYLDEDTIYHLQPSGRFVIGGPQGDAGLTGRKIIVDTYGGWGAHGGGAFSGKDYTKVDRSAAYAARW
VAKSLVKGGLCRRVLVQVSYAIGVSHPLSISIFHYGTSQKSERELLEIVKKNFDLRPGVIVRDLDLKKPIYQRTA
AYGHFGRDSFPWEVPKKLKY

FIGURE 810

ATGACACTCTGAGCGCTCCGGGAACGGACAGCCCGGCGGCTTCCCGAAGCCGGCGGCGCAGCTGCCCGGGGCGAG
GGGGAGAAAGGGAGAGAGGGAGGGGGAGGGCGGGCGAAGCGGGAGAGCCAGAGACTCCTCGGCGCTGAGCGCGGC
GGCGGCCCGGGCAGCCCCACGCCCCTGCCTCGCGCGCCGCCCGCGCCATGAAGCACATCCCGGTCCTCGAGGACG
GGCCGTGGAAGACCGTGTGCGTGAAGGAGCTGAACGGCCTTAAGAAGCTCAAGCGGAAAGGCAAGGAGCCGGCGC
GGCGCGCGAACGGCTATAAAACTTTCCGACTGGACTTGGAAGCGCCCGAGCCCCGCGCCGTAGCCACCAACGGGC
TGCGGGACAGGACCCATCGGCTGCAGCCGGTCCCGGTACCGGTGCCGGTGCCAGTCCCAGTGGCGCCGGCCGTTC
CCCCAAGAGGGGGCACGGACACAGCCGGGGAGCGCGGGGGCTCTCGGGCGCCCGAGGTCTCCGACGCGCGGAAAC
GCTGCTTCGCCCTAGGCGCAGTGGGGCCAGGACTCCCCACGCCGCCGCCGCCGCCGCCTCCTGCGCCCCAGAGCC
AGGCACCTGGGGGCCCAGAGGCACAGCCTTTCCGGGAGCCGGGTCCGCGTCCTCGCATCTTGCTGTGCGCACCGC
CCGCGCGCCCCGCGCCGTCAGCACCCCCAGCACCGCCAGCGCCCCCGGAGTCCACTGTGCGCCCTGCGCCCCCGA
CGCGCCCCGGGGAAAGTTCCTACTCGTCAATTTCACACGTAATTTACAATAACCACCAGGATTCCTCCGCGTCGC
CTAGGAAACGACCGGGCGAAGCGACTGCCGCCTCCTCCGAGATCAAAGCCCTGCAGCAGACCCGGAGGCTCCTGG
CGAACGCCAGGGAGCGGACGCGGGTGCACACCATCAGCGCAGCCTTCGAGGCGCTCAGGAAGCAGGTGCCGTGCT
ACTCATATGGGCAGAAGCTGTCCAAACTGGCCATCCTGAGGATCGCCTGTAACTACATCCTGTCCCTGGCGCGGC
TGGCTGACCTTGACTACAGTGCCGACCACAGCAACCTCAGCTTCTCCGAGTGTGTGCAGCGCTGCACCCGCACCC
TGCAGGCCGAGGGACGTGCCAAGAAGCGCAAGGAGTGACTGGCTGCAGGCAAGACCAAGGCCACCACTGTGGGCC
CTCCTTCCAGTCAGGCCTGAGGACAAGGTGAGCTCGCTGAGTCCAGCCTCGTGGTCTTCTCCAAGATGCCGCCAG
ATGCCCAGCCTACAGCCTCTCAGGGTCGGATCGGAGCACGCCTGCCTCCCTCTCCCCTCCGCCCTCACCCAGCCA
ATCCGAGGCTGCTTCGCACTTTGCCCTCTGCCTGGTGGGGAGGGGAGAGCTCAGCCCCCGACTCACTCAGACCCC
AAGGCCCACTGTCCAGCTGCAGAAATTCGTTGCCAAAGATTGGACAGAGACACCGAAGGAAATGGGGTGGTGAAA
CCCCACAGCGAAAAGCCACACCGTTGCTCTGTGACTTTTGCTCCTCCTGTTGCCTGAGCCCCATCTCAAGCCAAA
GATGAGTCAGTGGTTCTGCTAGGAACTCATGGAATGGATGGGCATTTGATGACCCCTGGGGGTCATCTTGGCCCT
CTGACCTGGTGCTCTCTCTCCACTGGGCCTTGTGCTGGCTGAGTGCAAGACAAGCCTTAGGGGCTGTGAGAGGGA
GGCTGGGGTGCCTGGGCGGGGCTGGGAGTGGGACCTGAGATCCCTGCCCACTCTCTCCCCTTCATTGGCTGCCCA
GGCCACTGGCCCCAGTTCTCAGTGTCCCTTGGGTCCAGGCTCCTTGGGCCCTAAGCATCACCAGAAGGGAGTAAG
CAGGGAGAGAAGCAATATTACTCCCTCCCCTACACCAGGGACTTGCCCCAGGGCAGCTACCTATGGGTCTTTGCT
TCCCCAGCCAGCCTCTCCTCACTGTGACCCACCCCCATGGGCCCCCGTCCCAGGCAGCCAGCACCATGGGCAGGC
CCTGCCATGGGCAGAAAAAGAGTTTTTCTCTTGTTCAGCCTGCACGTGGCCTGAGGAAGGAGTAGAGGCTGGGTT
GGCTGGAGCCGTCCTACTGGGCAAGATGGCGCCCCACTTGGAGGGCGGTGGTCTGTTACAGGGTGTGCAGGGGCA
GAGAAGGAAGGGACCAGGGGACTGGGCCAGTATGTGGAGGATGGGGCCTGCGTGTTCAAAGCCAAGGCCCGCCCC
TTCCTTGTGCTCAAATGGCCAAAGCTGTTCACGTCTGTGCTCAACCATCTGCTTCAAATTGAAGTAAAAGCCCCA
AAATGTCAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAG

FIGURE 811

MKHIPVLEDGPWKTVCVKELNGLKKLKRKGKEPARRANGYKTFRLDLEAPEPRAVATNGLRDRTHRLQPVPVPVP
VPVPVAPAVPPRGGTDTAGERGGSRAPEVSDARKRCFALGAVGPGLPTPPPPPPPAPQSQAPGGPEAQPFREPGP
RPRILLCAPPARPAPSAPPAPPAPPESTVRPAPPTRPGESSYSSISHVIYNNHQDSSASPRKRPGEATAASSEIK
ALQQTRRLLANARERTRVHTISAAFEALRKQVPCYSYGQKLSKLAILRIACNYILSLARLADLDYSADHSNLSFS
ECVQRCTRTLQAEGRAKKRKE

FIGURE 812

GGCACGAGGGATGGCGGTTGTATCTGCTGTTCGCTGGCTGGGCCTCCGCAGCAGGCTTGGCCAGCCGCTGACGGG
TCGGCGGGCGGGTTTGTGTGAACAGGCACGCAGCTGCAGATTTTATTCTGGTAGTGCAACCCTCTCAAAGGTTGA
AGGAACTGATGTAACAGGGATTGAAGAAGTAGTAATTCCAAAAAAGAAAACTTGGGATAAAGTAGCCGTTCTTCA
GGCACTTGCATCCACAGTAAACAGGGATACCACAGCTGTGCCTTATGTGTTTCAAGATGATCCTTACCTTATGCC
AGCATCATCTTTGGAATCTCGTTCATTTTTACTGGCAAAGAAATCCGGGGAGAATGTGGCCAAGTTTATTATTAA
TTCATACCCCAAATATTTTCAGAAGGACATAGCTGAACCTCATATACCGTGTTTAATGCCTGAGTACTTTGAACC
TCAGATCAAAGACATAAGTGAAGCCGCCCTGAAGGAACGAATTGAGCTCAGAAAAGTCAAAGCCTCTGTGGACAT
GTTTGATCAGCTTTTGCAAGCAGGAACCACTGTGTCTCTTGAAACAACAAATAGTCTCTTGGATTTATTGTGTTA
CTATGGTGACCAGGAGCCCTCAACTGATTACCATTTTCAACAAACTGGACAGTCAGAAGCATTGGAAGAGGAAAA
TGATGAGACATCTAGGAGGAAAGCTGGTCATCAGTTTGGAGTTACATGGCGAGCAAAAAACAACGCTGAGAGAAT
CTTTTCTCTAATGCCAGAGAAAAATGAACATTCCTATTGCACAATGATCCGAGGAATGGTGAAGCACCGAGCTTA
TGAGCAGGCATTAAACTTGTACACTGAGTTACTAAACAACAGACTCCATGCTGATGTATACACATTTAATGCATT
GATTGAAGCAACAGTATGTGCGATAAATGAGAAATTTGAGGAAAAATGGAGTAAAATACTGGAGCTGCTAAGACA
C<u>ATG</u>GTTGCACAGAAGGTGAAACCAAATCTTCAGACTTTTAATACCATTCTGAAATGTCTCCGAAGATTTCATGT
GTTTGCAAGATCGCCAGCCTTACAGGTTTTACGTGAAATGAAAGCCATTGGAATAGAACCCTCGCTTGCAACATA
TCACCATATTATTCGCCTGTTTGATCAACCTGGAGACCCTTTAAAGAGATCATCCTTCATCATTTATGATATAAT
GAATGAATTAATGGGAAAGAGATTTTCTCCAAAGGACCCGGATGATGATAAGTTTTTCAGTCAGCCATGAGCAT
ATGCTCATCTCTCAGAGATCTAGAACTTGCCTACCAAGTACATGGCCTTTTAAAAACCGGAGACAACTGGAAATT
CATTGGACCTGATCAACATCGTAATTTCTATTATTCCAAGTTCTTCGATTTGATTTGTCTAATGGAACAAATTGA
TGTTACCTTGAAGTGGTATGAGGACCTGATACCTTCAGCCTACTTTCCCCACTCCCAAACAATGATACATCTTCT
CCAAGCATTGGATGTGGCCAATCGGCTAGAAGTGATTCCTAAAATTTGGAAAGATAGTAAAGAATATGGTCATAC
TTTCCGCAGTGACCTGAGAGAAGAGATCCTGATGCTCATGGCAAGGGACAAGCACCCACCAGAGCTTCAGGTGGC
ATTTGCTGACTGTGCTGCTGATATCAAATCTGCGTATGAAAGCCAACCCATCAGACAGACTGCTCAGGATTGGCC
AGCCACCTCTCTCAACTGTATAGCTATCCTCTTTTTAAGGGCTGGGAGAACTCAGGAAGCCTGGAAAATGTTGGG
GCTTTTCAGGAAGCATAATAAGATTCCTAGAAGTGAGTTGCTGAATGAGCTTATGGACAGTGCAAAAGTGTCTAA
CAGCCCTTCCCAGGCCATTGAAGTAGTAGAGCTGGCAAGTGCCTTCAGCTTACCTATTTGTGAGGGCCTCACCCA
GAGAGTAATGAGTGATTTTGCAATCAACCAGGAACAAAAGGAAGCCCTAAGTAATCTAACTGCATTGACCAGTGA
CAGTGATACTGACAGCAGCAGTGACAGCGACAGTGACACCAGTGAAGGCAAA<u>TGA</u>AGTGGAGATTCAGGAGCAG
CAATGGTCTCACCATAGCTGCTGGAATCACACCTGAGAACTGAGATATACCAATATTTAACATTGTTACAAAGAA
GAAAAGATACAGATTTGGTGAATTTGTTACTGTGAGGTACAGTCAGTACACAGCTGACTTATGTAGATTTAAGCT
GCTAATATGCTACTTAACCATCTATTAATGCACCATTAAAGGCTTAGCATTTAAGTAGCAACATTGCGGTTTTCA
GACACATGGTGAGGTCCATGGCTCTTGTCATCAGGATAAGCCTGCACACCTAGAGTGTCGGTGAGCTGACCTCAC
GATGCTGTCCTCGTGCGATTGCCCTCTCCTGCTGCTGGACTTCTGCCTTTGTTGGCCTGATGTGCTGCTGTGATG
CTGGTCCTTCATCTTAGGTGTTCATGCAGTTCTAACACAGTTGGGGTTGGGTCAATAGTTTCCCAATTTCAGGAT
ATTTCGATGTCAGAAATAACGCATCTTAGGAATGACTAAACAAGATAATGGCAGTTTAGGCTGCACAACTGGTAA
AATGACTGTAGATAAATGTTGTAATTAGTGTACACGTTTGTATTTTTGTTAATATAGCCGCTGCCATAGTTTTCT
AACTTGAACAGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 813

MVAQKVKPNLQTFNTILKCLRRFHVFARSPALQVLREMKAIGIEPSLATYHHIIRLFDQPGDPLKRSSFIIYDIM
NELMGKRFSPKDPDDDKFFQSAMSICSSLRDLELAYQVHGLLKTGDNWKFIGPDQHRNFYYSKFFDLICLMEQID
VTLKWYEDLIPSAYFPHSQTMIHLLQALDVANRLEVIPKIWKDSKEYGHTFRSDLREEILMLMARDKHPPELQVA
FADCAADIKSAYESQPIRQTAQDWPATSLNCIAILFLRAGRTQEAWKMLGLFRKHNKIPRSELLNELMDSAKVSN
SPSQAIEVVELASAFSLPICEGLTQRVMSDFAINQEQKEALSNLTALTSDSDTDSSSDSDSDTSEGK

FIGURE 814

ACGCGGGCACGCACACACGGAAGCACGCCTCCACTTAACTCGCGCCGCCGCGGCAGCTCGAGTCCACCAGCAGCG
CCGTCCGCTTGACCGAG**ATG**CTGCGGGCCTGTCAGTTATCGGGTGTGACCGCCGCCGCCCAGAGTTGTCTCTGTG
GGAAGTTTGTCCTCCGTCCATTGCGACCATGCCGCAGATACTCTACTTCAGGCAGCTCTGGGTTGACTACTGGCA
AAATTGCTGGAGCTGGCCTTTTGTTTGTTGGTGGAGGTATTGGTGGCACTATCCTATATGCCAAATGGGATTCCC
ATTTCCGGGAAAGTGTAGAGAAAACCATACCTTACTCAGACAAACTCTTCGAGATGGTTCTTGGTCCTGCAGCTT
ATAATGTTCCATTGCCAAAGAAATCGATTCAGTCGGGTCCACTAAAAATCTCTAGTGTATCAGAAGTAATGAAAG
AATCTAAACAGTCTGCCTCACAACTCCAAAAACAAAAGGGAGATACTCCAGCTTCAGCAACAGCACCTACAGAAG
CGGCTCAAATTATTTCTGCAGCAGGTGATACCCTGTCGGTCCCAGCCCCTGCAGTTCAGCCTGAGGAATCTTTAA
AAACTGATCACCCTGAAATTGGTGAAGGAAAACCCACACCTGCACTTTCAGAAGAAGCATCCTCATCTTCTATAA
GGGAGCGACCACCTGAAGAAGTTGCAGCTCGCCTTGCACAACAGGAAAAACAAGAACAAGTTAAAATTGAGTCTC
TAGCCAAGAGCTTAGAAGATGCTCTGAGGCAAACTGCAAGTGTCACTCTGCAGGCTATTGCAGCTCAGAATGCTG
CGGTCCAGGCTGTCAATGCACACTCCAACATATTGAAAGCCGCCATGGACAATTCTGAGATTGCAGGCGAGAAGA
AATCTGCTCAGTGGCGCACAGTGGAGGGTGCATTGAAGGAACGCAGAAAGGCAGTAGATGAAGCTGCCGATGCCC
TTCTCAAAGCCAAAGAAGAGTTAGAGAAGATGAAAAGTGTGATTGAAAATGCAAAGAAAAAAGAGGTTGCTGGGG
CCAAGCCTCATATAACTGCTGCAGAGGGTAAACTTCACAACATGATAGTTGATCTGGATAATGTGGTCAAAAAGG
TCCAAGCAGCTCAGTCTGAGGCTAAGGTTGTATCTCAGTATCATGAGCTGGTGGTCCAAGCTCGGGATGACTTTA
AACGAGAGCTGGACAGTATTACTCCAGAAGTCCTTCCTGGATGGAAAGGAATGAGTGTTTCAGACTTAGCTGACA
AGCTCTCTACTGATGATCTGAACTCCCTCATTGCTCATGCACATCGTCGTATTGATCAGCTGAACAGAGAGCTGG
CAGAACAGAAGGCCACCGAAAAGCAGCACATCACGTTAGCCTTGGAGAAACAAAAGCTGGAAGAAAAGCGGGCAT
TTGACTCTGCAGTAGCAAAAGCATTAGAACATCACAGAAGTGAAATACAGGCTGAACAGGACAGAAAGATAGAAG
AAGTCAGAGATGCCATGGAAAATGAAATGAGAACCCAGCTTCGCCGACAGGCAGCTGCCCACACTGATCACTTGC
GAGATGTCCTTAGGGTACAAGAACAGGAATTGAAGTCTGAATTTGAGCAGAACCTGTCTGAGAAACTCTCTGAAC
AAGAATTACAATTTCGTCGTCTCAGTCAAGAGCAAGTTGACAACTTTACTCTGGATATAAATACTGCCTATGCCA
GACTCAGAGGAATCGAACAGGCTGTTCAGAGCCATGCAGTTGCTGAAGAGGAAGCCAGAAAAGCCCACCAACTCT
GGCTTTCAGTGGAGGCATTAAAGTACAGCATGAAGACCTCATCTGCAGAAACACCTACTATCCCGCTGGGTAGTG
CAGTTGAGGCCATCAAAGCCAACTGTTCTGATAATGAATTCACCCAAGCTTTAACCGCAGCTATCCCTCCAGAGT
CCCTGACCCGTGGGGTGTACAGTGAAGAGACCCTTAGAGCCCGTTTCTATGCTGTTCAAAAACTGGCCCGAAGGG
TAGCAATGATTGATGAAACCAGAAATAGCTTGTACCAGTACTTCCTCTCCTACCTACAGTCCCTGCTCCTATTCC
CACCTCAGCAACTGAAGCCGCCCCCAGAGCTCTGCCCTGAGGATATAAACACATTTAAATTACTGTCATATGCTT
CCTATTGCATTGAGCATGGTGATCTGGAGCTAGCAGCAAAGTTTGTCAATCAGCTGAAGGGGGAATCCAGACGAG
TGGCACAGGACTGGCTGAAGGAAGCCCGAATGACCCTAGAAACGAAACAGATAGTGGAAATCCTGACAGCATATG
CCAGCGCCGTAGGAATAGGAACCACTCAGGTGCAGCCAGAG**TGA**GGTTTAGGAAGATTTTCATAAAGTCATATTT
CATGTCAAAGGAAATCAGCAGTGATAGATGAAGGGTTCGCAGCGAGAGTCCCGGACTTGTCTAGAAATGAGCAGG
TTTACAAGTACTGTTCTAAATGTTAACACCTGTTGCATTTATATTCTTTCCATTTGCTATCATGTCAGTGAACGC
CAGGAGTGCTTTCTTTGCAACTTGTGTAACATTTTCTGTTTTTCAGGTTTTACTGATGAGGCTTGTGAGGCCAA
TCAAAATAATGTTTGTGATCTCTACTACTGTTGATTTTGCCCTCGGAGCAAACTGAATAAAGCAACAAGATG

FIGURE 815

MLRACQLSGVTAAAQSCLCGKFVLRPLRPCRRYSTSGSSGLTTGKIAGAGLLFVGGGIGGTILYAKWDSHFRESV
EKTIPYSDKLFEMVLGPAAYNVPLPKKSIQSGPLKISSVSEVMKESKQSASQLQKQKGDTPASATAPTEAAQIIS
AAGDTLSVPAPAVQPEESLKTDHPEIGEGKPTPALSEEASSSSIRERPPEEVAARLAQQEKQEQVKIESLAKSLE
DALRQTASVTLQAIAAQNAAVQAVNAHSNILKAAMDNSEIAGEKKSAQWRTVEGALKERRKAVDEAADALLKAKE
ELEKMKSVIENAKKKEVAGAKPHITAAEGKLHNMIVDLDNVVKKVQAAQSEAKVVSQYHELVVQARDDFKRELDS
ITPEVLPGWKGMSVSDLADKLSTDDLNSLIAHAHRRIDQLNRELAEQKATEKQHITLALEKQKLEEKRAFDSAVA
KALEHHRSEIQAEQDRKIEEVRDAMENEMRTQLRRQAAAHTDHLRDVLRVQEQELKSEFEQNLSEKLSEQELQFR
RLSQEQVDNFTLDINTAYARLRGIEQAVQSHAVAEEEARKAHQLWLSVEALKYSMKTSSAETPTIPLGSAVEAIK
ANCSDNEFTQALTAAIPPESLTRGVYSEETLRARFYAVQKLARRVAMIDETRNSLYQYFLSYLQSLLLFPPQQLK
PPPELCPEDINTFKLLSYASYCIEHGDLELAAKFVNQLKGESRRVAQDWLKEARMTLETKQIVEILTAYASAVGI
GTTQVQPE

FIGURE 816

TAGTGCCGCCGCTCCCTACTCTGGGGGTTGGGACTACCTCCTTTTCCGCGGGCCCCGCCCAGGCGGCTGCCCGTG
ACCTGCCTGGGCGCGGGGAACTGAAAGCCGGAAGGGGCAAGACGGGTTCAGTTCGTCATGGGGCTGTTTGGAAAG
ACCCAGGAGAAGCCGCCCAAAGAACTGGTCAATGAGTGGTCATTGAAGATAAGAAAGGAAATGAGAGTTGTTGAC
AGGCAAATAAGGGATATCCAAAGAGAAGAAGAAAAAGTGAAACGATCTGTGAAAGATGCTGCCAAGAAGGGCCAG
AAGGATGTCTGCATAGTTCTGGCCAAGGAGATGATCAGGTCAAGGAAGGCTGTGAGCAAGCTGTATGCATCCAAA
GCACACATGAACTCAGTGCTCATGGGGATGAAGAACCAGCTCGCGGTCTTGCGAGTGGCTGGTTCCCTGCAGAAG
AGCACAGAAGTGATGAAGGCCATGCAAAGTCTTGTGAAGATTCCAGAGATTCAGGCCACCATGAGGGAGTTGTCC
AAAGAAATGATGAAGGCTGGGATCATAGAGGAGATGTTAGAGGACACTTTTGAAAGCATGGACGATCAGGAAGAA
ATGGAGGAAGAAGCAGAAATGGAAATTGACAGAATTCTCTTTGAAATTACAGCAGGGGCCTTGGGCAAAGCACCC
AGTAAAGTGACTGATGCCCTTCCAGAGCCAGAACCTCCAGGAGCGATGGCTGCCTCAGAGGATGAGGAGGAGGAG
GAAGAGGCTCTGGAGGCCATGCAGTCCCGGCTGGCCACACTCCGCAGCTAGGGGCTGCCTACCCCGCTGGGTGTG
CACACACTCCTCTCAAGAGCTGCCATTTTATGTGTCTCTTGCACTACACCTCTGTTGTGAGGACTACCATTTTGG
AGAAGGTTCTGTTTGTCTCTTTTCATTCTCTGCCCAGGTTTTGGGATCGCAAAGGGATTGTTCTTATAAAAGTGG
CATAAATAAATGCATCATTTTTAGGAGTATAGACAGATATATCTTATTGTGGGGAGGGGAAAGAAATCCATCTGC
TCATGAAGCACTTCTGAAAATATAGGTGATTGCCTGAATGTCGAAGACTCTACTTTTGTCTATAAAACACTATAT
AAATGAATTTTAATAAATTTTTGCTTTAGCACTTGGCCCCATTGTAGATTGCCCTGTGCAGTAAACTTTCAAGGT
GTCGGCTGCCCCAGATTGCTTCATTTGCTGGGTGTGGAAAGAGTTGCTATGGCCAGGCATATGGGATTTGGAAGC
TCAGCAGAAGTGACTTCTGCTCTGTGGTTGCTGCTCCCCGGCTTTCACAGACATGGTATGGCAGCCATTCTTTTA
TCTATTTAACCAAGAGGATGCTGGGGAATTGTGCTGCTTGTCCTGTTGGCTGGTGGCTGCATTATGTCCTGGGGT
GTGCATGTGGGTCTATTTAGAGCTTCTGTCCCTTCCTTCCCATTGCAAGTTGCACCCAGATGAGACAGCTGTAGT
ACTAGGTCTCTTTCACCTCTCATTGCCTGTCCCTGCTTCGAGCTGGTTGTCTTGTGCGTGGGACATGGGCCTTCC
TATCTGTGTTTTCTCAAAGTCAGGAGCTGACCAGGAGCACACTAAGGTGTGGTCATGCATCATAACCAACATTCA
CTCATCTGGGACATTCTTAAGATACATTTATAAATCATTTCAGCAGTAGTACTTTGTATGTGTTGAGAGTTTACA
GAGCTCTTTGACATACGCGATCTTAGTCTTTACAAATAAGGAAAACAGCTCAGTTTGGGAAGTATCAGAGATGGG
ATTCAAACCCAGATCCTCTGGTCCAAGTTGTATGTGCACTGAACTAATCAGGCAGGAAAAAAGCCCAGCCACTGT
CTCACAGATTGTTTTTTGTATATTGTAGCAAAATCCTGAAACAATGGGGTCCTTCCAGTCTCATCATACAAAATG
GCAATCTTGGCTGGGTGCGGTGGTTCATGCCTATAATCCCAGTGCTTTACAAGGCTGAGGCAGGAGGCTCTCTTG
AGAATAGGAGTTCAAGACCAGCCTGGGCAACATAGCAAGATCCTGTCTCTCCAAAAAAAAAAAAAAAAAAAAAAA
AAAATTTCATTTTTGAGTCCAGAGGACCCTCCTATTACTCTTGATTTCATCTTCAGAGTGTAGTTAAAAAATTAT
TTTAAATAATTATTTTTTAAATCAGTTGTAGGTTCACAGCAAAAGTGGACAAAAAGAAATTTCTCATATATCCC
CTGCCCTCACACATGCATAGCCTCCCACCACTATCAGTATCCCACACCAGAGTGGTACATTTGTTACAATCAATA
AACCTCCATTGACACATCATTATCACCCAAAGTCCATAGTTTACATGAAGATTCACTCTGGTGTTGTACATTGTA
TGGGCTTAGACAAATGTATGATGATATCTACAATTATAGAATCATACAGAATAGTTTCACTGCCCTAAAACTTCT
CTATGCTTCACCTGTTCATCCCTTTCTTCCCTAATCCCCTGGCAACCACTTTAAAAAAAAAATTAGGTTCAGGGG
GTACATGTGCAGGTAAACTCGTGACAAGGGGGTTTGTTATACAGATTATTTAGTGACCCAGGTACTAAGCCTAGT
ACCCAATAGTTACTTTTCTGGTCCTGTCCCTTTTCCCACCCTCCACCCTCAGGTAGGCCCCAGTATGTTATTCCT
TTGTGTCCATGTTATTTCACTCCCACTTGTGAGAACATGGAATATTTGGTTTCCTGTTCCTATGTTAGTTTGTTA
AGGATAATGGCCTCCAGCCCCATCCATGTTCCTGCAAAGGACATGATCTTTCTTTGGCAACCACTTTTTACTGTC
GCCATAGTTCTTCCTTTTCTAGAATGTCATATTGGAATCATATAGTATGTAGCCTTTTCAGACTGGCTTCTTTCA
CTTAATAATATGCAATTAAGGTTCCTCCATGTCATTTCATGGCTTAATAGTGCATTTATTTTTAGCACTGAATAA
TACTCCATTGTCTAGATGAATAGTTTATCCATTCACCTATTGAAAGACTTCTTGGTGGTTTCCAAGTTTTGGCAA
TTATGAATAAAGCTGTTGTAAACATCTTTGTGCAGGTTTTTCTATGGGCATGTTTTTAATTCATTTGAATAAATA
CCAAGAGCTTCAGTGCTGGATCATA

FIGURE 817

CAGGACACAGCATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCCAAAT
GTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGG
CCAGTCAGAGTATTAGTAGCTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATA
AGGCGTCTAGTTTAGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCA
TCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCTCCCACATGGACGT
TCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT
GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCT
ACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGC
TCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCC

FIGURE 818

GCGGCCGTTACGGCGCTCAGGCGTCTCGACGCGCGCGATTTAAAACCAGCTCAGGAGACGCCAAGGAAAG**ATG**GG
ACCTCCCGGCCCAGCACTGCCAGCCACAATGAATAACTCTTCTTCAGAGACGCGAGGACACCCCCACAGTGCCTC
CTCTCCTTCAGAGCGTGTGTTCCCGATGCCCCTGCCCAGGAAGGCGCCTCTCAATATTCCTGGCACCCCAGTCCT
CGAAGACTTTCCTCAGAATGACGATGAGAAGGAGCGGCTGCAGCGGAGGCGCTCGAGGGTCTTTGATCTGCAGTT
CAGCACTGACTCACCTCGCTTATTGGCCTCCCCCTCCAGCAGGAGTATTGACATTTCAGCTACTATCCCCAAGTT
TACAAACACGCAGATTACGGAACATTACTCCACCTGTATCAAACTGTCCACTGAAAATAAAATCACTACCAAGAA
TGCTTTTGGTTTGCACTTGATTGATTTTATGTCAGAGATTCTTAAACAGAAAGACACCGAACCAACCAACTTTAA
AGTGGCTGCGGGTACTCTGGATGCCAGCACCAAGATCTATGCTGTGCGCGTGGATGCCGTCCATGCCGATGTATA
CAGAGTCCTTGGGGGGCTGGGCAAAGATGCACCGTCTTTGGAAGAAGTAGAAGGCCATGTTGCTGATGGAAGTGC
TACTGAAATGGGAACAACCAAAAAGGCTGTAAAGCCAAAGAAGAAGCACTTACACAGAACTATTGAGCAGAACAT
AAACAACCTCAATGTCTCCGAAGCAGATCGGAAGTGTGAGATTGATCCCATGTTTCAGAAGACAGCAGCCTCATT
TGATGAGTGCAGCACAGCAGGGGTGTTTCTGTCCACTCTCCACTGCCAGGACTACAGAAGTGAACTGCTGTTTCC
CTCTGATGTCCAGACTCTCTCCACGGGAGAACCTCTCGAGTTGCCAGAGTTAGGTTGTGTAGAAATGACAGATTT
AAAAGCGCCCTTGCAGCAGTGTGCAGAAGATCGCCAGATCTGCCCTTCCCTGGCCGGGTTCCAGTTTACACAGTG
GGACAGTGAAACACATAATGAGTCTGTGTCGGCCCTGGTAGACAAGTTTAAGAAGAATGACCAGGTATTTGACAT
CAATGCTGAAGTTGACGAGAGTGACTGTGGAGACTTCCCCGATGGGTCCCTGGGGGATGACTTTGATGCCAACGA
TGAACCTGACCACACCGCAGTTGGGGATCATGAAGAGTTCAGGAGCTGGAAGGAGCCCTGCCAGGTTCAGAGCTG
CCAGGAAGAAATGATTTCCCTTGGGGATGGAGACATCAGGACCATGTGCCCCCTTCTGTCTATGAAACCTGGAGA
ATATTCTTATTTCAGTCCTCGGACCATGTCGATGTGGGCTGGCCCGGATCACTGGCGCTTTAGGCCTCGACGCAA
ACAAGATGCTCCTTCCCAATCAGAAAACAAAAAGAAGAGTACAAAAAAAGATTTTGAAATTGACTTTGAAGATGA
TATTGACTTTGATGTATATTTTAGAAAAACAAAGGCTGCTACTATTCTGACCAAGTCCACTTTGGAGAACCAGAA
TTGGAGAGCTACCACCCTTCCTACAGATTTCAACTACAATGTTGACACTCTGGTCCAGCTTCACCTCAAACCAGG
CACCAGGTTACTTAAGATGGCCCAGGGCCATAGGGTAGAGACTGAGCATTATGAAGAAATTGAAGACTATGATTA
CAACAACCCTAACGACACCTCCAACTTTTGCCCTGGATTACAGGCTGCTGACAGTGATGATGAAGATTTGGATGA
CTTATTTGTGGGACCTGTTGGGAACTCTGACCTCTCACCTTATCCTTGCCATCCACCTAAGACAGCACAACAGAA
TGGTGACACTCCAGAAGCCCAAGGATTAGACATCACAACATATGGGGAGTCAAACTTGGTAGCTGAGCCTCAGAA
GGTAAATAAAATTGAAATTCACTATGCCAAGACTGCCAAAAAGATGGACATGAAGAAACTGAAGCAGAGCATGTG
GAGTCTGCTGACAGCGCTCTCCGGAAAGGAGGCAGATGCAGAGGCAAACCACAGGGAAGCTGGAAAAGAAGCGGC
CCTGGCAGAAGTGGCTGACGAGAAGATGCTTAGCGGGCTCACGAAGGACCTGCAGAGGAGCCTGCCCCCTGTCAT
GGCTCAGAACCTCTCCATACCTCTGGCTTTTGCCTGTCTCCTACATTTAGCCAATGAAAAGAATCTAAAACTGGA
AGGAACAGAGGACCTCTCTGATGTTCTTGTGAGGCAAGGAGAT**TGA**GTTCACTATGGAGAAGTCAGCAGCAGGAG
GCCCATCCCTTACTCAGTTGCCGGGACATCCCCAGTCTCGGGGGAAGAAGATGCCATGGGCTTATACCCAGGCTG
TAGCCAACTACCAACGTGCCTGTTTGTTTGTTGCTCTTTCCTTCTCTCCATCATAGTCTGGGTGCCAGCGCCCTG
AAGCTCCGTGCTCAACTGATTAAACTTTACTGCCCTATGGTGACCATCTAGGAGAGGGGAGGGCAGAGGGGGTGA
GGGTACTATTCTGGATTGAGAAAACCTATATCCATTCTTTATATCAATGTATAGTTTTAGTCTCCTAAATTGATC
TGTTATTTTCCAAACTATTCTCTTGTAGAAAATTTTCCAGTGGGCACTTAATGGTGCCCTTGAAGAACTTCCTAA
TCCATGTACATAAAATACATCATATGTACACTTATAAATGTATATAGAATGCTCAAAAATAAAATTCTTAATAAT
AGAACTGGCAAAATA

FIGURE 819

MGPPGPALPATMNNSSSETRGHPHSASSPSERVFPMPLPRKAPLNIPGTPVLEDFPQNDDEKERLQRRRSRVFDL
QFSTDSPRLLASPSSRSIDISATIPKFTNTQITEHYSTCIKLSTENKITTKNAFGLHLIDFMSEILKQKDTEPTN
FKVAAGTLDASTKIYAVRVDAVHADVYRVLGGLGKDAPSLEEVEGHVADGSATEMGTTKKAVKPKKKHLHRTIEQ
NINNLNVSEADRKCEIDPMFQKTAASFDECSTAGVFLSTLHCQDYRSELLFPSDVQTLSTGEPLELPELGCVEMT
DLKAPLQQCAEDRQICPSLAGFQFTQWDSETHNESVSALVDKFKKNDQVFDINAEVDESDCGDFPDGSLGDDFDA
NDEPDHTAVGDHEEFRSWKEPCQVQSCQEEMISLGDGDIRTMCPLLSMKPGEYSYFSPRTMSMWAGPDHWRFRPR
RKQDAPSQSENKKKSTKKDFEIDFEDDIDFDVYFRKTKAATILTKSTLENQNWRATTLPTDFNYNVDTLVQLHLK
PGTRLLKMAQGHRVETEHYEEIEDYDYNNPNDTSNFCPGLQAADSDDEDLDDLFVGPVGNSDLSPYPCHPPKTAQ
QNGDTPEAQGLDITTYGESNLVAEPQKVNKIEIHYAKTAKKMDMKKLKQSMWSLLTALSGKEADAEANHREAGKE
AALAEVADEKMLSGLTKDLQRSLPPVMAQNLSIPLAFACLLHLANEKNLKLEGTEDLSDVLVRQGD

FIGURE 820A

TTCCAAGAAGAAGGATTTGCACCCTCGGGATATTGATGCATTTTGGCTGCAGCGGCAGCTCAGTCGTTTCTATGA
TGATGCCATCGTGTCGCAGAAGAAGGCAGATGAAGTATTGGAGATTTTGAAGACGGCCAGTGATGATCGGGAATG
TGAAAATCAGCTGGTTCTGCTGCTTGGTTTCAACACCTTTGATTTCATTAAAGTGTTGCGGCAGCACAGGATGAT
GATTTTATACTGTACCTTGCTGGCCAGTGCACAAAGTGAAGCTGAAAAGGAAAGGATTATGGGAAAGATGGAAGC
TGACCCAGAGCTATCCAAGTTCCTCTACCAGCTTCATGAAACCGAGAAGGAGGATCTGATCCGAGAGGAAAGGTC
CCGGAGAGAGCGAGTGCGTCAGTCTCGAATGGACACAGATCTGGAAACCATGGATCTCGACCAGGGTGGAGAGGC
ACTGGCTCCACGGCAGGTTCTGGACTTGGAGGACCTGGTTTTACCCAAGGGAGCCACTTTATGGCCAATAAACG
CTGTCAGCTTCCTGATGGATCCTTCCGTCGCCAGCGTAAGGGCTATGAAGAGGTGCATGTGCCTGCTCTGAAGCC
CAAGCCCTTTGGCTCAGAAGAACAACTGCTTCCAGTGGAAAAGCTGCCAAAGTATGCCCAGGCTGGGTTTGAGGG
CTTCAAAACACTGAATCGGATCCAGAGTAAGCTCTACCGTGCTGCCCTTGAGACGGATGAGAATCTGCTGCTGTG
TGCTCCTACTGGTGCTGGGAAGACCAACGTGGCCCTGATGTGCATGCTCCGAGAGATTGGGAAACACATAAACAT
GGACGGCACCATCAATGTGGATGACTTCAAGATTATCTACATTGCCCCCATGCGCTCCTTGGTGCAGGAGATGGT
GGGCAGCTTTGGAAAGCGCCTGGCCACTTATGGCATCACTGTTGCTGAACTGACTGGGGACCACCAGCTGTGCAA
AGAAGAGATCAGTGCCACTCAGATCATCGTCTGCACCCCCGAGAAGTGGGACATCATCACCCGCAAGGGTGGTGA
GCGCACCTACACCCAGCTGGTGCGGCTCATCATTCTGGATGAGATTCATCTTCTCCACGATGACAGAGGTCCTGT
CTTAGAAGCTTTAGTGGCCAGGGCCATCCGAAACATTGAGATGACCCAAGAGGATGTCCGACTCATTGGTCTCAG
TGCCACCCTACCCAACTATGAAGATGTAGCCACCTTTCTACGTGTTGACCCTGCCAAGGGTCTCTTTTACTTTGA
CAACAGCTTCCGTCCAGTGCCTCTGGAACAGACATATGTGGGTATCACAGAGAAAAAAGCTATCAAGCGTTTCCA
GATCATGAATGAAATCGTCTATGAAAAAATCATGGAACATGCTGGAAAAAATCAGGTGCTGGTGTTTGTCCACTC
CCGGAAGGAGACTGGAAAGACAGCCAGGGCCATCCGGGACATGTGCCTAGAAAAGGACACTCTGGGTCTGTTTCT
GAGGGAGGGCTCAGCCTCCACAGAAGTCCTGCGAACAGAAGCTGAGCAGTGCAAGAACCTAGAGCTGAAGGATCT
TCTGCCTTATGGCTTTGCTATTCATCACGCAGGCATGACCAGGGTTGACCGAACACTCGTGGAGGATCTTTTTGC
TGATAAACATATTCAGGTTTTAGTTTCCACAGCAACTCTAGCTTGGGGTGTGAATCTCCCTGCACATACAGTCAT
CATCAAAGGCACCCAGGTGTACAGTCCAGAGAAGGGGCGTTGGACAGAACTGGGAGCACTGGACATTCTGCAGAT
GCTGGGACGTGCCGGAAGACCCCAGTATGACACCAAGGGTGAAGGCATACTCATCACATCTCATGGGGAGCTACA
GTACTACCTGTCCCTCCTCAATCAACAACTTCCTATTGAAAGCCAGATGGTTTCAAAGCTTCCTGACATGCTCAA
TGCAGAAATCGTGCTAGGAAATGTCCAGAATGCCAAGGATGCGGTGAACTGGCTGGGCTATGCCTACCTCTATAT
CCGAATGCTGCGATCCCCAACCCTCTATGGCATCTCTCATGATGACCTCAAGGGAGATCCCCTGCTGGACCAGCG
CCGACTAGATCTGGTTCATACAGCTGCCCTGATGCTGGACAAGAACAATCTGGTCAAGTACGACAAGAAGACGGG
CAACTTCCAGGTGACAGAACTGGGCCGTATAGCCAGCCACTACTACATCACCAATGATACAGTGCAGACTTACAA
CCAGCTGCTGAAGCCCACCCTGAGTGAGATTGAGCTTTTCAGGGTCTTCTCATTGTCCTCTGAGTTCAAGAACAT
CACAGTGAGAGAGGAGGAGAAGCTGGAGCTGCAGAAGTTGCTGGAGAGGGTGCCTATCCCTGTAAAGGAGAGCAT
TGAGGAACCCAGTGCTAAGATCAACGTTCTTCTGCAAGCCTTCATCTCACAGCTGAAATTGGAGGGCTTTGCACT
GATGGCTGACATGGTGTATGTCACACAGTCGGCTGGCCGGTTGATGCGAGCGATATTTGAAATTGTCCTGAACCG
AGGTTGGGCACAGCTTACAGACAAGACCCTGAACCTCTGCAAGATGATCGACAAACGCATGTGGCAGTCCATGTG
TCCTCTGCGCCAGTTCCGGAAACTCCCTGAGGAAGTAGTGAAGAAGATTGAGAAGAAGAATTTCCCCTTTGAGCG
TCTGTACGACCTGAATCATAATGAGATTGGGGAGCTTATCCGCATGCCAAAGATGGGGAAGACCATCCACAAATA
TGTCCATCTGTTTCCCAAGTTGGAGTTGTCAGTGCACCTGCAGCCTATCACACGCTCCACCCTGAAGGTGGAGCT
GACCATCACGCCAGACTTCCAGTGGGATGAAAAGGTGCATGGTTCATCCGAGGCTTTTTGGATTCTGGTGGAGGA
TGTGGACAGCGAGGTGATTCTGCACCATGAGTATTTTCTCCTCAAGGCCAAGTACGCCCAGGACGAGCACCTCAT
TACATTCTTCGTGCCTGTCTTTGAACCGCTGCCCCCTCAGTACTTCATCCGAGTGGTGTCTGACCGCTGGCTCTC
TTGTGAGACCCAGCTGCCTGTCTCCTTCCGGCACCTGATCTTGCCGGAGAAGTACCCCCCTCCAACCGAACTTTT
GGACCTGCAGCCCTTGCCCGTGTCTGCTCTGAGAAACAGTGCCTTTGAGAGTCTTTACCAAGATAAATTTCCTTT
CTTCAATCCCATCCAGACCCAGGTGTTTAACACTGTATACAACAGTGACGACAACGTGTTTGTGGGGGCCCCCAC
GGGCAGCGGGAAGACTATTTGTGCAGAGTTTGCCATCCTGCGAATGCTGCTGCAGAGCTCGGAGGGGCGCTGTGT
GTACATCACCCCCATGGAGGCCCTGGCAGAGCAGGTATACATGGACTGGTACGAGAAGTTCCAGGACAGGCTCAA
CAAGAAGGTGGTACTCCTGACAGGCGAGACCAGCACAGACCTGAAGCTGCTGGGCAAAGGGAACATTATCATCAG
CACCCCTGAGAAGTGGGACATACTTTCCCGGCGATGGAAGCAGCGCAAGAACGTGCAGAACATCAACCTCTTCGT

FIGURE 820B

GGTGGATGAGGTCCACCTTATCGGGGGCGAGAATGGGCCTGTCTTAGAAGTGATCTGCTCCCGAATGCGCTACAT
CTCCTCCCAGATTGAGCGGCCCATTCGCATTGTGGCACTCAGCTCTTCGCTCTCCAATGCCAAGGATGTGGCCCA
CTGGCTGGGCTGCAGTGCCACCTCCACCTTCAACTTCCATCCCAATGTGCGTCCCGTCCCCTTGGAGCTGCACAT
CCAGGGCTTCAACATCAGCCATACACAAACCCGCCTGCTCTCCATGGCCAAGCCTGTGTACCATGCTATCACCAA
GCACTCGCCCAAGAAGCCTGTCATTGTCTTTGTGCCGTCTCGCAAGCAGACCCGCCTCACTGCCATTGACATCCT
CACCACCTGTGCAGCAGACATCCAACGGCAGAGGTTCTTGCACTGCACCGAGAAGGATCTGATTCCGTACCTGGA
GAAGCTAAGTGACAGCACGCTCAAGGAAACGCTGCTAAATGGGGTGGGCTACCTGCATGAGGGGCTCAGCCCCAT
GGAGCGACGCCTGGTGGAGCAGCTCTTCAGCTCAGGGGCTATCCAGGTGGTGGTGGCTTCTCGGAGTCTCTGCTG
GGGCATGAACGTGGCTGCCCACCTGGTAATCATCATGGATACCCAGTACTACAATGGCAAGATCCACGCCTATGT
GGATTACCCCATCTATGACGTGCTTCAGATGGTGGGCCACGCCAACCGCCCTTTGCAGGACGATGAGGGGCGCTG
TGTCATCATGTGTCAGGGCTCCAAGAAGGATTTCTTCAAGAAGTTCTTATATGAGCCATTGCCAGTAGAATCTCA
CCTGGACCACTGTATGCATGACCACTTCAATGCTGAGATCGTCACCAAGACCATTGAGAACAAGCAGGATGCTGT
GGACTACCTCACCTGGACCTTTCTGTACCGCCGCATGACACAGAACCCCAATTACTACAACCTGCAGGGCATCTC
CCATCGTCACTTGTCGGACCACTTGTCAGAGCTGGTGGAGCAGACCCTGAGTGACCTGGAGCAGTCCAAGTGCAT
CAGCATCGAGGACGAGATGGACGTGGCGCCTCTGAACCTAGGCATGATCGCCGCCTACTATTACATCAACTACAC
CACCATTGAGCTCTTCAGCATGTCCCTCAATGCCAAGACCAAGGTGCGAGGGCTTATCGAGATCATCTCCAATGC
AGCAGAGTATGAGAACATTCCCATCCGGCACCATGAAGACAATCTCCTGAGGCAGTTGGCTCAGAAGGTCCCCCA
CAAGCTGAATAACCCTAAGTTCAATGATCCGCACGTCAAGACCAACCTGCTCCTGCAGGCTCACTTGTCTCGCAT
GCAGCTGAGTGCTGAGTTGCAGTCAGATACGGAGGAAATCCTTAGTAAGGCAATCCGGCTCATCCAGGCCTGCGT
GGATGTCCTTTCCAGCAATGGGTGGCTCAGCCCTGCTCTGGCAGCTATGGAACTGGCCCAGATGGTCACCCAAGC
CATGTGGTCCAAGGACTCATACCTGAAGCAGCTGCCACACTTCACCTCTGAGCATATCAAACGTTGCACAGACAA
GGGAGTGGAGAGTGTTTTCGACATCATGGAGATGGAGGATGAAGAACGGAACGCGTTGCTTCAGCTGACTGACAG
CCAGATTGCAGATGTGGCTCGCTTTTGTAACCGCTACCCTAATATCGAACTATCTTATGAGGTGGTAGATAAGGA
CAGCATCCGCAGTGGCGGCCAGTTGTGGTGCTGGTGCAGCTGGAGCGAGAGGAGGAAGTCACAGGCCCTGTCAT
TGCGCCTCTCTTCCCGCAGAAACGTGAAGAGGGCTGGTGGGTGGTGATTGGAGATGCCAAGTCCAATAGCCTCAT
CTCCATCAAGAGGCTGACCTTGCAGCAGAAGGCCAAGGTGAAGTTGGACTTTGTGGCCCCAGCCACTGGTGCCCA
CAACTACACTCTGTACTTCATGAGTGACGCTTACATGGGATGTGACCAGGAGTACAAATTCAGCGTGGATGTGAA
AGAAGCTGAGACAGACAGTGATTCAGATTGAGTCCTGAGGCATTTACTTTTGGGTAAAGGAGAGTTGAGCCTGAA
TTAGGAATGTGTACATTGTAGGAATCCTGGTTGTGGGGACCAGGTCTGTGGGCCTCAGGTCTGGCCAGCCAGGGC
TGGTGCTGTCCCCGCCTACCTCCACTTCCTTTCCCTTGCTCACTCTGGATCCAGTGACAGCAGGTGTCATGGGTC
AAGCATAAATCATATATAGCATTTTCAGGCATGTTCCTGGTAGTTCTTTTGAGTCTGACATTCTAATAAAATAAT
TTGTAGAAACC

FIGURE 821

MADVTARSLQYEYKANSNLVLQADRSLIDRTRRDEPTGEVLSLVGKLEGTRMGDKAQRTKPQMQEERRAKRRKRD
EDRHDINKMKGYTLLSEGIDEMVGIIYKPKTKETRETYEVLLSFIQAALGDQPRDILCGAADEVLAVLKNEKLRD
KERRKEIDLLLGQTDDTRYHVLVNLGKKITDYGGDKEIQNMDDNIDETYGVNVQFESDEEEGDEDVYGEVREEAS
DDDMEGDEAVVRCTLSANLVASGELMSSKKKDLHPRDIDAFWLQRQLSRFYDDAIVSQKKADEVLEILKTASDDR
ECENQLVLLLGFNTFDFIKVLRQHRMMILYCTLLASAQSEAEKERIMGKMEADPELSKFLYQLHETEKEDLIREE
RSRRERVRQSRMDTDLETMDLDQGGEALAPRQVLDLEDLVFTQGSHFMANKRCQLPDGSFRRQRKGYEEVHVPAL
KPKPFGSEEQLLPVEKLPKYAQAGFEGFKTLNRIQSKLYRAALETDENLLLCAPTGAGKTNVALMCMLREIGKHI
NMDGTINVDDFKIIYIAPMRSLVQEMVGSFGKRLATYGITVAELTGDHQLCKEEISATQIIVCTPEKWDIITRKG
GERTYTQLVRLIILDEIHLLHDDRGPVLEALVARAIRNIEMTQEDVRLIGLSATLPNYEDVATFLRVDPAKGLFY
FDNSFRPVPLEQTYVGITEKKAIKRFQIMNEIVYEKIMEHAGKNQVLVFVHSRKETGKTARAIRDMCLEKDTLGL
FLREGSASTEVLRTEAEQCKNLELKDLLPYGFAIHHAGMTRVDRTLVEDLFADKHIQVLVSTATLAWGVNLPAHT
VIIKGTQVYSPEKGRWTELGALDILQMLGRAGRPQYDTKGEGILITSHGELQYYLSLLNQQLPIESQMVSKLPDM
LNAEIVLGNVQNAKDAVNWLGYAYLYIRMLRSPTLYGISHDDLKGDPLLDQRRLDLVHTAALMLDKNNLVKYDKK
TGNFQVTELGRIASHYYITNDTVQTYNQLLKPTLSEIELFRVFSLSSEFKNITVREEEKLELQKLLERVPIPVKE
SIEEPSAKINVLLQAFISQLKLEGFALMADMVYVTQSAGRLMRAIFEIVLNRGWAQLTDKTLNLCKMIDKRMWQS
MCPLRQFRKLPEEVVKKIEKKNFPFERLYDLNHNEIGELIRMPKMGKTIHKYVHLFPKLELSVHLQPITRSTLKV
ELTITPDFQWDEKVHGSSEAFWILVEDVDSEVILHHEYFLLKAKYAQDEHLITFFVPVFEPLPPQYFIRVVSDRW
LSCETQLPVSFRHLILPEKYPPPTELLDLQPLPVSALRNSAFESLYQDKFPFFNPIQTQVFNTVYNSDDNVFVGA
PTGSGKTICAEFAILRMLLQSSEGRCVYITPMEALAEQVYMDWYEKFQDRLNKKVVLLTGETSTDLKLLGKGNII
ISTPEKWDILSRRWKQRKNVQNINLFVVDEVHLIGGENGPVLEVICSRMRYISSQIERPIRIVALSSSLSNAKDV
AHWLGCSATSTFNFHPNVRPVPLELHIQGFNISHTQTRLLSMAKPVYHAITKHSPKKPVIVFVPSRKQTRLTAID
ILTTCAADIQRQRFLHCTEKDLIPYLEKLSDSTLKETLLNGVGYLHEGLSPMERRLVEQLFSSGAIQVVVASRSL
CWGMNVAAHLVIIMDTQYYNGKIHAYVDYPIYDVLQMVGHANRPLQDDEGRCVIMCQGSKKDFFKKFLYEPLPVE
SHLDHCMHDHFNAEIVTKTIENKQDAVDYLTWTFLYRRMTQNPNYYNLQGISHRHLSDHLSELVEQTLSDLEQSK
CISIEDEMDVAPLNLGMIAAYYYINYTTIELFSMSLNAKTKVRGLIEIISNAAEYENIPIRHHEDNLLRQLAQKV
PHKLNNPKFNDPHVKTNLLLQAHLSRMQLSAELQSDTEEILSKAIRLIQACVDVLSSNGWLSPALAAMELAQMVT
QAMWSKDSYLKQLPHFTSEHIKRCTDKGVESVFDIMEMEDEERNALLQLTDSQIADVARFCNRYPNIELSYEVVD
KDSIRSGGPVVVLVQLEREEEVTGPVIAPLFPQKREEGWWVVIGDAKSNSLISIKRLTLQQKAKVKLDFVAPATG
AHNYTLYFMSDAYMGCDQEYKFSVDVKEAETDSDSD

FIGURE 822

GTTTCCATCCCTCCTCTGGAGGCTTTTGAAGTCACCGGGAGACAGATGTGCTCTGTGGCAGGCAGGGGAGTGGGG
GTGCTCAGGCACTTGGGAGGTCTGGGAGCTCCTCAGTGTGACCGCTGGGACCCACCAGGACTTTTTCCTTTGTCA
GAAGCCTTTGGTTGCTTTGCTGCTCTGCATGTGTCACTGTGGAGGGGCAATAGAGCAAGGCCTTACATGGCATGG
TCATTTCTCGGGCCCAGGAGGCTTAGAGGCCTGCCCCTGGCGCTCAAGTATTGAACCAGAACCATGGGGTGGCAC
TGAAGCCTCCTCACCACATCATGATAAATAACGGGGACATTCACAGAGCAGGCACTGTTTCCTCAGTCCATGGCT
GAGTACATCACCGGTGTTTTCTCTCTTATTCCTCCCATCAAGCCTAAAAGGAATCTCTATTGGAGATACTGCCAT
TAGTGTTCCTTTTATAGGTGAGGAACTGAGGCATAGAGGGTTCCCCAGTTGAACCAACTGATAAATAGTAGAACT
TGGATTTTAATTCAGTCTTGATGCCAGGGATAAGGCTCTTACTTTCTACCTTAGGCTATTTCTAGGAAACGCAGG
AGAGTGTTGAAGGGGCAGAGAAAGGGATCCAGTTCCTTTCTGTCCCGCATCCTAGTCCCTGAGAAGCAAAGAAGA
ATGTGTGGCTTCTTTTGCTTTGCTTTTGTTGTCATCCCACACATCTCCAGGGGACCTGGGCTCTTGATCTTGGCC
TCTTCCCCTTTAACTGTTAAGTGGGAGCAGGTAAGGGGGTACAGTAGGGCTGGCCTGGAGTTAGAGGCTTGGATG
CCTTAGCTCCTCTGTCTGCACTCCAGAACTGCCTGACTTCATTTCGTATGTTGTCCTTTGTTTTGACAATTGATC
CATGTCCCAGTCCGTCTCTTCTTCCTTCTTGATACTTACACTGCTTCTTTCTGTTGGTTTCCAGTGTTTAACACT
GTATACAACAGTGACGACAACGTGTTTGTGGGGGCCCCCACGGGCAGCGGGAAGACTATTTGTGCAGAGTTTGCC
ATCCTGCGAATGCTGCTGCAGAGCTCGGAGGGGCGCTGTGTGTACATCACCCCCATGGAGGCCCTGGCAGAGCAG
GTATGACGTGGCGCTGTGTCATGTGAATTTCCCAAGAAGCATTTCATCTGTGATTCCGTATGAAGGCTTTCTAAG
CCCTGAAATTTGCAGGGTCATTTCCTCAGTTTGTGTATTAAAGAAAAGCTGCCCCAGCCAAGCGTGGTGGCTCAC
GCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCAGATCTCCGGAGATCAGGAGTTCGAGACCAGCCTGGCC
AACATGGTGAAACCCTGTCTCTACTAAAAATACAGAAATTAGCTGGGCGTGGTGGTGTGCGCCTGTAATCCCAGC
TACTTGGAAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGTTCGCACCACT
GCACTCCAGCCTGGGCAACAAGAGCGAGACTTCATCTCA

FIGURE 823

GCGGAAGGCGCGGGAGCTTGCGTGCTGCTGGGCCTGAGCTGTCTGTCTCGTTTCTGTCCGCGCGCCCTGCATCCC
GGCCCCGGGCGCCCGCTGGAGGTCGCCGAGGAGCCACAGGGCTGACTGGTCTGCTGCCCGGGCCCAGGAGTGCCT
GGTGTAGCAGTCGCGGAGCCATCCCGGCGTCTGCTGCCATGACCGACTCTCCCCTCAGAGGAGACTCTTCCTCAG
CGGTGGCTGCAGAGACAGATGAGCGGCGGCTCCTGGCCGCGGGACCGTGAGACGGGTTCGTGGCCGGCCATTTAG
GGGGACGCTGCGACCACCGCCTGCGCCCCTCCGGACTGGTTCCTTGGGCCCCGGAAGCTCGCGGCGGGCCCTGCG
GGAGGCGGCATGCTCCCGCGGAGGCTGCTGGCCGCCTGGCTGGCGGGACGCGGGGCGGGGGCCTGCTGGCGCTT
CTGGCCAATCAGTGCCGCTTCGTCACGGGCCTGCGCGTGCGGCGCGCGCAGCAGATCGCGCAGCTCTACGGCCGC
CTCTACTCCGAGAGCTCACGCCGCGTTCTCCTCGGCCGCCTCTGGCGCCGGCTGCACGGCCGTCCTGGCCATGCC
TCTGCCTTGATGGCGGCGTTAGCCGGCGTCTTCGTTTGGGACGAGGAGAGGATCCAGGAGGAGGAGTTGCAGAGA
TCTATTAATGAGATGAAGCGGTTGGAAGAAATGTCAAATATGTTTCAGAGCTCTGGAGTCCAGCACCACCCTCCA
GAACCAAAAGCCCAAACAGAAGGGAATGAAGATTCAGAGGGCAAAGAGCAACGTTGGGAAATGGTGATGGATAAG
AAACACTTTAAGCTGTGGCGGCGCCCAATTACAGGCACCCACCTTTACCAGTACCGAGTTTTTGGAACCTACACA
GATGTGACACCTCGGCAGTTCTTCAATGTTCAGCTGGACACAGAGTATAGAAAAAAATGGGATGCCCTGGTAATC
AAGCTGGAGGTGATTGAGAGGGATGTGGTTAGTGGTTCCGAGGTTCTTCACTGGGTAACCCATTTTCCTTATCCA
ATGTACTCACGGGATTATGTTTATGTTCGGCGGTATAGTGTGGATCAGGAAAACAACATGATGGTGTTGGTGTCG
CGTGCTGTGGAGCATCCGAGTGTGCCAGAGTCTCCAGAATTCGTCAGGGTCAGATCATATGAATCCCAAATGGTT
ATCCGTCCCCACAAGTCATTTGATGAGAATGGCTTTGACTACTTACTAACATACAGTGACAATCCCCAAACGGTG
TTTCCTCGCTACTGTGTTAGTTGGATGGTTTCCAGTGGCATGCCAGATTTCCTGGAGAAGCTGCACATGGCCACT
CTGAAAGCCAAGAATATGGAGATTAAAGTAAAGGACTACATCTCAGCTAAGCCTCTGGAAATGAGTAGTGAAGCC
AAGGCCACCAGCCAGTCCTCTGAGCGAAAGAACGAGGGCAGCTGTGGCCCTGCTCGGATTGAGTATGCTTGACAG
GCTTTGGGATAAGAAGGGACAAGGTGCTTCTAGCCCTGTCTCAGTCCGTTATCACTCTGCTGTAGAAGGGGGACA
TGCCACATGTATTAGAAGGCATCTGCTGTAACTTCCAGTGCAAGATAATTCAATAACTGATGTCCCATTTCATTC
AGAGCCCTTATTGCTCTTATCAAAACAGAAGAAGGCTACATTTGTGGGAGTGTTGTCATATTCTCAGGCCAACTG
TTTTGAAATTCGGTATCTCACTGAGCTAATCTGGAACAAACCTCTCACCTCAGGCCAGAAGGGGATGACCTCCAT
TTGCTTCTCTGAGTAGTTTCCTCTGCTGACATTCCAAATCCCACCATCGATTGTGCAGCGCTTTGGATTTCCTTC
AGTTCTCCAGGTCCACCTGGAAAGTATAGTTGGCCAGTTGAGTCTCTCAAATGAGGGGCTACTGGGAGTGCTCTT
GGTAACAATCATGATGTGAATGGGTGTGAACGATACTTGGCTATGTTAAGTGCCTTGTCCGCACCTTGCTTTTAT
CTCTAGAGACATGAAGTTATTATTAATTTTTTTTTTTTTTAAGTAGAGATGGAGTTTCACTCTGTTTCCCAGGCT
GGTCTTGAACTCCTGGGCCATGCCTGGCCAGGGACATGAATTTGTACAAAGAAATTTCCCTCCCTGCCTGCACAA
TATCACCCATTGACTCACCTTATCCAAAGCAAGTTTCCTGTGAATCGGCCAGTTCTTCTATATTCATTGGATCAT
TGCCTCCTTCCTAACCTTCCCCATTTACCAAGAACACTGGGAGACTAATCCTTTTAGATAGTAGCTTTTTGATGC
TCAAAACATCACATTTAAATTTAGTTTAAAAATTTTTTAACTTTTGTGTCAAATAGGAGTTGAGGAATTGAGCAG
GATTCTACCCTAGTCCGATTGTATAGAAAACACCATTTTGATTCAGGTATTATTTTTCATATTTCAGGTTTGACT
TGTTCTTTTCAGAAGGCTAAAGTCAGAGGAATGGGGGCTGGGCCACTCCCTTGGAGCTCTCAGATCTACAGACAA
GCTGTGTGAATGCATAGATGTAATCTTGTCTCAAATACTAATACAGTGGAGATTTGGTTTATGTTACCATTAAGT
TCCTCTAAAAAGTTTTTCTTCCTCTCTTCAGAGCCAAAATAAAAGTGAACTACACTGTTCAGATAAGGTCACAAT
CTGATGCTGTCAGTTTGACCGAGCTGGTTTTGCTTATGGTCATGCTGCAATTTGTTAGAATAATAGGGATCAAGT
TTTAAATCCTCCTCCTTCCCTTTTTTCTGGAGTCTTGAGGGCCAGAGTTTTTGTTTTTGTTTTTGTTTTTGTTTT
CCTGCTTGCTACTGTTTTGTGGTGTTGAAAAGTGGTTTAAACCTGAGACTAACTTAAACACTTCCTTGACCTTCT
TGTTGCCTGTTCATTTTTGTGCCAAGGAAGTAGCTGCCCCAGTGTATGTCTTGCCTTCTCCGCGTCATTGTTGGA
AGAGGAGAGATGCATCGAGCAGTCCCAGCTGCTTTTCATTTATTACTTCTTCTTTCCAGGACCTGACAGAAGTCA
GGGAAGAGTCCCTGGGTTATGTCCAAACTTAGCACCTGCAATTGTTGGGATGTGGATGGATGTGTGCATAAGAGA
GAGAGAGAATATGTGTGTGTGTGTGTGCGTCTGCGAGCGCACACACATGCACAAGTGCGAAGGAGTTGCGGTTGC
TCCATGTTCTGACTTAGGGCAATTTGATTCTGCACTTGGGGTCTGTCTGTACAGTTACTCATGTCATTGTAATGA
TTTCACTCCTAACTGTGACATTTTTATCAAATGTGTGAATAAATACATAAAGATTGGTAC

FIGURE 824A

CGCGCTTAGGGATCCGGCCGTGGCCGAGCGCGCGGCCGTAAGACCGCGGGTGACTAGCATGCAGATACCCATGCT
CTGACTTTCTGCCCCTCCACTGACATGGCCCACCGGGGTGGGGAGAGGGACTTCCAGACTTCAGCTCGACGCATG
GGCACCTCGCTGCTCTTCCAGCTTTCAGTGCATGAACGGGAGCTGGACCTGGTTTTTCTGGATCATAGCTATGCC
AAGCCTTGGAGTGCCCACCCAGATGCCAGTAGTGCCCGCCCCACCCGCATGCTCTTTGTCACTCCCCGGCGGCAG
CACGAAAGTACCATTGAATCAGACGTCCCAATAGATGTGGAGACGGTCACATCAACGCCTATGCCACTCTATGAC
AATCAGAAGGCACGCAGCGTGATGAATGAGTGTGAACGGCATGTCATCTTTGCCAGGACTGATGCAGATGCCCCT
CCTCCACCAGAGGACTGGGAGGAGCATGTCAACAGGACTGGCTGGACAATGGCCCAGAACAAGCTATTCAACAAG
ATCCTCAAAGCCCTGCAGTCTGACCGGCTTGCCCGCTTGGCCAACGAAGGGGCTTGTAATGAGCCAGTGCTGCGC
CGTGTTGCTGTGGACAAGTGTGCAAGGAGAGTGCGGCAGGCTCTGGCAAGTGTGAGCTGGGATACCAAGCTGATC
CAGTGGCTGCACACCACCCTTGTGGAGACCTTGAGTCTGCCCATGCTGGCAGCCTACCTGGATGCTTTGCAGACG
CTGAAGGGGAAGATCCCAACCTTGATTGACCGGATGCTTGTGTCATCCAACACAAAGACTGGGGCTGCAGGAGCT
GAGGCCTTGTCTCTCCTACTGAAGAGGCCCTGGGACCCTGCTGTGGGTGTGCTTTCTCATAACAAACCAAGCAAA
CTCCCTGGCTCTCCGCTGATTCTCATCGCCTCCTCTGGTCCCTCCAGCTCTGTGTTTCCCACTTCACGCCGCCAC
CGCTTCTGGCAATCTCAGCTGTCCTGCTTGGGCAAGGTCATCCCTGTAGCCACCCATCTGCTGAACAATGGCAGT
GGGGTAGGAGTTCTACAGTGTCTCGAGCATATGATTGGGGCAGTGAGAAGCAAAGTGCTGGAGATTCACAGCCAT
TTCCCACACAAACCCATTATCTTGATTGGCTGGAACACAGGAGCTTTGGTGGCCTGTCATGTGTCAGTAATGGAG
TATGTCACTGCAGTTGTCTGCCTTGGGTTTCCTCTGCTTACTGTGGATGGCCCCAGAGGGGATGTAGATGATCCC
CTCTTGGATATGAAGACTCCAGTCCTCTTTGTCATTGGTCAGAATTCCCTTCAATGTCACCCTGAAGCCATGGAG
GACTTCCGGGAGAAGATTCGAGCTGAGAACAGCTTGGTGGTGGTTGGGGGAGCTGATGACAATCTCAGAATAAGC
AAAGCAAAGAAGAAATCAGAAGGGTTGACTCAGAGCATGGTGGACAGATGTATTCAGGATGAGATTGTGGACTTT
CTGACTGGAGTGCTCACTCGTGCTGAGGGTCACATGGGCTCTGAACCTCGGGATCAGGATGCTGAGAAGAAGAAG
AAGCCCCGCGATGTGGCCCGCAGAGACTTGGCCTTTGAAGTCCCTGAGCGGGGCAGTCGACCTGCCTCCCCAGCT
GCCAAGCTGCCCGCCTCACCCTCAGGCTCAGAGGATCTCTCCAGTGTGTCCAGCAGCCCCACCTCCAGTCCCAAG
ACCAAAGTGACCACAGTGACCTCTGCCCAGAAGTCCAGTCAGATTGGAAGTTCTCAGCTGCTGAAGAGACATGTG
CAGCGGACAGAAGCTGTGCTGACCCACAAACAAGCTCAAGCACAGTTTGCTGCTTTTCTGAAACAAAATATGCTG
GTGAGGAAAGCTCTTCCTCCTGGCACCTCCTCCTGTCTCTTTGTTCCCATTTCATCAGAACCACCAGAGGAAGGA
GAGAAAGAGGATCTTAGGGTTCAGCTGAAGCGACACCATCCCTCGAGTCCCCTTCCTGGCAGTAAGACCTCCAAA
CGACCGAAGATCAAGGTGTCCCTTATCTCCCAAGGGGACACAGCTGGAGGGCCTTGTGCTCCTTCCCAAGGAAGT
GCTCCAGAAGCTGCAGGTGGGAAGCCCATCACCATGACACTGGGGCAGGCTTCAGCAGGGGCCAAGGAGCTCACA
GGACTTCTCACCACAGCCAAGTCCAGTTCTTCTGAAGGTGGAGTCTCAGCCAGCCCAGTCCCTTCAGTGGTCTCC
AGCAGCACTGCACCCAGTGCCTTGCACACACTGCAGAGCCGCCTGGTGGCCACATCTCCTGGCAGCTCCCTCCCA
GGGGCCACATCAGCCAGCAGCCTCCTCCAAGGCCTCAGCTTCAGCTTGCAGGATATCAGCAGCAAGACCTCTGGC
CTTCCAGCAAATCCCTCCCCAGGACCAGCCCCACAGGCTTGAAGGTCCCCACCACCATTACTCTGACACTTCGTG
GCCAGCCGAGCAGGATCACTACACTGAGCCCTATGGGCTCAGGAGCAGCCCCATCCGAGGAGTCCTCTTCCCAGG
TGCTGCCCTCCAGCTCACAGCGCCTGCCTCCAGCACCCTGAAGATGCTGTGTGATATGTCCTCCTTACCAAGTTG
GTGATGGCTGCCTCATGGTGGGCCCTGGACAGGTGTGTGGTCCTGCTGAGCTGTCCACGTGTCGGAAGACCTGTT
TAAGACAGTCATTTTTGCCTCTCCGCCAACTGTCTTCAGAGAAACCATTAGGTTAGGTGATACGGTGCCAGCAAG
GGAAGCACCATCGTCCAGGATCTGCAAATCTGGTTCCTGGGAACCCCAGACTCCTCAGCAGATCTGGCTGTACAT
GGATCAGAACCACTTCTTCCCCCGCTTAAGCTGTGGTTTGACCCAAGGGTCAGCATATAGGACTGCCTGCTGCAT
TTAATGAAGGTGTTTCCTTTTGGAAGTCTGTGCTACCCTCTGCGCCTAGTTGGGAGGAGACATCCATCTGGTCTG
GGATTTCGGGAGTTAGAATGGAAAGCTCTTTGCTAAAGACTGGAGTCATCCTGGCCTGCCAACTGGTGGTTCAGA
GCCGGACGGGCTTGTTTTGGACATCACTGTTGCCTTCACTCAGCAGCCACGGGAGAGTGCTCCCCATGCAACTCC
ACCTTAGAAACCACGTCAGATACTGAGTAGCTTGCTGACTCCTGGAAACTTCTGGTTTTTGTTAGTATCATAATG
AAGGCAAAGAGAACTAGGCTGTCATCTTTCAGCCTCTTTGACTTACTCTAGATGTTGGGAGCAGTGGTTGCCAGG
TGAAACCTGGGCCCTTTGTCTTTTTCACCATGCTTTGGGCAGTTTCTGTATCCAGAGAGTCCGCAGGTTCAGATA
AGCTGAAGAAGAGTAATAGAACAGCAAAGGAAGTGGCTTGAAGGATGTGCTAGTAAGCCCTGTGGTTTGTGCTTA
GGTCTCTGCTCTGCTACCCAAGGAACTGGTGGTTCAGCTGGAGATAAAAAGAAGAATTTGCCAAGTCAGAGAAGA
AACCCCAACCCCGGAAAATCCTCTGTCTCCAGTCTCTGGAGGTGAAGCAGGGACAATAAGCTAAGGTAGTATCTT

FIGURE 824B

GGCCATCCCAGGAAACTTGTGGCATTAGGACGATGAAGGCCATGCTTCAGTGTTTTCGTTTCTATTTCATGAGAC
TTTTTGTCTTCCTGCTTACAAGTGGGAAGATGATTGACAGTGACTCTACTATGCAGGGCTGTTGGTACCAACCTG
AGCCCTATAGGTGGCAGTCCCTGGAGAAGTGGTCACAGAAGATGGAGCTCTGATCCCCTGCTTACCTCTTCACAA
CACTTGTGTGCAAAGATAGTTTTAGATTTGGTTTAGAAGCTATCCTCCAGAACAGGCTCCCATACTTAGAATGTT
TCTAGTTAAGGTAATAAATTAGGCAACCCAAGTGTGACTCCACTCAAGTGTCCTTTTCTGTAGGCAGGAAGGGCC
CACAACATGGCTTAAAATGTAGTCCATGGTTCTGGCCCACAGTACAGTGTGTATCTATACCAGGTCACCTGTGTT
CAATCTGGGAGCCTTCCTGGCCAGTCTGAGTGGCAGCCAGAAGGGAGCTCATAGTGTCTAGGAGTCTCAGGCAAG
GTAGGTCAGGGTACTGTGGGCAGGGGGGATGTGTGTGATAGGAGAGGGTACCCTAAACCCCATACCTTCCCTCCC
TGACCTGAAAAGCTGATCTCAACAGGGATTCACACAGAATTAGGCTGTGTTTTTGCATTAGCTGGTAGGTGACTT
TCTCAAAATTCTTAAATTCAGAAAGTATTTAGTAAACTTGAGGAAGGTATGAAATCTGGAGGAGGCATCCAGGAC
CCAGGGGTTTGATAGCTTTACAGGTAGGATCATACCACACCAAAAGAGCAGTGGACAATAAGACTATATGAGCTA
TATGAAGCTTTTAGGAATCATTTAGGACAGACAGAGCCCTAAACAACCCATTCATGACTTAAGTTGTTGGCTCAG
TGTATGCTGGGGACAAAGAAAAACTAACAAGCCGACCTGCCTTTATGATAAATTCTAGTGTGCTTACAAGGGATG
ACTTCCTGAGGTGTGATCTGTCCACCTTGAAGAACTCCACAACTGAAGAAGGGGAGCTGTGAGAACGTGGATTGT
TCTACAACTTGCACAGGGTAACAGAGGAAGTGGCTGAGGCCTAGAGTCACGTTTTCCAGTTCCCTTCGCAAACTA
TATTTCTTGGAACGCGAAAGGAAGCTTTACCTATTTCATAGAAGACCTGGAATCCATAACCTCAGAAGGCAATAT
TATTGATAGAAAATGTGGAAGGATCAGGAAGTTCTTAGATTCTTGGATGACAGATGCATGTTGATGCCCTATGGA
GATGTCCTTGTGTTTTGAGGTCACTGAGGTAGGAAGACCTGTCTACTCTTGGTTTCACCACTAGAACAGTCTTGG
GCTGGATGGGTTATAGAGCTGAGCGGCTGTGATGGTTCTGTTTTTACATTAACAAAAACAATTAAAAACACCAAA
AAC

FIGURE 825

CACACCCTGCAGGACACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAGTGGGGTGACATGTAC
CTGTCGGCCATCTGTGAGTACCAGTTGGAAGAGATCCAGCGGGTGTTTGAGGGCCCCTATAAGGAGTACCATGAG
GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCTCGGCCTGGCTCGTGCATTAACAACTGGCAT
CGGCGCCACGGCTACACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAGAAGCACCCGCTGATG
GAGGAGCAGGTGGGGCCTCGGTGGAGCCGCCCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC
GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTCATTGACACAGGAGACGGCTGGCTGCTCAAG
GCTGTGAGCCTGGGGCCCTGGGTTCACCTGATTGAGGAGCTGCAGCTGTTTGACCAGGAGCCCATGAGAAGCCTG
GTGCTATCTCAGAGCAAGAAGCTGCTCTTTGCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC
ATGAAGTATCGCTCCTGTGCAGACTGTGTCCTCGCCCGGGACCCCTATTGCGCCTGGAGCGTCAACACCAGCCGC
TGTGTGGCCGTGGGTGGCCACTCTGGATCTCTACTGATCCAGCATGTGATGACCTCGGACACTTCAGGCATCTGC
AACCTCCGTGGCAGTAAGAAAGTCAGGCCCACTCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTGCTG
CCCTGCCACCTCTCCTCCAACTTGGCCCATGCCCGCTGGACCTTTGGGGGCCGGGACCTGCCTGCGGAACAGCCC
GGGTCCTTCCTCTACGATGCCCGGCTCCAGGCCCTGGTTGTGATGGCTGCCCAGCCCCGCCATGCCGGGGCCTAC
CACTGCTTTTCAGAGGAGCAGGGGGCGCGGCTGGCTGCTGAAGGCTACCTTGTGGCTGTCGTGGCAGGCCCGTCG
GTGACCTTGGAGGCCCGGGCCCCCCTGGAAAACCTGGGGCTGGTGTGGCTGGCGGTGGTGGCCCTGGGGGCTGTG
TGCCTGGTGCTGCTGCTGCTGGTGCTGTCATTGCGCCGGCGGCTGCGGGAAGAGCTGGAGAAAGGGGCCAAGGCT
ACTGAGAGGACCTTGGTGTACCCCCTGGAGCTGCCCAAGGAGCCCACCAGTCCCCCCTTCCGGCCCTGTCCTGAA
CCAGATGAGAAACTTTGGGATCCTGTCGGTTACTACTATTCAGATGGCTCCCTTAAGATAGTACCTGGGCATGCC
CGGTGCCAGCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGGCATCCCAGGCCAGCCTCTGCCTTCTCCAACTCGG
CTTCACCTGGGGGGTGGGCGGAACTCAAATGCCAATGGTTACGTGCGCTTACAACTAGGAGGGGAGGACCGGGGA
GGGCTCGGGCACCCCCTGCCTGAGCTCGCGGATGAACTGAGACGCAAACTGCAGCAACGCCAGCCACTGCCCGAC
TCCAACCCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCGCGTCGGCGGGAAGCGTGGGAGGTGTAGCTCCTA
CTTTTGCACAGGCACCAGCTACCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGGGACAGATACTGCCCAGCA
CCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACTGCCACTTGGTGTGGCTCACCAGGGCACCAGCCT
CGCAGAAGGCATCTTCCTCCTCTCTGTGAATCACAGACACGCGGGACCCCAGCCGCCAAAACTTTTCAAGGCAGA
AGTTTCAAGATGTGTGTTTGTCTGTATTTGCACATGTGTTTGTGTGTGTGTGTATGTGTGTGTGCACGCGCGTGC
GCGCTTGTGGCATAGCCTTCCTGTTTCTGTCAAGTCTTCCCTTGGCCTGGGTCCTCCTGGTGAGTCATTGGAGCT
ATGAAGGGGAAGGGGTCGTATCACTTTGTCTCTCCTACCCCCACTGCCCCGAGTGTCGGGCAGCGATGTACATAT
GGAGGTGGGGTGGACAGGGTGCTGTGCCCCTTCAGAGGGAGTGCAGGGCTTGGGGTGGGCCTAGTCCTGCTCCTA
GGGCTGTGAATGTTTTCAGGGTGGGGGAGGGAGATGGAGCCTCCTGTGTGTTTGGGGGGAAGGGTGGGTGGGGC
CTCCCACTTGGCCCCGGGGTTCAGTGGTATTTTATACTTGCCTTCTTCCTGTACAGGGCTGGGAAAGGCTGTGTG
AGGGGAGAGAAGGGAGAGGGTGGGCCTGCTGTGGACAATGGCATACTCTCTTCCAGCCCTAGGAGGAGGGCTCCT
AACAGTGTAACTTATTGTGTCCCCGCGTATTTATTGTTGTAAATATTTGAGTATTTTTATATTGACAATAAAAT
GGAGAAAATGAAAAAAAAAAAAAAAAAAAA

FIGURE 826

MYLSAICEYQLEEIQRVFEGPYKEYHEEAQKWDRYTDPVPSPRPGSCINNWHRRHGYTSSLELPDNILNFVKKHP
LMEEQVGPRWSRPLLVKKGTNFTHLVADRVTGLDGATYTVLFIDTGDGWLLKAVSLGPWVHLIEELQLFDQEPMR
SLVLSQSKKLLFAGSRSQLVQLPVADCMKYRSCADCVLARDPYCAWSVNTSRCVAVGGHSGSLLIQHVMTSDTSG
ICNLRGSKKVRPTPKNITVVAGTDLVLPCHLSSNLAHARWTFGGRDLPAEQPGSFLYDARLQALVVMAAQPRHAG
AYHCFSEEQGARLAAEGYLVAVVAGPSVTLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLREELEKGA
KATERTLVYPLELPKEPTSPPFRPCPEPDEKLWDPVGYYYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLPSP
TRLHLGGGRNSNANGYVRLQLGGEDRGGLGHPLPELADELRRKLQQRQPLPDSNPEESSV

FIGURE 827

CGGAAGTTTTGCTGCTAGTCGCGGACGCA**ATG**GCTTCAAGGTTACTTCGCGGAGCTGGAACGCTGGCCGCGCAGG
CCCTGAGGGCTCGCGGCCCCAGTGGCGCGGCCGCGATGCGCTCCATGGCATCTGGAGGTGGTGTTCCCACTGATG
AAGAGCAGGCGACTGGGTTGGAGAGGGAGATCATGCTGGCTGCAAAGAAGGGACTGGACCCATACAATGTACTGG
CCCCAAAGGGAGCTTCAGGCACCAGGGAAGACCCTAATTTAGTCCCCTCCATCTCCAACAAGAGAATAGTAGGCT
GCATCTGTGAAGAGGACAATACCAGCGTCGTCTGGTTTTGGCTGCACAAAGGCGAGGCCCAGCGATGCCCCCGCT
GTGGAGCCCATTACAAGCTGGTGCCCCAGCAGCTGGCACAC**TGA**GCACCTGCACTAAATTACTCAAAATGTGCTG
TAAAGTTTCTTCTTTCCAGTAAAGACTAGCCATTGCATTGGCTCCTTCTCCCATAAAAAAAAAAAAAAAAAAA

FIGURE 828

MASRLLRGAGTLAAQALRARGPSGAAAMRSMASGGGVPTDEEQATGLEREIMLAAKKGLDPYNVLAPKGASGTRE
DPNLVPSISNKRIVGCICEEDNTSVVWFWLHKGEAQRCPRCGAHYKLVPQQLAH

FIGURE 829

TTGCAGCCGCCGGCAGCTACTGCAAGGCAAAAGCCGGAGTGGACGTGTCTTTTGAAACTGCTGCTCTTTCACTTC
TCAGGCGTCACCGAGAGCTCAGCACCCAGGCTGAACTCTGTACCATTTGGAAGA<u>ATG</u>GAAGCTGATGCATCTGTT
GACATGTTTTCCAAAGTCCTGGAGCATCAGCTGCTTCAGACTACCAAACTGGTGGAAGAACATTTGGATTCTGAA
ATTCAAAAACTGGATCAGATGGATGAGGATGAATTGGAACGCCTTAAAGAAAAGAGACTCCAGGCACTAAGGAAA
GCTCAACAGCAGAAACAAGAATGGCTTTCTAAAGGACATGGGGAATACAGAGAAATCCCTAGTGAAAGAGACTTT
TTTCAAGAAGTCAAGGAGAGTGAAAATGTGGTTTGCCATTTCTACAGAGACTCCACATTCAGGTGTAAAATACTA
GACAGACATCTGGCAATATTGTCCAAGAAACACCTCGAGACCAAATTTTTGAAGCTGAATGTGGAAAAAGCACCT
TTCCTTTGTGAGAGACTGCATATCAAAGTCATTCCCACACTAGCACTGCTAAAAGATGGGAAAACACAAGATTAT
GTTGTTGGGTTTACTGACCTAGGAAATACAGATGACTTCACCACAGAAACTTTAGAATGGAGGCTCGGTTCTTCT
GACATTCTTAATTACAGTGGAAATTTAATGGAGCCACCATTTCAGAACCAAAAGAAATTTGGAACAAACTTCACA
AAGCTGGAAAAGAAAACTATCCGAGGAAAGAAATATGATTCAGACTCTGATGATGAT<u>TAG</u>AGCTCAATAATTCTT
TGTAAATTGTCTTTTTTTTTCTGCTTCAGATTTAAATGTGTTTTTAAAATTCTATTAATGTCTATACATTGGTCA
CCTAAATACTCATATTCTCGAGTTTTATACAGTTGTATCACATCGAAAAGTGTCTTTACTGTTTTCTGTGTGGCC
ATCATGTTTAAGTTGAGGAAAACTCAGTTCTTAAATTATCTGGGAAGGGTCTGGATTCTCTATTTTTGAGATTGA
CTTTATCACAATATGATTCTTACATCTTTATACCATTTACAATTGTGTTTTAGATCTACAGAGTTAGAAATTCGA
AAACTATTCCAGGACTAATTCTTAATCGGCATTATTTATACAAGAGGTCAAGTAACATTTACTAGCGCAATACTG
CACTTGTAAATGAATTATAAACGCTCTTCTGGAATATATTTAAATAACCATTAAAGAACTGCTTATTCATTCTGG
ACACTGCATGTTGATGTTGAATCAACTGATGCCAGCAGAAAGCTATTTTGATTTGTGAACATACTGCCTTATTTA
AAGGGTCCTGATTGCTTGTATTTTAAGACATTCATTAAAAAGAAACCAGGAAACACTTTTGAAATAACAGCATAA
GGAACTTCACTGTCTCTGCTCAATAAAATACCTGTAACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 830

MEADASVDMFSKVLEHQLLQTTKLVEEHLDSEIQKLDQMDEDELERLKEKRLQALRKAQQQKQEWLSKGHGEYRE
IPSERDFFQEVKESENVVCHFYRDSTFRCKILDRHLAILSKKHLETKFLKLNVEKAPFLCERLHIKVIPTLALLK
DGKTQDYVVGFTDLGNTDDFTTETLEWRLGSSDILNYSGNLMEPPFQNQKKFGTNFTKLEKKTIRGKKYDSDSDD
D

FIGURE 831A

CGCGGGTCTGTGGAGAGCCGGGTGCGAGCGGCGGCAGCACGAGGGGAAAAGAGCTGAGCGGAGACCAAAGTCAGC
CGGGAGACAGTGGGTCTGTGAGAGACCGAATAGAGGGGCTGGGGCCACGAGCGCCATTGACAAGCAATGGGGAAG
AAACAGAAAAACAAGAGCGAAGACAGCACCAAGGATGACATTGATCTTGATGCCTTGGCTGCAGAAATAGAAGGA
GCTGGTGCTGCCAAAGAACAGGAGCCTCAAAAGTCAAAAGGGAAAAAGAAAAAAGAGAAAAAAAAGCAGGACTTT
GATGAAGATGATATCCTGAAAGAACTGGAAGAATTGTCTTTGGAAGCTCAAGGCATCAAAGCTGACAGAGAAACT
GTTGCAGTGAAGCCAACAGAAAACAATGAAGAGGAATTCACCTCAAAAGATAAAAAAAAGAAAGGACAGAAGGGC
AAAAAACAGAGTTTTGATGATAATGATAGCGAAGAATTGGAAGATAAAGATTCAAAATCAAAAAAGACTGCAAAA
CCGAAAGTGGAAATGTACTCTGGGAGTGATGATGATGATGATTTTAACAAACTTCCTAAAAAAGCTAAAGGGAAA
GCTCAAAAATCAAATAAGAAGTGGGATGGGTCAGAGGAGGATGAGGATAACAGTAAAAAAATTAAAGAGCGTTCA
AGAATAAATTCTTCTGGTGAAAGTGGTGATGAATCAGATGAATTTTTGCAATCTAGAAAAGGACAGAAAAAAAAT
CAGAAAAACAAGCCAGGTCCTAACATAGAAAGTGGGAATGAAGATGATGACGCCTCCTTCAAAATTAAGACAGTG
GCCCAAAAGAAGGCAGAAAAGAAGGAGCGCGAGAGAAAAAAGCGAGATGAAGAAAAAGCGAAACTGCGGAAGCTG
AAAGAAAAAGAAGAGTTAGAAACAGGTAAAAAGGATCAGAGTAAACAAAAGGAATCTCAAAGGAAATTTGAAGAA
GAAACTGTAAAATCCAAAGTGACTGTTGATACTGGAGTAATTCCTGCCTCTGAAGAGAAAGCAGAGACTCCCACA
GCTGCAGAAGATGACAATGAAGGAGACAAAAAGAAGAAAGATAAGAAGAAAAAGAAAGGAGAAAAGGAAGAAAAA
GAGAAAGAGAAGAAAAAAGGACCTAGCAAAGCCACTGTTAAAGCTATGCAAGAAGCTCTGGCTAAGCTTAAAGAG
GAAGAAGAAAGACAGAAGAGAGAAGAGGAAGAACGTATAAAACGGCTTGAAGAATTAGAAGCCAAGCGTAAAGAA
GAGGAACGATTGGAACAAGAAAAAAGAGAAAGGAAAAAGCAAAAAGAAAAAGAAAGAAAAGAACGCTTGAAAAAA
GAAGGGAAACTTTTAACTAAATCCCAGAGAGAAGCCAGAGCCAGAGCCGAAGCTACTCTTAAACTGCTACAAGCT
CAGGGTGTTGAAGTGCCATCAAAAGACTCTTTGCCAAAGAAGAGGCCAATTTATGAAGATAAAAAGAGGAAAAAA
ATACCACAGCAGCTAGAAAGTAAAGAAGTGTCTGAATCAATGGAATTATGTGCTGCTGTAGAAGTTATGGAACAA
GGAGTACCAGAAAAGGAAGAGACACCACCTCCTGTTGAACCAGAAGAAGAAGAAGATACTGAGGATGCTGGATTG
GATGATTGGGAAGCTATGGCCAGTGATGAGGAGACAGAAAAAGTAGAAGGAAACAAAGTTCATATAGAAGTAAAA
GAAAACCCTGAAGAGGAGGAGGAGGAGGAAGAAGAGGAAGAAGAAGATGAAGAAAGTGAAGAAGAGGAGGAAGAG
GAGGGAGAAAGTGAAGGCAGTGAAGGTGATGAGGAAGATGAAAAGGTGTCAGATGAGAAGGATTCAGGGAAGACA
TTAGATAAAAAGCCAAGTAAAGAAATGAGCTCAGATTCTGAATATGACTCTGATGATGATCGGACTAAAGAAGAA
AGGGCTTATGACAAAGCAAAACGGAGGATTGAGAAACGGCGACTTGAACATAGTAAAAATGTAAACACCGAAAAG
CTAAGAGCCCCTATTATCTGCGTACTTGGGCATGTGGACACAGGGAAGACAAAAATTCTAGATAAGCTCCGTCAC
ACACATGTACAAGATGGTGAAGCAGGTGGTATCACACAACAAATTGGGGCCACCAATGTTCCTCTTGAAGCTATT
AATGAACAGACTAAGATGATTAAAAATTTTGATAGAGAGAATGTACGGATTCCAGGAATGCTAATTATTGATACT
CCTGGGCATGAATCTTTCAGTAATCTGAGAAATAGAGGAAGCTCTCTTTGTGACATTGCCATTTTAGTTGTTGAT
ATTATGCATGGTTTGGAGCCCCAGACAATTGAGTCTATCAACCTTCTCAAATCTAAAAAATGTCCCTTCATTGTT
GCACTCAATAAGATTGATAGGTTATATGATTGGAAAAAGAGTCCTGACTCTGATGTGGCTGCTACTTTAAAGAAG
CAGAAAAAGAATACAAAAGATGAATTTGAGGAGCGAGCAAAGGCTATTATTGTAGAATTTGCACAGCAGGGTTTG
AATGCTGCTTTGTTTTATGAGAATAAAGATCCCCGCACTTTTGTGTCTTTGGTACCTACCTCTGCACATACTGGT
GATGGCATGGGAAGTCTGATCTACCTTCTTGTAGAGTTAACTCAGACCATGTTGAGCAAGAGACTTGCACACTGT
GAAGAGCTGAGAGCACAGGTGATGGAGGTTAAAGCTCTCCCGGGGATGGGCACCACTATAGATGTCATCTTGATC
AATGGGCGTTTGAAGGAAGGAGATACAATCATTGTTCCTGGAGTAGAAGGGCCCATTGTAACTCAGATTCGAGGC
CTCCTGTTACCTCCTCCTATGAAGGAATTACGAGTGAAGAACCAGTATGAAAAGCATAAAGAAGTAGAAGCAGCT
CAGGGGGTAAAGATTCTTGGAAAAGACCTGGAGAAAACATTGGCTGGTTTACCCCTCCTTGTGGCTTATAAAGAA
GATGAAATCCCTGTTCTTAAAGATGAATTGATCCATGAGTTAAAGCAGACACTAAATGCTATCAAATTAGAAGAA
AAAGGAGTCTATGTCCAGGCATCTACACTGGGTTCTTTGGAAGCTCTACTGGAATTTCTGAAAACATCAGAAGTG
CCCTATGCAGGAATTAACATTGGCCCAGTGCATAAAAAAGATGTTATGAAGGCTTCAGTGATGTTGGAACATGAC
CCTCAGTATGCAGTAATTTTGGCCTTCGATGTGAGAATTGAACGAGATGCACAAGAAATGGCTGATAGTTTAGGA
GTTAGAATTTTTAGTGCAGAAATTATTTATCATTTATTTGATGCCTTTACAAAATATAGACAAGACTACAAGAAA
CAGAAACAAGAAGAATTTAAGCACATAGCAGTATTTCCCTGCAAGATAAAAATCCTCCCTCAGTACATTTTTAAT
TCTCGAGATCCGATAGTGATGGGGGTGACGGTGGAAGCAGGTCAGGTGAAACAGGGGACACCCATGTGTGTCCCA
AGCAAAAATTTTGTTGACATCGGAATAGTAACAAGTATTGAAATAAACCATAAACAAGTGGATGTTGCAAAAAAA

FIGURE 831B

GGACAAGAAGTTTGTGTAAAAATAGAACCTATCCCTGGTGAGTCACCCAAAATGTTTGGAAGACATTTTGAAGCT
ACAGATATTCTTGTTAGTAAGATCAGCCGGCAGTCCATTGATGCACTCAAAGACTGGTTCAGAGATGAAATGCAG
AAGAGTGACTGGCAGCTTATTGTGGAGCTGAAGAAAGTATTTGAAATCATCTAATTTTTTCACATGGAGCAGGAA
CTGGAGTAAATGCAATACTGTGTTGTAATATCCCAACAAAAATCAGACAAAAAAATGGAACAGACGTATTTGGACA
CTGATGGACTTAAGTATGGAAGGAAGAAAAATAGGTGTATAAAATGTTTTCCATGAGAAACCAAGAAACTTACAC
TGGTTTGACAGTGGTCAGTTACATGTCCCCACAGTTCCAATGTGCCTGTTCACTCACCTCTCCCTTCCCCAACCC
TTCTCTACTTGGCTGCTGTTTTAAAGTTTGCCCTTCCCCAAATTTGGATTTTTATTACAGATCTAAAGCTCTTTC
GATTTTATACTGATTAAATCAGTACTGCAGTATTTGATTAACC

FIGURE 832

CTTCCTTTCCAACTTGGACGCTGCAGA**ATG**GCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCC
ATCAACGAAGTGGTAACCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGT
GCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAGGAGATGGGAACTCCAGATGTGCGCATTGACACC
AGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAA
CGTAATGAGGATGAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAAT
CTACAGACAGTCAATGTGGATGAGAAC**TAA**TCGCTGATCGTCAGATCAAATAAAGTTATAAAATTGC

FIGURE 833

MAPAKKGGEKKKGRSAINEVVTREYTINIHKRIHGVGFKKRAPRALKEIRKFAMKEMGTPDVRIDTRLNKAVWAK
GIRNVPYRIRVRLSRKRNEDEDSPNKLYTLVTYVPVTTFKNLQTVNVDEN

FIGURE 834

ATGCCCGGCGGAGGGGCGAGCGCGGCGTCTGGCCGGCTTCTCACCGCCGCGGAGCAAAGAGGGTCCCGGGAAGCG
GCAGGGTCGGCGTCCAGGAGCGGCTTCGGGGGCTCCGGCGGCGGCAGAGGCGGAGCAAGCGGCCCCGGGTCCGGG
AGCGGAGGCCCTGGGGGCCCCGCGGGCAGGATGAGCTTGACCCCGAAGGAGCTCTCGAGCCTGCTGAGCATCATA
TCGGAGGAGGCGGGCGGCGGCAGCACCTTCGAGGGCCTGTCCACCGCCTTCCACCACTACTTCAGCAAGGCCGAC
CACTTCCGCCTGGGCTCGGTGCTCGTCATGCTGCTCCAGCAGCCCGACCTGCTGCCTAGCGCGGCGCAGCGCCTC
ACGGCGCTCTACCTGCTCTGGGAGATGTACCGCACCGAGCCGCTGGCCGCCAACCCCTTCGCCGCCAGCTTCGCG
CACCTGCTCAACCCCGCGCCGCCCGCCCGCGGCGGCCAGGAACCCGACCGCCCTCCGCTCTCAGGATTTTTACCT
CCTATAACTCCACCAGAAAAGTTTTTCTTTCCCAGCTGATGCTGGCACCCCCACGGGAACTCTTCAAAAAGACG
CCTCGCCAGATTGCACTGATGGACGTTGGAAACATGGGCCAGTCTGTGGACATTAGTGGGCTTCAGTTAGCCTTG
GCCGAACGCCAATCTGAATTGCCAACGCAAAGCAAAGCGAGCTTCCCCAGTATTCTCAGTGACCCAGACCCGGAT
TCTTCTAATTCTGGATTTGACAGCTCAGTTGCCTCTCAGATCACAGAAGCTTTAGTCAGCGGACCAAAGCCACCT
ATTGAAAGCCATTTTCGACCAGAGTTTATTCGTCCACCGCCTCCACTCCACATTTGTGAGGATGAACTTGCTTGG
CTAAACCCCACGGAGCCTGACCACGCGATCÇAGTGGGATAAATCGATGTGTGTTAAGAATAGCACTGGTGTGGAG
ATCAAACGAATAATGGCCAAAGCCTTCAAAAGCCCCTTATCCTCTCCCCAACAAACACAGCTACTTGGTGAGTTG
GAAAAAGACCCCAAACTTGTCTACCATATTGGCCTCACCCCAGCCAAACTTCCTGACCTTGTGGAAAACAACCCT
TTAGTCGCTATAGAAATGTTGCTGAAATTAATGCAGTCAAGCCAGATCACTGAGTATTTCTCTGTCCTGGTCAAT
ATGGACATGTCTTTACATTCAATGGAAGTTGTAAATCGACTAACTACAGCTGTTGATCTACCTCCTGAATTTATT
CACCTTTATATATCAAATTGCATCTCTACTTGTGAACAGATTAAGGATAAATATATGCAGAATCGGTTGGTGCGT
CTTGTGTGTGTGTTTCTCCAATCCTTGATCCGTAACAAAATTATTAATGTACAGGATTTGTTTATAGAAGTGCAG
GCATTCTGTATTGAATTCAGTAGGATACGAGAAGCTGCTGGTCTTTTCCGGTTGTTGAAGACATTGGATACTGGG
GAAACACCTTCTGAGACCAAAATGTCAAAA**TAA**

FIGURE 835

MPGGGASAASGRLLTAAEQRGSREAAGSASRSGFGGSGGGRGGASGPGSGSGGPGGPAGRMSLTPKELSSLLSII
SEEAGGGSTFEGLSTAFHHYFSKADHFRLGSVLVMLLQQPDLLPSAAQRLTALYLLWEMYRTEPLAANPFAASFA
HLLNPAPPARGGQEPDRPPLSGFLPPITPPEKFFLSQLMLAPPRELFKKTPRQIALMDVGNMGQSVDISGLQLAL
AERQSELPTQSKASFPSILSDPDPDSSNSGFDSSVASQITEALVSGPKPPIESHFRPEFIRPPPPLHICEDELAW
LNPTEPDHAIQWDKSMCVKNSTGVEIKRIMAKAFKSPLSSPQQTQLLGELEKDPKLVYHIGLTPAKLPDLVENNP
LVAIEMLLKLMQSSQITEYFSVLVNMDMSLHSMEVVNRLTTAVDLPPEFIHLYISNCISTCEQIKDKYMQNRLVR
LVCVFLQSLIRNKIINVQDLFIEVQAFCIEFSRIREAAGLFRLLKTLDTGETPSETKMSK

FIGURE 836

AGGGTACGGGCCGGGACCGCCGCAGCCCGGGGCGGGGGCACGGCAACCGCGAGGCCTGGGGGCGCCCGCCCCCCG
CGCCCCACGCCCGGTGCCAGCGAGCCGAGGCGTGCATCTCCTTATATGGTCAAATGACACGGCGGGGTTTCTCGA
GGGCGGGAGCTGCGCAGCGCTCCACTCGGCCGGCAGCGGAGCCGCAGCCACCAGCCGCCCGCGCCCTCCAGCCCC
GTCCGGGAGTCCCCGGCCCGCTGCGGTGCCGTGAGTACCTCCAACCCCCTGCGCCCCGGAGGGAGGCCGAGGGGC
TTAGCCACCAGGGCTCGGAAGTGGGGGCCGAATCCGGTGCGAGACCCAAGGAGAGGGGAGCAGAGCCGGAGTTGG
GGAGACTGTGGCTGAAAACTGTGTCTTCCTGGAGACTAGGCTGGCATTTTGACTTTGGGACGGAGTCTCGCTTTG
TCGCCCAGGCTGGAGTGCAGTGGCACGATCTCAGCTCACTGCAAGCTCTACCTCTTGGTTCACGCCATTCTCCTG
CCCCAGCCTCCCAAGTAGCTGGGACTACAGGTTGCTGAAAAGCCAGGAGTCAAA<u>ATG</u>ACTGAGCGCTTTGACTGC
CACCATTGCAACGAATCTCTCTTTGGCAAGAAGTACATCCTGCGGGAGGAGAGCCCCTACTGCGTGGTGTGCTTT
GAGACCCTGTTCGCCAACACCTGCGAGGAGTGTGGGAAGCCCATCGGCTGTGACTGCAAGGACTTGTCTTACAAG
GACCGGCACTGGCATGAAGCCTGTTTCCACTGCTCGCAGTGCAGAAACTCACTGGTGGACAAGCCCTTTGCTGCC
AAGGAGGACCAGCTGCTCTGTACAGACTGCTATTCCAACGAGTACTCATCCAAGTGCCAGGAATGCAAGAAGACC
ATCATGCCAGGTACCCGCAAGATGGAGTACAAGGGCAGCAGCTGGCATGAGACCTGCTTCATCTGCCACCGCTGC
CAGCAGCCAATTGGAACCAAGAGTTTCATCCCCAAAGACAATCAGAATTTCTGTGTGCCCTGCTATGAGAAACAA
CATGCCATGCAGTGCGTTCAGTGCAAAAAGCCCATCACCACGGGAGGGGTCACTTACCGGGAGCAGCCCTGGCAC
AAGGAGTGCTTCGTGTGCACCGCCTGCAGGAAGCAGCTGTCTGGGCAGCGCTTCACAGCTCGCGATGACTTTGCC
TACTGCCTGAACTGCTTCTGTGACTTGTATGCCAAGAAGTGTGCTGGGTGCACCAACCCCATCAGCGGACTTGGT
GGCACAAAATACATCTCCTTTGAGGAACGGCAGTGGCATAACGACTGCTTTAACTGTAAGAAGTGCTCCCTCTCA
CTGGTGGGGCGTGGCTTCCTCACAGAGAGGGACGACATCCTGTGCCCCGACTGTGGGAAAGACATC<u>TGA</u>ATTCAA
CACAGAGAAGTTGCTGCTTGTGATCTCACACACAGATTTTTATGTTTTCTTTCTCACCCAGGCAATCTTGCCTTC
TGGTTTCTTCCAGCCACATTGAGACTTTCTTCTAGTGCTTTTCAGTGATACTCACGTTTGCTTAAACCCTTTAGT
GCTTTGTGATAGTTCAGTCCCAGGGAAAGAGAAAACTCGCCCTAGGCCCTAGGTGGGAAGATGGTTTGAAATTTT
TGTAATCGAGTAAGGCACACCCAAATGTAAAAATCCTTTTGAATGATGCCTTTATAAATCTTTCTCTCACTGTCT
ATTTAAGTGCAATTAACATATGTCACGAACTTGAAAGTTTCTAAACTCAATAAGGTAATGACCAGTTGTTATTT
ACAGCTCTGTAACCTCCCGTTGCGTCAAGTCTAAACCAAGATTATGTGACTTGCAATAAAGTTATTCAGAACAGA
AAAAAAAAAAAAAAAAA

FIGURE 837

MTERFDCHHCNESLFGKKYILREESPYCVVCFETLFANTCEECGKPIGCDCKDLSYKDRHWHEACFHCSQCRNSL
VDKPFAAKEDQLLCTDCYSNEYSSKCQECKKTIMPGTRKMEYKGSSWHETCFICHRCQQPIGTKSFIPKDNQNFC
VPCYEKQHAMQCVQCKKPITTGGVTYREQPWHKECFVCTACRKQLSGQRFTARDDFAYCLNCFCDLYAKKCAGCT
NPISGLGGTKYISFEERQWHNDCFNCKKCSLSLVGRGFLTERDDILCPDCGKDI

FIGURE 838

AGTCTTCTGGCCCCGAGAGGGAGAGGTGGGGATAGGACCTTCCTTTAGTCCCCTCCGTAGTGGAACGAAGGATTC
TTTATGGTCATCTGTGGTGTTCATTTCGTAAAGAAGCATCTGCAGGGTAAGAAGGAAAAACGTCCACCTTGCAAA
TATATCCCAGGCACATGCCTCCTGAGAAGTGACCCCCTCCTCCCTCCGCCTCCCCCGGCACGTCCTGGGGCTTCT
CCAGTCTCCCGCTCCTGGGACCAGGCAGAGATCCCGGCGTGGGCAGACCCCTGCCACCGCGCCCAGGCCTCGTCC
GAAACTCGCGCCCGAGAGCCCACGCCGGAGGCGACGCTCCCGATAACTACTGTGCTCCCAAGACCCGGAGGGCAC
GAAGAAAGGAGCCCTGGCAAACAAAGGGTTGCTGAAAAGCCAGGAGTCAAAATGACTGAGCGCTTTGACTGCCAC
CATTGCAACGAATCTCTCTTTGGCAAGAAGTACATCCTGCGGGAGGAGAGCCCCTACTGCGTGGTGTGCTTTGAG
ACCCTGTTCGCCAACACCTGCGAGGAGTGTGGGAAGCCCATCGGCTGTGACTGCAAGGTACCTGCTGCGGGCCTC
TGCGGGTCCCCGGCGCTCCCCTAGGAAACACGGGTTTCTCTGTGGTTTGTGCTGAAGCCCTGATCCACCACTGAA
GTCTGTCTCTTGAGCCCCCTCTGAGGGGCGTGGACCCTGCGTGTAGCCTTTCGGAAGCTTCTTCCCTCTAGCGAA
TGTGATCTCTGCCCACAAGCACTGGGTGAGGGCCTTGCCAGGACTTTTGTGCTTAGTATCTCTAAGTACATTTTC
TGTATTCTAGCAATTAGTGCCCTTATCTAACTACCCAGCTGCCTACCAATACTGGAACTTTCTTAAGGGTGGTGC
TCTCTTCCTCTTGTCTGTTTGCCCCGTGGTGAGTAACGTGGAGCAGGTGCTGTGCTCAGTCAATATTTGATGAAT
GAATGTGTACATGAGAGAACCAGAGTTGGTTCCTGGATAAATGGGCACATAAAAGCACAAAGTCCTTGG

FIGURE 839

AAGGACTCCATGAAAGATGACAGAAGAAGTTATTGTGATAGCCAAGTGGGACTACACCGCCCAGCAGGACCAGGA
GCTGGACATCAAGAAGAACGAGCGGCTGTGGTTGCTGGACGACTCCAAGACGTGGTGGCGGGTGAGGAACGCGGC
CAACAGGACGGGCTATGTACCGTCCAACTACGTGGAGCGGAAGAACAGCCTGAAGAAGGGCTCCCTCGTGAAGAA
CCTGAAGGACACACTAGGCCTCGGCAAGACGCGCAGGAAGACCAGCGCGCGGGATGCGTCCCCCACGCCCAGCAC
GGACGCCGAGTACCCCGCCAATGGCAGCGGCGCCGACCGCATCTACGACCTCAACATCCCGGCCTTCGTCAAGTT
CGCCTATGTGGCCGAGCGGGAGGATGAGTTGTCCCTGGTGAAGGGGTCGCGCGTCACCGTCATGGAGAAGTGCAG
CGACGGTTGGTGGCGGGGCAGCTACAACGGGCAGATCGGCTGGTTCCCCTCCAACTACGTCTTGGAGGAGGTGGA
CGAGGCGGCTGCGGAGTCCCCAAGCTTCCTGAGCCTGCGCAAGGGCGCCTCGCTGAGCAATGGCCAGGGCTCCCG
CGTGCTGCATGTGGTCCAGACGCTGTACCCCTTCAGCTCAGTCACCGAGGAGGAGCTCAACTTCGAGAAGGGGGA
GACCATGGAGGTGATTGAGAAGCCGGAGAACGACCCCGAGTGGTGGAAATGCAAAAATGCCCGGGGCCAGGTGGG
CCTCGTCCCCAAAAACTACGTGGTGGTCCTCAGTGACGGGCCTGCCCTGCACCCTGCGCACGCCCCACAGATAAG
CTACACCGGGCCCTCGTCCAGCGGGCGCTTCGCGGGCAGAGAGTGGTACTACGGGAACGTGACGCGGCACCAGGC
CGAGTGCGCCCTCAACGAGCGGGGCGTGGAGGGCGACTTCCTCATTAGGGACAGCGAGTCCTCGCCCAGCGACTT
CTCCGTGTCCCTTAAAGCGTCAGGGAAGAACAAACACTTCAAGGTGCAGCTCGTGGACAATGTCTACTGCATTGG
GCAGCGGCGCTTCCACACCATGGACGAGCTGGTGGAACACTACAAAAAGGCGCCCATCTTCACCAGCGAGCACGG
GGAGAAGCTCTACCTCGTCAGGGCCCTGCAGTGACGGCGCCCCGGCCCCACACTCGCCTCCCGGGCCCCACGGTG
GAGCTGCCCGCCCGGCCTTGTGGCAGAGGCTCCTCCCGCGGGGACGGCCCCGACGGCTTCTCTG

FIGURE 840

MTEEVIVIAKWDYTAQQDQELDIKKNERLWLLDDSKTWWRVRNAANRTGYVPSNYVERKNSLKKGSLVKNLKDTL
GLGKTRRKTSARDASPTPSTDAEYPANGSGADRIYDLNIPAFVKFAYVAEREDELSLVKGSRVTVMEKCSDGWWR
GSYNGQIGWFPSNYVLEEVDEAAAESPSFLSLRKGASLSNGQGSRVLHVVQTLYPFSSVTEEELNFEKGETMEVI
EKPENDPEWWKCKNARGQVGLVPKNYVVVLSDGPALHPAHAPQISYTGPSSSGRFAGREWYYGNVTRHQAECALN
ERGVEGDFLIRDSESSPSDFSVSLKASGKNKHFKVQLVDNVYCIGQRRFHTMDELVEHYKKAPIFTSEHGEKLYL
VRALQ

FIGURE 841

TGGAACCATGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACTGACAAGCCCTTGCACCTGCC
TCTCCAGGATGTCTACAAAATTGGTGGTATTGGTAGTGTTCCTGTTGGCCGAGTGGAGACTGGTGTTCTCAAACC
TGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACAGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTT
GAGTGAAGCTCTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCGTCATGGCAA
CGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGTTTCACTGCTCAGGTGATTATCCTGAACCA
TCCAGGCCAAATAAGCACTGGCTATGCCCCTGTATTGGATTGCCACACGGCTCATATTGCATGCAAGTTTGCTGA
GCTGAAGGAAAAGATTGATCACCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTCTTTGGGTTGCTTTG
CTGTTCGTGATATGAGACAGATAGTT

FIGURE 842

AAAAGCCAAAATGGGAAAGGAAAAGACTCATACCAACATTGTCGTCATTGGACACATAGATTCGGGCAAGTCCAC
CACTACTGGCCATCTGATCTACAAAGGCGGTGGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGC
TGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGTGTGAACATGGTATCAC
CATTGATACCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCGTTGATGCCCCAGGACACAGAGA
CTTCATCAAAAACATGATTACAGAGACATCTCAGGCTGACTGTGCTGTCCTGATTGTTGCTGCTGGTGTTGGTGA
ATTTGAAGCTGGTATCTCCAAGAATGGGCAAACCCAAGAGCATGCCCTTCTGGCTTACACACTGGGTGTGAAACA
ACTAATTGTTGGTGTTAACAAAATGGATTCTACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAACTACAAA
ATTGGTGGTATTGGTAGTGTTCCTGTTGGCCGAGTGGAGACTGGTGTTCTCAAACCTGGTATGGTGGTCACCTTT
GCTCCAGTCAACGTTACAACAGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCCTGGG
GACAATGTGG

FIGURE 843

AACAGATCTTCATGAATGTCGCTATCTTTGAGGATGAAGTTTTTGCTGGAGTTACCACACACCAGGAACTCTTTC
CACACAGCCTGCTGAGTGTGATTGCCAACTTCATCCCTTTCTCTGATCTCAACCAGAGTCCACGGAACATGTACC
AATGCCAGATGGGTAAGCAAACTATGGGCTTTCCACTTCTCACTTATCAAGACCGATCGGATAACAAACTGTATC
GTCTTCAGACTCCTCAGAGTCCCTTGGTGAGACCCTCCATGTATGATTATTATGACATGGATAACTATCCAATTG
GGACCAATGCCATCGTTGCTGTGATTTCTTACACTGGCTATGATATGGAAGATGCCATGATTGTGAATAAGGCCT
CTTGGGAACGAGGCTTTGCCCATGGAAGTGTCTACAAGTCTGAGTTCATAGACCTCTCTGAAAAAATTAAACAAG
GAGATAGTAGCCTGGTGTTTGGCATCAAACCTGGTGACCCACGCGTTCTGCAGAAGTTAGATGACGATGGATTGC
CGTTTATAGGAGCAAAACTGCAGTACGGAGATCCGTATTACAGCTACCTCAACCTCAACACCGGGGAAAGTTTTG
TGATGTACTATAAGAGTAAAGAAAATTGTGTTGTGGATAACATCAAAGTGTGCAGTAATGACACTGGGAGTGGAA
AATTCAAGTGTGTTTGCATCACTATGAGAGTGCCTCGGAACCCAACTATCGGAGATAAATTTGCCAGTCGCCATG
GGCAGAAGGGCATTTTAAGCAGATTGTGGCCGGCTGAGGACATGCCTTTTACTGAGAGTGGGATGGTCCCAGACA
TTCTGTTCAATCCCCATGGTTTTCCATCCCGCATGACCATTGGGATGTTAATTGAGAGTATGGCCGGGAAGTCTG
CAGCTTTGCATGGTCTCTGCCATGATGCTACACCCTTCATCTTCTCAGAGGAGAACTCGGCCTTAGAATACTTTG
GTGAGATGTTAAAGGCTGCTGGCTACAATTTCTATGGCACCGAGAGGTTATATAGTGGCATCAGTGGGCTAGAAC
TGGAAGCAGACATCTTCATAGGAGTGGTTTATTATCAGCGCTTACGCCATATGGTCTCAGACAAATTTCAAGTAA
GGACAACTGGAGCCCGAGACAGAGTCACCAACCAGCCTATTGGGGGAAGAAATGTCCAGGGTGGAATCCGTTTTG
GGGAGATGGAACGGGATGCGCTTTTAGCTCATGGTACATCTTTTCTCCTTCATGACCGCCTCTTCAACTGCTCAG
ATCGGTCGGTAGCCCATGTGTGTGAAGTGTGGCAGTTTACTCTCTCCACTGTTGGAGAAGCCACCCCCTTCTTGG
TCTGCCATGCGCAACAGAAAATACAACTGTACTCTGTGTAGTCGCAGTGACACTATCGATACTGTTTCTGTGCCT
TATGTTTTTCGGTATTTTGTAGCTGAACTGGCAGCTATGAACATCAAAGTGAAACTGGATGTTGTTTAACTTGAT
GTTGACCTTTTGGATTAAGGGGACTATCAGATTAAAGCAAAATGTAATTTTAATTCAATGAAGATATCATTACCA
GGTTACTCTTGAGATTTTTCAACGGTGTTAGAACTCTCAACCAAGACCTGAAAACCAAGTATGCAAGGTTTCTGA
ATCTCTCTGGTAGATTAACTATTGACAATGATTTTCTGTTATCTTTGTTCAAAAAGTTCATGTCTTCTCAAAATA
TGAAATATTGATAAATGGAAGAGCATACGGTGACAAGTCTCCTTTCCAACCCCAGGTTCCCTACACCCTGCTCTC
AGCAGGCAGTGAGTGTCACACACCTGTTAATCCATCTTGAGCAGGACAGTACTATACAAATAGAATGCAAGCTGT
AATGTAATTTTATATTTTCTTATAGCCACGTTGAAGTAAAAACAAACAGGTACAGTGTTTTTTACCAGCTTTATA
GAAGTACAGTTGTTACATATTTAATGAATACAATTTGATGGGTCTGACTATATGCACACACCTTTGATACCATCA
CCACAATCAGGGTAATAAACATACCTGTCATCTCCACAAGTTTCCTCCTGCCCCTTTGTTTTTTGCTTTTTGGTT
GCTGTTGAGTTTTTGTTTTGTCTTCTGTGGTAAGAACACTTAACTCAAGACCTACCCTCTTAACAAATCTTTAAG
TGCACGATATAGTATTGTTAATTCCAGGCACCATGTTGTACAACAGATCTTTAGACCTTACTTGTCTTGCATAAC
TGAAGCTTTATACCTGTTGAACAACTCTCCATTTCCCTGGCCCCTAGCAACCACCCTTCTACCCTGTTTCTATGA
GTTTGACTATTACAGATATCTCATATAGTGGGATCATGCAATATTTGTCCTGTGACTGGCTTATTTCACTTAGCA
TAGTGAAATAAGATTCATCCATTTTGGAAGCCAGGCATGGTGCTGTGCATCTATAGTCCCTGCTATTTGAGAGGC
TGAGGTGGGAGGATCATTTGAGTGCAGGAGTTCAAGGACAGCCTGGGTAATATAGGAAGACCCCTGTCTTGAAGAC
CCTGACCTCAAGTGATCCACCCACCTCGGCCTCCGAAAGTGCTAGGATTACAGGTGTGAGCCACTGTGCCTGGCC
TCCGGTGAGTATTTTATATTTAGTCTACACTTCCATACTTGGCTTTTTTCTGCTTTTATGTTGATCTGCTTTCAT
AGCAGTGTGTAGAGTGCCACTTATGTTTTCTTTCTTGTGTACAGTATTTTATTGTATGGATTTACCATCCCCTGT
GTATTTAAGTTGTTCCATTCTTTGGCCATTATAACTTTTTTCTGCAAATATTCTGGTGACTTATCTTTGGCCATT
ATAAACTGTTGATAATAAAAAAAAAAAAAAAAA

FIGURE 844

MNVAIFEDEVFAGVTTHQELFPHSLLSVIANFIPFSDLNQSPRNMYQCQMGKQTMGFPLLTYQDRSDNKLYRLQT
PQSPLVRPSMYDYYDMDNYPIGTNAIVAVISYTGYDMEDAMIVNKASWERGFAHGSVYKSEFIDLSEKIKQGDSS
LVFGIKPGDPRVLQKLDDDGLPFIGAKLQYGDPYYSYLNLNTGESFVMYYKSKENCVVDNIKVCSNDTGSGKFKC
VCITMRVPRNPTIGDKFASRHGQKGILSRLWPAEDMPFTESGMVPDILFNPHGFPSRMTIGMLIESMAGKSAALH
GLCHDATPFIFSEENSALEYFGEMLKAAGYNFYGTERLYSGISGLELEADIFIGVVYYQRLRHMVSDKFQVRTTG
ARDRVTNQPIGGRNVQGGIRFGEMERDALLAHGTSFLLHDRLFNCSDRSVAHVCEVWQFTLSTVGEATPFLVCHA
QQKIQLYSV

FIGURE 845

GAGCTGTCCCCGGTGCCGCCGACCCGGGCCGTGTGCCCGTGGCTCCAGCCGCTGTCGCCTCGATCTCCTCGTCTC
CCGCTCCGCCCTCCCTTTTCCCTGGATGAACTTGCGTCCTTTCTCTTCTCCGCCATGGAATTCTGCTCCGTGCTT
TTAGCCCTCCTGAGCCAAAGAAACCCCAGACAACAGATGCCCATACGCAGCGTATAGCAGTAACTCCCCAGCTCG
GTTTCTGTGCCGTAGTTTACAGTATTTAATTTTATATAATATATATTATTTATTATAGCATTTTTGATACCTCAT
ATTCTGTTTACACATCTTGAAAGGCGCTCAGTAGTTCTCTTACTAAACAACCACTACTCCAGAGA**ATG**GCAACGC
TGATTACCAGTACTACAGCTGCTACCGCCGCTTCTGGTCCTTTGGTGGACTACCTATGGATGCTCATCCTGGGCT
TCATTATTGCATTTGTCTTGGCATTCTCCGTGGGAGCCAATGATGTAGCAAATTCTTTTGGTACAGCTGTGGGCT
CAGGTGTAGTGACCCTGAAGCAAGCCTGCATCCTAGCTAGCATCTTTGAAACAGTGGGCTCTGTCTTACTGGGGG
CCAAAGTGAGCGAAACCATCCGGAAGGGCTTGATTGACGTGGAGATGTACAACTCGACTCAAGGGCTGCTGATGG
CCGGCTCAGTCAGTGCTATGTTTGGTTCTGCTGTGTGGCAACTCGTGGCTTCGTTTTTGAAGCTCCCTATTTCTG
GAACCCATTGTATTGTTGGTGCAACTATTGGTTTCTCCCTCGTGGCAAAGGGGCAGGAGGGTGTCAAGTGGTCTG
AACTGATAAAAATTGTGATGTCTTGGTTCGTGTCCCCACTGCTTTCTGGAATTATGTCTGGAATTTTATTCTTCC
TGGTTCGTGCATTCATCCTCCATAAGGCAGATCCAGTTCCTAATGGTTTGCGAGCTTTGCCAGTTTTCTATGCCT
GCACAGTTGGAATAAACCTCTTTTCCATCATGTATACTGGAGCACCGTTGCTGGGCTTTGACAAACTTCCTCTGT
GGGGTACCATCCTCATCTCGGTGGGATGTGCAGTTTTCTGTGCCCTTATCGTCTGGTTCTTTGTATGTCCCAGGA
TGAAGAGAAAAATTGAACGAGAAATAAAGTGTAGTCCTTCTGAAAGCCCCTTAATGGAAAAAAAGAATAGCTTGA
AAGAAGACCATGAAGAAACAAAGTTGTCTGTTGGTGATATTGAAAACAAGCATCCTGTTTCTGAGGTAGGGCCTG
CCACTGTGCCCCTCCAGGCTGTGGTGGAGGAGAGAACAGTCTCATTCAAACTTGGAGATTTGGAGGAAGCTCCAG
AGAGAGAGAGGCTTCCCAGCGTGGACTTGAAAGAGGAAACCAGCATAGATAGCACCGTGAATGGTGCAGTGCAGT
TGCCTAATGGGAACCTTGTCCAGTTCAGTCAAGCCGTCAGCAACCAAATAAACTCCAGTGGCCACTACCAGTATC
ACACCGTGCATAAGGATTCCGGCCTGTACAAAGAGCTACTCCATAAATTACATCTTGCCAAGGTGGGAGATTGCA
TGGGAGACTCCGGTGACAAACCCTTAAGGCGCAATAATAGCTATACTTCCTATACCATGGCAATATGTGGCATGC
CTCTGGATTCATTCCGTGCCAAAGAAGGTGAACAGAAGGGCGAAGAAATGGAGAAGCTGACATGGCCTAATGCAG
ACTCCAAGAAGCGAATTCGAATGGACAGTTACACCAGTTACTGCAATGCTGTGTCTGACCTTCACTCAGCATCTG
AGATAGACATGAGTGTCAAGGCAGAGATGGGTCTAGGTGACAGAAAAGGAAGTAATGGCTCTCTAGAAGAATGGT
ATGACCAGGATAAGCCTGAAGTCTCTCTCCTCTTCCAGTTCCTGCAGATCCTTACAGCCTGCTTTGGGTCATTCG
CCCATGGTGGCAATGACGTAAGCAATGCCATTGGGCCTCTGGTTGCTTTATATTTGGTTTATGACACAGGAGATG
TTTCTTCAAAAGTGGCAACACCAATATGGCTTCTACTCTATGGTGGTGTTGGTATCTGTGTTGGTCTGTGGGTTT
GGGGAAGAAGAGTTATCCAGACCATGGGGAAGGATCTGACACCGATCACACCCTCTAGTGGCTTCAGTATTGAAC
TGGCATCTGCCCTCACTGTGGTGATTGCATCAAATATTGGCCTTCCCATCAGTACAACACATTGTAAAGTGGGCT
CTGTTGTGTCTGTTGGCTGGCTCCGGTCCAAGAAGGCTGTTGACTGGCGTCTCTTTCGTAACATTTTTATGGCCT
GGTTTGTCACAGTCCCCATTTCTGGAGTTATCAGTGCTGCCATCATGGCAATCTTCAGATATGTCATCCTCAGAA
TG**TGA**AGCTGTTTGAGATTAAAATTTGTGTCAATGTTTGGGACCATCTTAGGTATTCCTGCTCCCCTGAAGAATG
ATTACAGTGTTAACAGAAGACTGACAAGAGTCTTTTTATTTGGGAGCCAGAGGAGGGAAGTGTTACTTGTGCTAT
AACTGCTTTTGTGCTAAATATGAATTGTCTCAAAATTAGCTGTGTAAAATAGCCCGGGTTCCACTGGCTCCTGCT
GAGGTCCCCTTTCCTTCTGGGCTGTGAATTCCTGTACATATTTCTCTACTTTTTGTATCAGGCTTCAATTCCATT
ATGTTTTAATGTTGTCTCTGAAGATGACTTGTGATTTTTTTTCTTTTTTTTAAACCATGAAGAGCCGTTTGACA
GAGCATGCTCTGCGTTGTTGGTTTCACCAGCTTCTGCCCTCACATGCACAGGGATTTAACAACAAAAATATAACT
ACAACTTCCCTTGTAGTCTCTTATATAAGTAGAGTCCTTGGTACTCTGCCCTCCTGTCAGTAGTGGCAGGATCTA
TTGGCATATTCGGGAGCTTCTTAGAGGGATGAGGTTCTTTGAACACAGTGAAAATTTAAATTAGTAACTTTTTTG
CAAGCAGTTTATTGACTGTTATTGCTAAGAAGAAGTAAGAAAGAAAAAGCCTGTTGGCAATCTTGGTTATTTCTT
TAAGATTTCTGGCAGTGTGGGATGGATGAATGAAGTGGAATGTGAACTTTGGGCAAGTTAAGTGGGACAGCCTTC
CATGTTCATTTGTCTACCTCTTAACTGAATAAAAAAGCCTACAGTTTTTAG

FIGURE 846

MATLITSTTAATAASGPLVDYLWMLILGFIIAFVLAFSVGANDVANSFGTAVGSGVVTLKQACILASIFETVGSV
LLGAKVSETIRKGLIDVEMYNSTQGLLMAGSVSAMFGSAVWQLVASFLKLPISGTHCIVGATIGFSLVAKGQEGV
KWSELIKIVMSWFVSPLLSGIMSGILFFLVRAFILHKADPVPNGLRALPVFYACTVGINLFSIMYTGAPLLGFDK
LPLWGTILISVGCAVFCALIVWFFVCPRMKRKIEREIKCSPSESPLMEKKNSLKEDHEETKLSVGDIENKHPVSE
VGPATVPLQAVVEERTVSFKLGDLEEAPERERLPSVDLKEETSIDSTVNGAVQLPNGNLVQFSQAVSNQINSSGH
YQYHTVHKDSGLYKELLHKLHLAKVGDCMGDSGDKPLRRNNSYTSYTMAICGMPLDSFRAKEGEQKGEEMEKLTW
PNADSKKRIRMDSYTSYCNAVSDLHSASEIDMSVKAEMGLGDRKGSNGSLEEWYDQDKPEVSLLFQFLQILTACF
GSFAHGGNDVSNAIGPLVALYLVYDTGDVSSKVATPIWLLLYGGVGICVGLWVWGRRVIQTMGKDLTPITPSSGF
SIELASALTVVIASNIGLPISTTHCKVGSVVSVGWLRSKKAVDWRLFRNIFMAWFVTVPISGVISAAIMAIFRYV
ILRM

FIGURE 847

ACCAACCTCTTCGAGGCACAAGGCACAACAGGCTGCTCTGGGATTCTCTTCAGCCAATCTTCATTGCTCAAGTGT
CTGAAGCAGCC**ATG**GCAGAAGTACCTGAGCTCGCCAGTGAAATGATGGCTTATTACAGTGGCAATGAGGATGACT
TGTTCTTTGAAGCTGATGGCCCTAAACAGATGAAGTGCTCCTTCCAGGACCTGGACCTCTGCCCTCTGGATGGCG
GCATCCAGCTACGAATCTCCGACCACCACTACAGCAAGGGCTTCAGGCAGGCCGCGTCAGTTGTTGTGGCCATGG
ACAAGCTGAGGAAGATGCTGGTTCCCTGCCCACAGACCTTCCAGGAGAATGACCTGAGCACCTTCTTTCCCTTCA
TCTTTGAAGAAGAACCTATCTTCTTCGACACATGGGATAACGAGGCTTATGTGCACGATGCACCTGTACGATCAC
TGAACTGCACGCTCCGGGACTCACAGCAAAAAAGCTTGGTGATGTCTGGTCCATATGAACTGAAAGCTCTCCACC
TCCAGGGACAGGATATGGAGCAACAAGTGGTGTTCTCCATGTCCTTTGTACAAGGAGAAGAAAGTAATGACAAAA
TACCTGTGGCCTTGGGCCTCAAGGAAAAGAATCTGTACCTGTCCTGCGTGTTGAAAGATGATAAGCCCACTCTAC
AGCTGGAGAGTGTAGATCCCAAAAATTACCCAAAGAAGAAGATGGAAAAGCGATTTGTCTTCAACAAGATAGAAA
TCAATAACAAGCTGGAATTTGAGTCTGCCCAGTTCCCCAACTGGTACATCAGCACCTCTCAAGCAGAAAACATGC
CCGTCTTCCTGGGAGGGACCAAAGGCGGCCAGGATATAACTGACTTCACCATGCAATTTGTGTCTTCC**TAA**AGAG
AGCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGGAACAGAAAGGTTTT
TGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCCCAACTGCCTGCCTTAGGGTAGTGCTAAGA
GGATCTCCTGTCCATCAGCCAGGACAGTCAGCTCTCTCCTTTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAG
GCCTCTCTCACCTCTCCTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCT
CTGTCATTCGCTCCCACATTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTTGTTTGTTTTATTCA
TTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTAGTTTTTAATAGCTATGGAAT
CAATTCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATT
ATTTAAATGGGAATATTTATAAATGAGCAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCTCTGAAG

FIGURE 848

MAEVPELASEMMAYYSGNEDDLFFEADGPKQMKCSFQDLDLCPLDGGIQLRISDHHYSKGFRQAASVVVAMDKLR
KMLVPCPQTFQENDLSTFFPFIFEEEPIFFDTWDNEAYVHDAPVRSLNCTLRDSQQKSLVMSGPYELKALHLQGQ
DMEQQVVFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINNK
LEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSS

FIGURE 849

AGGCACCATGACTCCTGTGAGGATGCAGCACTCCCTGGCAGGTCAGACCTATGCCGTGCCCCTCATCCAGCCAGA
CCTGCGGTGAGAGGAGGCCGTCCAGCAGATGGCAGATGCCCTGCAGTACCTGCAGAAGGTCTCTGGAGACATCTT
CAGCAGTGAGAGCGGCCTTGCTGCGGCCAAAGAACATGGAAAAGCATGAGTGGGGTGATGTGTGCCTTAAAGCAT
CAGACACTTGGGCCTCGGGCATCAGGAGCCAGCCACAGGGATGTCTGGGGAAATGGCGTTCCATGAGATGCAAGC
ACACAAGAATGCACTTGGCACATCTGGGGAACAGCAGGCAGCTGATATCACTGGGCCCACCCTGCACCAGGGAGG
ATGGAAGCAGGTAGAGCAGAGCCGGAGCCAGGTGCAGGCCATTGGAGAGAAGGTCTCCTTGGCCCAGGCCAAGAT
TGAGAAGATCAAGGGCAGCAAGAAGGCCATCAAGGTGTTCTCCAGTGCCAAGTACCCTGCTCCAGAGCGCCTGCA
GGAATATGGCTCCATCTTCACGGGCGCCCAGGACCCTGGCCTGCAGAGACGCCCCCGCCACAGGATCCAGAGCAA
GCACCGCCCCCTGGACGAGCGGGCCCTGCAGGAGAAGCTGAAGGACTTTCCTGTGTGCGTGAGCACCAAGCCGGA
GCCCGAGGACGATGCAGAAGAGGGACTTGGGGGTCTTCCCAGCAACATCAGCTCTGTCAGCTCCTTGCTGCTCTT
CAACACCACCTAGAACCT

FIGURE 850

AGCGCGGGGGAACCGGAGGCTGCAGGATGGTCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCA
ACGCAGTGCGCGACCGGGAGCTGGACCTCCGGGGGTATAAAATTCCCGTCATTGAAAATCTAGGTGCTACGTTAG
ACCAGTTTGATGCTATTGATTTTTCTGACAATGAGATCAGGAAACTGGATGGTTTTCCTTTGTTGAGAAGACTGA
AAACATTGTTAGGGAACAACAACAGAATATGCCGTATAGGTGAGGGACTTGATCAGGCTCTGCCCTGTCTGACAG
AACTCATTCTCACCAATAATAGGCTCGTGGAACTGGGTGATCTGGACCCTCTGGCATCTCTCAAATCGCTGACTT
ACCTAAGTATCCTAAGAAATCTGGTAACCAATAAGAAGCATTACAGATTGTATGTGATTTATAAAGTTCCGCAAG
TCAGAGTACTGGATTTCCAGAAAGTGAAACTAAAAGTTTTAATCCAGGTGCTGGTTTGCCAACTGACAAAAAGAA
AGGTGGGCCATCGCCAGGGGATGTAGAAACAATCAAGAATGCTATAGCAAATGCTTCAACTCTGGCTGAAGTGGA
GCGGCTGAAGGGGTTGCTGCAGTCTGGTCAGATCCCTGGCAGAGAACGCAAATCGGGGCC

FIGURE 851A

GATGGGCTGTGCAAAGGGCGCGGCTGCTGAGGACAGGGCTGTGGCTGGAGAACCTGCTGCTTCCTGAAGCCGAGC
CCCACCCTAAAGGACCGAGAGCACAGGCCATGGGAGAGGAATCGAGTAGGGATGCAGAGCCTGGTGGCACTGTCC
TGAGAGAGGAGGAGGCTGGGCAGGGCCCCGGCGCTGGAGAGGTGCCCTGCATATGGGACCTCTCAGAGGTGCACA
AGAGCTGTGTGCCCAGGTACCCCTGTCTCCTCTCCTCCTCCAGCCCCCAGCCTACTCTCCTAATGGTCTGTGTCT
TTCAGGGATGAGATTTACTGCCAGATCTGCAAGCAGCTCTCGGAGAACTTCAAAACAAGCAGCCTGGCCCGGGGC
TGGATCCTGCTCAGCCTCTGCCTCGGCTGCTTCCCACCCTCAGAGAGGTTCATGAAGTATCTACTGAACTTCATC
GGCCAAGGGCCGGCGACCTACGGCCCCTTCTGTGCCGAGCGCCTGAGACGCACCTATGCCAATGGGGTGCGTGCG
GAGCCCCCCACCTGGCTGGAGCTGCAGGCTGTCAAGTCCAAGAAGCACATCCCCATCCAAGTCATCTTGGCCACT
GGAGAGAGCCTAACCGTCCCCGTGGACTCAGCCTCCACATCTCGGGAAATGTGCATGCACATCGCTCACAAGCAG
GGCCTCAGCGACCACCTGGGCTTCTCCCTCCAGGTCGCCGTGTACGACAAGTTCTGGTCCCTGGGCAGCGGGCGC
GACCACATGATGGATGCCATCGCCCGGTGTGAGCAGATGGCCCAGGAGAGGGGCGAGAGCCAGCGCCAGTCACCC
TGGCGCATCTACTTCCGGAAGGAATTCTTCACCCCCTGGCACGACTCCCGGGAGGACCCTGTCAGCACCGAGCTT
ATTTACCGCCAAGTCCTCCGAGGAGTCTGGTCTGGCGAGTACAGCTTCGAGAAGGAGGAAGAGCTGGTTGAGCTG
CTGGCCCGGCACTGCTACGTGCAGCTCGGCGCCTCAGCAGAGAGCAAGGCTGTCCAGGAGCTGCTGCCCAGCTGC
ATCCCCCACAAGCTGTACAGGACCAAGCCCCCAGACAGGTGGGCGAGCCTCGTCACTGCCGCCTGCGCCAAGGCC
CCATACACTCAGAAGCAAGTCACACCACTGGCCGTGCGAGAGCAGGTGGTGGACGCCGCCCGCCTGCAGTGGCCG
CTGCTCTTCTCCCGGCTCTTCGAAGTCATCACACTCTCAGGCCCCCGCCTGCCCAAGACGCAGCTGATCTTGGCT
GTTAACTGGAAGGGGCTTTGCTTCCTGGACCAGCAGGAGAAGATGCTGCTGGAACTCTCTTTCCCAGAGGTCATG
GGTCTGGCCACCAACAGGGAGGCCCAGGGCGGGCAGAGGCTGCTGCTCTCCACGATGCATGAGGAGTACGAGTTT
GTGTCACCCAGCAGTGTGGCCATCGCTGAGCTGGTGGCCCTGTTCCTGGAGGGCCTGAAGGAGAGGTCCATTTTC
GCCATGGCCCTGCAGGACAGGAAGGCCACAGATGACACCACCCTCCTGGCCTTCAAGAAGGGGGACCTGTTGGTC
CTCACAAAGAAGCAGGGGCTGCTGGCCTCTGAGAACTGGACCCTCGGCCAGAACGACAGGACAGGCAAGACGGGG
CTGGTGCCCATGGCCTGCCTCTACACCATCCCCACGGTCACTAAGCCCTCGGCACAGCTGCTGAGCTTGCTTGCC
ATGTCACCAGAGAAGAGGAAGCTGGCGGCTCAGGAGGGGCAGTTCACAGAGCCACGTCCTGAGGAGCCACCCAAG
GAAAAGCTGCACACCCTGGAGGAGTTCTCCTATGAGTTCTTCAGGGCTCCAGAGAAGGACATGGTGAGCATGGCC
GTGCTGCCCCTGGCCCGTGCCCGTGGCCACCTGTGGGCCTATTCCTGCGAGCCGCTGCGACAGCCGCTGCTCAAG
CGAGTCCACGCCAACGTCGACCTCTGGGACATCGCCTGCCAGATCTTTGTCGCCATCCTCCGGTACATGGGCGAC
TACCCTTCTCGGCAGGCCTGGCCCACCCTGGAGCTCACCGACCAGATCTTCACACTGGCCCTGCAGCACCCGGCC
CTCCAGGACGAGGTCTACTGCCAGATCCTGAAGCAGCTGACGCACAACTCCAACAGGCACAGCGAAGAGCGGGGC
TGGCAGCTGCTGTGGCTGTGCACGGGCCTCTTCCCGCCCAGCAAGGGGCTGCTGCCCCATGCCCAGAAGTTTATA
GACACTCGGAGGGGGAAGCTGCTGGCCCCCGACTGCAGCCGCCGAATCCAGAAGGTCCTGAGGACGGGGCCCCGG
AAGCAGCCCCCGCACCAGGTGGAGGTGGAGGCCGCAGAGCAGAACGTCTCCCGCATCTGCCACAAGATCTACTTC
CCCAATGACACCAGTGAGATGCTGGAGGTGGTTGCCAACACACGGGTGCGGGATGTGTGTGACAGCATTGCCACC
AGGCTGCAGCTGGCCTCCTGGGAGGGCTGCAGCCTCTTCATCAAGATTTCAGACAAGGTGGGCCGGGCTGGGGCT
GGGCAGACGGTGGGCGGACGGGCAGTGAGCGAGGCCCTAGGTGCTGCCTGTGGGGGCCTCAGCCTACCAGGGGCA
CCCATGCTGGACCAGGCTGCACGGCCAGGGCTGCTGGGACAGAGGTAGGTGGGGTCCTGGAGCAGAGCCAGCTCC
ACACGCCAATAGCCCACGCACAGCCGACTCCAGCGCAGCACCCAGGCCGTAGGCGGCCACTGGACCAGAACCCAG
CAGGTTCTCAGGAGGACAGTCCCCGGAAGCCACCCAACTTCCCTGTACCTTCCCCTTCCCCAGGTCATCAGCCAG
AAGGAGGGAGACTTCTTCTTTGATTCCTTGAGGGAGGTGTCTGACTGGGTGAAGAAGAACAAGCCCCAGAAAGAA
GGGGCCCCCGTGACGCTCCCCTACCAGGTGTACTTCATGCGGAAATTGTGGCTCAACATATCTCCAGGGAAGGAT
GTGAATGCAGACACCATACTCCATTACCACCAGGAGCTGCCCAAGTACCTGCGCGGATTCCACAAGTGTTCGCGG
GAGGATGCCATCCACCTGGCGGGCCTCATCTACAAGGCCCAGTTCAACAACGACCGGTCCCAGCTGGCTAGTGTC
CCCAAGATCCTGAGGGAACTGGTGCCTGAGAACCTCACACGCCTGATGTCCTCGGAGGAGTGGAAAAAGAGCATC
CTTCTAGCCTATGACAAGCATAAGGACAAGACAGTGGAGGAGGCCAAGGTGGCCTTCCTGAAGTGGATCTGCCGG
TGGCCCACCTTCGGATCCGCCTTCTTCGAGGTGAAGCAAACCTCGGAGCCTTCCTACCCGGACGTCATCCTCATC
GCCATCAACCGACATGGGGTTCTGCTCATCCACCCCAAGACCAAGGACCTGCTCACCACCTATCCCTTCACCAAG
ATCTCCAGCTGGAGCAGCGGCAGCACCTACTTCCACATGGCGCTGGGGAGCCTGGGCCGTGGCAGCCGCCTGCTG
TGCGAGACCTCCCTGGGCTATAAGATGGATGACCTGCTGACCTCATATGTGCAGCAGCTCCTGAGTGCCATGAAC

FIGURE 851B

AAGCAGCGGGGCTCCAAGGCCCCAGCCCTGGCCAGCACCTAGCAGCGGATGCTGGCGTGTCTGCTCAGGCGCCCT
TCCCGACCTCTAGCCTGGCGGCACCTTCCCAGGCCCTCTCAACCCAGGGCCTGTCCTTGGCGGGCAGCCTTCCAT
GCTGCCCCCCATACAAAGCCCACTCAGCCCCGCAGGCGGCCCCCTCTGTCCTGGGCGCTGCCCAGGGAGGCCAAA
AGACGGGCCCAGAATGGGGTCGGGAGTCTCGGACCCCCAGGCTATTGGTGGATGACTGACTGACAGGACACCTCC
CAACCCCACCCCACCCCACCAGAATGTTCAATAAAAACTCCTGGAGCAGGA

FIGURE 852

MKYLLNFIGQGPATYGPFCAERLRRTYANGVRAEPPTWLELQAVKSKKHIPIQVILATGESLTVPVDSASTSREM
CMHIAHKQGLSDHLGFSLQVAVYDKFWSLGSGRDHMMDAIARCEQMAQERGESQRQSPWRIYFRKEFFTPWHDSR
EDPVSTELIYRQVLRGVWSGEYSFEKEEELVELLARHCYVQLGASAESKAVQELLPSCIPHKLYRTKPPDRWASL
VTAACAKAPYTQKQVTPLAVREQVVDAARLQWPLLFSRLFEVITLSGPRLPKTQLILAVNWKGLCFLDQQEKMLL
ELSFPEVMGLATNREAQGGQRLLLSTMHEEYEFVSPSSVAIAELVALFLEGLKERSIFAMALQDRKATDDTTLLA
FKKGDLLVLTKKQGLLASENWTLGQNDRTGKTGLVPMACLYTIPTVTKPSAQLLSLLAMSPEKRKLAAQEGQFTE
PRPEEPPKEKLHTLEEFSYEFFRAPEKDMVSMAVLPLARARGHLWAYSCEPLRQPLLKRVHANVDLWDIACQIFV
AILRYMGDYPSRQAWPTLELTDQIFTLALQHPALQDEVYCQILKQLTHNSNRHSEERGWQLLWLCTGLFPPSKGL
LPHAQKFIDTRRGKLLAPDCSRRIQKVLRTGPRKQPPHQVEVEAAEQNVSRICHKIYFPNDTSEMLEVVANTRVR
DVCDSIATRLQLASWEGCSLFIKISDKVGRAGAGQTVGGRAVSEALGAACGGLSLPGAPMLDQAARPGLLGQR

FIGURE 853

AAGTGCATGACTCAGGACTGGGTGGGAGGGGGCTGTCCCTGAGGCCCTGGTCTCCCCCAGCCAAGTCCTGGCAGG
GGGATGCTGTTCTTCAGGATCCCATGACCTGGGGCTCTTGGGGAGCCCCAGCCCGGAGAGTGACCTGTGGCTTTG
CTGGGGAAAGGGGCTTGGAGGGTACAGGGCAGTGTCCAGGATTGCAGTCTCAAATCCGAGGCCCACAGGGGAGCT
GCCTCTGTGATCGCCATTAAGGCTGTGGCCTGGGGTCTCAGGGCAGCCCAGGAACCAAAAATAGCCTGTAACTTG
TCACTTTGTAAGTCCTGCCCTCCAGACACACTTCCCTTTCTTCTCCCCAAGCCTCTCTTCCCAGTTAGCTCCCCT
GACTTGGAGTCACCTCTAAGCCTTGGCCCAGGCCCCTCTGCAGTGAGATGGAGGGACTCATCCCCCGGAGAGTGG
CATCTGCAGGCCCACTGGCTGCCTGTGGTCACCCCCTAGGGTTCTAGCGGGGCTGCCTCCCATTTTCCTCAGAGC
ATCCCTGCCAGCTGGCTGGTTCTCACTCTCCTGTTTCTAGGAAAAGAAAGTGGGGAGAGACAGGAACAGGGTCC
GGAGCAGCCCCAGCAGCAGCATTGAGGTGGAGCAATATGTCGGACGCCTTGGCCAACGCCGTGTGCCAGCGCTGC
CAGGCCCGCTTCTCCCCCGCCGAGCGCATTGTCAACAGCAATGGGGAGCTGTACCATGAGCACTGCTTCGTGTGT
GCCCAGTGCTTCCGGCCCTTCCCCGAGGGGCTCTTCTATGAGTTTGAAGGCCGGAAGTACTGCGAACACGACTTC
CAAATGCTGTTTGCTCCGTGCTGTGGATCCTGCGGTGAGTTCATCATTGGCCGCGTCATCAAGGCCATGAACAAC
AACTGGCACCCGGGCTGCTTCCGCTGCGAGCTGTGTGATGTGGAGCTGGCTGACCTGGGCTTTGTGAAGAATGCC
GGCAGGCATCTCTGCCGGCCTTGCCACAACCGTGAGAAGGCCAAGGGCCTGGGCAAGTACATCTGCCAGCGGTGC
CACCTGGTCATCGACGAGCAGCCCCTCATGTTCAGGAGCGACGCCTACCACCCTGACCACTTCAACTGCACCCAC
TGTGGGAAGGAGCTGACAGCCGAGGCCCGCGAGCTGAAGGGTGAGCTCTACTGCCTGCCCTGCCATGACAAGATG
GGCGTCCCCATCTGCGGGGCCTGCCGCCGGCCCATCGAGGGCCGAGTGGTCAACGCGCTGGGCAAGCAGTGGCAC
GTGGAGCACTTTGTCTGTGCCAAGTGTGAGAAGCCATTCCTGGGGCACCGGCACTATGAGAAGAAGGGCCTGGCC
TACTGCGAGACTCACTACAACCAGCTCTTCGGGGACGTCTGCTACAACTGCAGCCATGTGATTGAAGGCGATGTG
GTGTCGGCCCTCAACAAGGCCTGGTGTGTGAGCTGCTTCTCCTGCTCCACCTGCAACAGCAAGCTCACCCTGAAG
AACAAGTTTGTGGAGTTCGACATGAAGCCCGTGTGTAAGAGGTGCTACGAGAAGTTCCCGCTGGAGCTGAAGAAG
CGGCTGAAGAAGCTGTCGGAGCTGACCTCCCGCAAGCCCAGCCCAAGGCCACAGACCTCAACTCTGCCTGAAGGC
CCTCTTGCGCAGTGCCTCTCGGCCCCTCCGCCTTCTCCCCTCCTGCTGTCCATGCTTGGCCCCCTCGTCCCCATC
CACCTGTGCCCTCCGCATCTTACCCTCCCTTTCTCTTTCCTCATTGCCTTCTCCCTTCCTGTTCCCTCATCTCTG
CCTTCCCCATGTCTCTCCTCTCCTTGGCCGTGGCTTCTGTCTGTGAGGAGGCAGGAGCTGGGGAGTGGGAGCCTA
TGACCCCACGTCTGACAGCCATGTCCACCTGTGCCCACAGCTTCCGCCCACAGACCTCCAGGGACAGGAGCAAAT
TGCACCACAGCTCCCCGCCTGGCCTGGCCCTCCCCAGGCGGCTCAGTGGCTCATGCTGTCCTGTGAGAGCCCCTG
CCCCAGAGCGGCCCCACTAAGCGCATGTGGCTCCTGGGCTACCCACAGCCAGGGCAGCCTGCTGGAGCCACAGGG
CCAGGGCCATGCAGATGGAGGCCTCTGGGAGCCACCTCCAATCCCTCACCACTCACTCAACCAGTGGCACAGTGT
CCTTGTGCCCACACTGAGCCAGCAAGTCCTGCTGTCCACACCCACAAGCTACCTGGAGGGACAGGACCCACCTCC
ATCCTTCGGAAGGCCTTCCTGGAATCCCACCTTGGCCTCCGCCCTCGGTTCCGCCCCGCCCCTCTCCCCCCGACC
TTGGGGCTTGTGTCGAGCCCTTGGGTGGGGCCAGGAGGAGGTGATGGCGTCAGAGGAGGTGTGGTCAGAGGTGAC
TTGTTCCCACCTCCAGGGAGGACGCTTCGTCTTCGGCCAGCGCAGACCTGGTGTTTGTTTGTTGGGCTCACGCTT
GCACAATGAAGGCTTGTTCACAC

FIGURE 854

CCGACACCCACGGGCGGAGATCACCTGCTGCCCCGCAGACCCCTGTCCCTTCCTCCCGGACCAGCAGCTAGAGGA
TGTCCAAACGGAGTTGGTGGGCTGGATCCAGAAAGCCCCCAAGAGAGATGCTGAAACTCTCAGGCTCTGACTCCA
GCCAAAGCATGAATGGCCTTGAAGTGGCTCCCCCAGGTCTGATCACCAACTTCTCCCTGGCCACGGCAGAGCAAT
GTGGCCAGGAGACGCCACTGGAGAACATGCTGTTCGCCTCCTTCTACCTTCTGGATTTTATCCTGGCTTTAGTTG
GCAATACCCTGGCTCTGTGGCTTTTCATCCGAGACCACAAGTCCGGGACCCCGGCCAACGTGTTCCTGATGCATC
TGGCCGTGGCCGACTTGTCGTGCGTGCTGGTCCTGCCCACCCGCCTGGTCTACCACTTCTCTGGGAACCACTGGC
CATTTGGGGAAATCGCATGCCGTCTCACCGGCTTCCTCTTCTACCTCAACATGTACGCCAGCATCTACTTCCTCA
CCTGCATCAGCGCCGACCGTTTCCTGGCCATTGTGCACCCGGTCAAGTCCCTCAAGCTCCGCAGGCCCCTCTACG
CACACCTGGCCTGTGCCTTCCTGTGGGTGGTGGTGGCTGTGGCCATGGCCCCGCTGCTGGTGAGCCCACAGACCG
TGCAGACCAACCACACGGTGGTCTGCCTGCAGCTGTACCGGGAGAAGGCCTCCCACCATGCCCTGGTGTCCCTGG
CAGTGGCCTTCACCTTCCCGTTCATCACCACGGTCACCTGCTACCTGCTGATCATCCGCAGCCTGCGGCAGGGCC
TGCGTGTGGAGAAGCGCCTCAAGACCAAGGCAGTGCGCATGATCGCCATAGTGCTGGCCATCTTCCTGGTCTGCT
TCGTGCCCTACCACGTCAACCGCTCCGTCTACGTGCTGCACTACCGCAGCCATGGGGCCTCCTGCGCCACCCAGC
GCATCCTGGCCCTGGCAAACCGCATCACCTCCTGCCTCACCAGCCTCAACGGGGCACTCGACCCCATCATGTATT
TCTTCGTGGCTGAGAAGTTCCGCCACGCCCTGTGCAACTTGCTCTGTGGCAAAAGGCTCAAGGGCCCGCCCCCCA
GCTTCGAAGGGAAAACCAACGAGAGCTCGCTGAGTGCCAAGTCAGAGCTGTGAGCGGGGGGCGCCGTCCAGGCCG
AGCGCAGACTGTTTAGGACTCAGCAGACCCAGCAAGAGGCATCTGCCCTTTCCCCAGCCACCTCCCCAGCAAGCA
ACCTGAAATCTCAGCAGATGCCCACCATTTCTCTAGATCGCCTAGTCTCAACCCATAAAAAGGAAGAACTGACAA
AGGGGATCCATCGGCCACCCCTCTGCAGGGGCTTGTGATGGCTACAATGGCTCCTAGACACTCAACGACTTCATC
TGTGGCAGGGAGAGAGGAGGCCGGAAGAACAACCCCTGAACAATGGAGGCCTTTCTTTCCCGCTAGGCTCCCAGC
CTCCTTCCCGCTACAGAATCGCTCATCGGCGAGGCTCAGCAGAAAGACCCTGAAGGCAGGCTGCAAATGACCCAG
AAGAGGGACCTGGGAGTCCTGGTGGGGACGGGGAGGGAGTCTCAATACTCCTTTGCAGCGCAAGGTACTCTGAGT
CCCCTCTGTAGTGCCTCTGCCAGACACACACTGCCTGAGTTGAAGAGACACAGGCCACACATTTCAGGCTGGTTG
CCAGCGGACGTCAGCACTCACGGCCTGCGGGGACTCAGCACAGCTCTGGATTCTGGATCTCTCCTGCTGTAACCC
CACGCACAAGCCTGCAACCCCCAGAGCTCTTTGACAGGCTCCCAGGCCTCCCAGTCCTGGACAAGCATGTGCAGT
CACGGGAGCTCAGCTCAGGCCAGGGCTGGGCTGTGCACCTGCCTCCCACTGACCCAGACCCACTTCCTCCAGAGA
GGCCTCTCTCCGCCTGAGCTATTTCCCTTGCTAGTGTGCAGATATTTCCCTAACATGTCCTTTTTGTATTTGTT
TGTACGGACCATAAATATAACTGTAGCTTTAAGACTAAAAAAAAA

FIGURE 855

MSKRSWWAGSRKPPREMLKLSGSDSSQSMNGLEVAPPGLITNFSLATAEQCGQETPLENMLFASFYLLDFILALV
GNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFL
TCISADRFLAIVHPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSL
AVAFTFPFITTVTCYLLIIRSLRQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSVYVLHYRSHGASCATQ
RILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLKGPPPSFEGKTNESSLSAKSEL

FIGURE 856A

GGGGAAGATGGCGGCTGCTCCTTTGGAGGAGCGGGATTGAGAGGATCGGGGTGGGGAGACCAAACAAGAGAGACA
TTTCTGGCTCTGAAGGCGAACGCTTCGCTGGCCATTTAGGAGCTCTGCTCAAAGCCAGACGTATCCTAGAAGGAA
AACATCACCATGGCTACAGAAATTGGTTCTCCTCCTCGTTTTTCCATATGCCAAGGTTCCAGCACCAGGCACCT
CGACAGCTGTTTATAAGCGACCTGATTTTGCACAACAGCAAGCAATGCAACAGCTTACTTTTGATGGAAAACGA
ATGAGAAAAGCTGTGAACCGAAAAACCATAGACTACAATCCATCTGTAATTAAGTATTTGGAGAACAGAATATGG
CAAAGAGACCAGAGAGATATGCGGGCAATTCAGCCTGATGCAGGTTATTACAATGATCTGGTCCCACCTATAGGA
ATGTTGAATAATCCTATGAATGCAGTAACAACAAAATTTGTTCGGACATCAACAAATAAAGTAAAGTGTCCTGTA
TTTGTTGTTAGGTGGACTCCAGAAGGAAGACGCTTGGTCACTGGAGCTTCTAGTGGGGAGTTTACCCTGTGGAAT
GGACTCACTTTCAATTTTGAAACAATATTACAGGCTCACGACAGCCCAGTGAGGGCCATGACGTGGTCACATAAT
GACATGTGGATGTTGACAGCAGACCACGGAGGATATGTGAAATATTGGCAGTCGAACATGAACAACGTCAAGATG
TTCCAGGCACATAAGGAGGCGATTAGAGAGGCCAGTTTCTCACCCACGGATAATAAATTTGCTACATGCTCTGAT
GACGGCACTGTTAGAATCTGGGACTTTCTTCGTTGCCATGAGGAAAGAATTCTCCGAGGGCATGGTGCTGATGTG
AAATGTGTAGACTGGCATCCAACCAAAGGGTTAGTTGTTTCAGGAAGTAAAGATAGTCAACAGCCAATCAAGTTC
TGGGATCCCAAGACTGGGCAGAGTCTTGCAACACTTCATGCCCATAAAAACACAGTAATGGAAGTGAAATTAAAC
CTCAATGGCAATTGGCTACTCACAGCATCACGTGATCATCTCTGTAAACTTTTTGATATCAGAAACCTAAAAGAA
GAGCTTCAAGTCTTCCGAGGTCATAAGAAAGAAGCCACAGCTGTGGCCTGGCATCCTGTTCATGAAGGACTTTTT
GCCAGTGGAGGGTCTGATGGTTCTTTGTTATTCTGGCATGTTGGGGTAGAGAAGGAAGTGGGTGGGATGGAGATG
GCTCACGAAGGGATGATCTGGAGTCTGGCTTGGCATCCTCTTGGGCATATTCTCTGCTCAGGCTCAAATGACCAT
ACTAGCAAATTCTGGACTCGAAACCGACCAGGTGATAAAATGCGAGATCGATATAATCTAAACCTTTTACCTGGA
ATGTCTGAAGATGGAGTAGAATATGATGACCTCGAACCTAATAGCCTGGCAGTAATTCCAGGAATGGGAATACCA
GAACAACTAAAATTAGCTATGGAACAAGAACAGATGGGGAAAGATGAATCAAATGAAATTGAAATGACAATTCCA
GGTTTAGATTGGGGAATGGAGGAAGTGATGCAAAAGGATCAGAAAAAAGTACCTCAGAAGAAAGTTCCTTATGCA
AAACCCATTCCTGCTCAGTTCCAGCAGGCTTGGATGCAAAATAAAGTTCCAATTCCTGCTCCAAATGAGGTGCTG
AATGACAGAAAAGAAGACATTAAATTGGAAGAGAAGAAAAAAACACAAGCAGAAATTGAGCAAGAAATGGCTACA
TTACAATATACTAACCCACAACTTCTGGAGCAACTTAAAATTGAAAGACTTGCACAGAAACAAGTTGAGCAAATT
CAGCCTCCTCCCTCATCTGGCACCCCTCTCCTCGGACCCCAGCCTTTTCCAGGACAAGGTCCAATGTCTCAGATT
CCTCAAGGTTTTCAACAGCCCCATCCATCTCAGCAGATGCCAATGAACATGGCTCAAATGGGGCCTCCAGGTCCA
CAGGGACAGTTTAGGCCTCCTGGACCCCAGGGACAAATGGGACCACAAGGTCCTCCACTGCATCAGGGAGGTGGG
GGGCCACAAGGATTCATGGGACCACAGGGGCCCCAGGGCCCGCCCCAGGGGTTGCCACGGCCTCAGGACATGCAT
GGGCCCCAAGGAATGCAGAGGCATCCTGGACCTCATGGCCCTTTGGGACCTCAAGGGCCACCTGGACCACAAGGT
AGTTCTGGTCCTCAAGGTCATATGGGTCCTCAGGGTCCACCTGGCCCACAGGGTCACATAGGCCCCCAAGGCCCG
CCTGGCCCTCAGGGTCACTTGGGCCCACAGGGGCCTCCGGGTACTCAAGGTATGCAGGGACCACCTGGTCCCAGA
GGAATGCAAGGGCCTCCTCATCCTCATGGGATCCAAGGCGGACCAGGGTCTCAAGGGATCCAAGGTCCTGTGTCT
CAGGGACCTCTGATGGGATTGAATCCAAGAGGAATGCAGGGGCCTCCAGGCCCCCGGGAGAACCAGGGTCCTGCT
CCCCAAGGGATGATTATGGGCCACCCGCCTCAAGAGATGAGAGGACCTCACCCTCCAGGTGGACTACTGGGACAC
GGCCCTCAGGAAATGAGAGGTCCTCAGGAGATCCGAGGCATGCAGGGGCCTCCACCCCAAGGATCAATGCTGGGA
CCTCCCCAGGAATTGCGAGGGCCTCCAGGCTCACAAAGTCAGCAGGGGCCGCCCCAGGGCTCTTTAGGACCTCCA
CCCCAGGGTGGCATGCAAGGACCCCCCGGACCTCAGGGACAGCAGAACCCAGCAAGAGGGCCACATCCATCTCAA
GGGCCAATACCATTCCAGCAACAGAAAACGCCTCTGCTAGGTGATGGGCCCCGGGCCCCCTTCAACCAGGAAGGA
CAGAGCACAGGCCCCCCACCCCTGATACCAGGCCTAGGGCAGCAGGGAGCACAAGGTCGCATTCCCCCTCTGAAC
CCCGGACAAGGACCTGGCCCCAACAAAGTTTCAGAAGAGGAGCCCCGCCGAGGCATGAGGGCCGTGCTCCCCCCA
GAGGAAGGGATGGTTTTCCTGGTCCTGAAGACTTTGGTCCAGAGGAGAATTTTGATGCTTCTGAGGAAGCGGCCC
GAGGACGAGATCTCAGAGGTCGAGGTCGGGGTACCCCACGAGGAGGAAGGAAGGGTTTACTTCCCACTCCTGACG
AGTTCCCTCGCTTTGAAGGAGGGCGGAAGCCAGATTCCTGGGATGGAAACAGAGAGCCTGGGCCAGGTCATGAAC
ATTTTCGTGATACTCCCCGCCCTGATCATCCCCCTCACGACGGTCATTCCCCAGCCAGCAGAGAACGCTCCTCTT
CTCTCCAAGGCATGGACATGGCATCCCTACCTCCCCGAAAGCGCCCCTGGCATGATGGCCCAGGCACTTCTGAGC
ACAGAGAGATGGAGGCCCCAGGAGGCCCTTCTGAAGACCGAGGAGGCAAAGGCCGAGGGGGCCCAGGACCTGCTC
AGAGAGTGCCCAAATCTGGGCGTTCCAGCTCCTTAGACGGAGAGCACCACGATGGATACCACAGAGATGAACCTT

FIGURE 856B

TTGGGGGCCCTCCAGGCAGTGGCACCCCTTCTCGAGGGGGCCGGAGTGGCAGTAACTGGGGTAGAGGGAGTAACA
TGAACTCTGGCCCGCCGAGGCGAGGAGCTTCACGGGGTGGTGGAAGGGGTCGGTAGAAGCTGGAACTGAGTACCC
TGAGGCCTCTCTGGACAGTATGTAAGAACTTCTTGTGGACTCACCAAGAGAAACAAAAGGAAGCCTGCACCATTG
TAGCCCTGAACTCTTTTCTGGGCACCTGAATCCCAGGAACCCTCAATGAGGTCTTCAAGATGAAGAGACTGCTGC
CAGCTACCAGCCTGGCTGGCCCTGTCCTGTCCACCCTCATTGCCCCAACTCCCATGTTGTTTTGTGAAGATAAAA
GCTGGGATCTTTTTCTTTTTTTTAAGTCTCACAAGACATGGGGCATCTCCACAAATTTAAGTTCCTGTCCATTTG
GAAATTTGTTTCTATGTGTACAGTTTGTCAGAGAAAAACAAAGTTTTTGTATGAATACAGAATGTGATTTACGCA
AGAATTGACAGAAAACTAGTTGTGAAGTGCTTGCCTTAAGGAAACCTTTGGTTTCCATCGCATCCCATCTGCCAA
GGAATGCACGGTTGTTGCTGATGTTCATGAGCATATTAACCACTAGGTTATCTAAATTAATCTCAGCTGTGAACT
TTGTGTTTTTCAACACATTCTGTCACACCATTTTTGTGACAGAAAAATACTTGAAAATTATTCTAATGTAGTTTG
TAGTAGGTTCAAATTTTTATTCAGACATGCTCTGACAGATGGAAAATTGTACTCTGAAGAGAAAATGCAATCTTC
TGGATGTCCAACGAGGGAGCTTCCCCTTGGAAGCATCTCCTAAGAATCACAGTTTAGGTTTGAATCGCCTTGTTA
TGATGAGGAGAGGAACTTGATGTTAGTCAGAAATAAAGTCACATGCCCTTTAGATAACTTGAAATCACACATGGA
GTTGATAAGGAATGGACCAAAATAGGTCCTCAAACAATTTTGCAACACTTAATTAAGTTTTCCTCTCTTCCTCTT
CCATACTATGTGGAAATACCAGTGTTACGGCAGGGCGTACTTCTAACTCACAGTAAGCCAGATAGATCTTGTCCA
TGGCAAATTCCTTGTTTAAAATAAACATACCATTTAGCCCAGTTTGGATTGGAAGCCAAAAATTCAGTTTGTTAT
ATACCCCATGATACTTTCTATACTGACCTTTATTTTGGTTTTACATGGAAGCTTTTATTAAAAGGACTGTCCTAT
GGCCACCTTAACATTTCATTACATTGGCAGCTTCAGTTTTGGCATCAGTCAAATTTATTTGGCAAATTTAGTGGT
GCTGGAAGTTTCTTTTTTTCTTTTCCTTTTTTGACAGAGTCTTGCTCTGTCACCCAGCCAGGAGTGCAGTGGTGC
AATCACGGCTCACTTCAGCTTTGACCCTGCCTCAGCCTCCCTAGTAGCTAGGACTACAGGCATATGCCACCATGC
CCAGCTAATTTTTTGTGTGTGTGTTTTTTGTAGAGATGGAGTTTCACCACTTTGTCTATGCTGGTTTCAAACTCC
TGGGCTCAAGCGGTCCACCTGCTGTGGCCTCCCAAAGTGCTGGGATTGCAGATCTGAGCCACAGTACCTGGCCGC
TGGTGCTGGAAGTTTCAATGGTTGCTTAGAAAAGGCATACTGATATAGTTTAACAGGATATGAAAATTTAACTGG
TTCTCTATGAATGTAAAAAACAGCAAAAGCTAATTGATTTCTGTGGAGTGAGAAAATGTCAGCCATATACACTGC
TTTTCAGTGTTAGAATCTAGAGACTATTTTTTTTTTAACTTTGAAATTACAGCTTATTTAATCAGCGCTCCACCA
TAAACATGCTATTAGGAGGCTCAAGATTGCTTTAGGTTATGGGTATTTCTTCACTCACCCCCAACTGGTATAGCT
TAAAGAGAGAGAAACTGTAATCAAATTTCATGAAGCTAAAACCGGATCCAGAGACCAAACCCATATCAAGATTAG
ACTTTTTTTCCCTGAGATTCTAGTGGAAAAATTTTCATTATTTGGGCTTTAACTTTAGAAACATAGTATCTCAG
TAAGCAGATAACCAGATCACATTTAAAAATTTTCATTTTACCTTGAAGCTCTACTGGACTTGACAGATCACATTT
TGAGAGTGAATTCATTTAAACAATAAACCTCTACATTATACTTAT

FIGURE 857

AGAACATCCAGTCACGGATAAAAATGAGCTGGTTCAGAAGGCCAAACTGGCCGAGCAGGCTGAGCAATATGATGA
CATGGCAGCCTGCATGAAGTCTGTAACTAAGCAAGGAGCTGAATTATCCAATGAGGAGAGGAATCTTCTCTCAGT
TGCTTATAAAAATGTTGTAGGAGCCCGTAAGTCATCTTGGAGGGTCGTCTCAAGTATTGAACAAAAAACGGAAGG
TGCTGAGAAAAAACAGCAGATGGCTCGAGAACACAGAGAGAAAATTGAGACGGAGCTAAGAGATATCTGTAATGA
TGTATTGTCTCTTTTGGAAAAGTTCTTGATCCCCAATGCTTCACAAGCAGAGAGCAAAGTCTTCTATTTGAAAAT
GAAAGGAGATTACTACCGTTACTTGACTGAGGTTACTGCTGGTGATGACAAGATAGGGATTGTGGATCAGTCACA
ACAAGCATACCAAGAAGCTTTTGAAATCAGCAAAAAAGAAATGCAACCAACACATCCTGTCAGATTGGGTCTGGC
CCTTAACTTCTGTGTTCTATTATGAGATTCTGAACTCCCCAGAGAAAGCCTGCTGTCTTGCAAAGACCGCTTTTG
ATGAAGCCATTGCTGAACTTGATACATTAAGTGAAGAGTCATACAAAGACAGCATGCTAATAATGCAATTACTGA
GAGACAACTTGACATTGTGGACATCGGATACCCAAGGAGACGAAGCTGAAGCAGGAGAAGGAGGGGAAAATTAAC
CGGCCTTCCAACTTTTGTCTGCCTCATTCTAAAATTTACACAGTAGACCATTTGTCATCCATGCTGTCCCACAAA
TAGTTTTTTGTTTATGATTTATGACAGGTTTATGTTACTTCTATTTGGATTTCTATATTTCCCATGTGGTTTTTA
TGTTTAATATTAAGGGAGTAGAGCCAGTCAACATTTAGGGAGGTATCTGTTTTCATCTTGAGGTGGCCAATATTG
GGATGTGGAATTTTTATACAAGTTATAAATGTTTGGCATAGTACTTTTGGTACATTGTGGCTTCACAAGGGCCAG
TGTAAAACTGCTTCCATGTCTAAGCAAAGAAAACTGCCTACATATTGGTTTGTCCTGGTGGAGAATAAAAGGGAT
CATTGATTCCAGTCAGAGGTGTAGTAATTGTGGGTACTTTTAAGGTTTGGAGCACTTTACAAGGCTGTGGTAGAA
ACATACCCCATGGATACCACATGTTAAACCATGTATATCTGTGGAATACTCAGTCTCATTGTGCACACCTTTGAC
TACAGCTGCAGAAGTTTTCCTTTAGATAAAGTTGTGACCCATTTTACTCTGGATAAGGGCAGAAACAGTTCACAT
TCCATTATTTGTAAAGTTACCTGCTGTTAGCTTTCATTATTTTTGCTACACTCATTTTATTTGTATTTAAATGTT
TTAGGCAACCTAAGAACAAATGTAAAAGTAAAGATGCAGTAAAAATGAATTGCTTGGTATTCATTGCTTCATGTA
TATCAAGCACAGCAGTAAAACAAAAACCCATGTATTTAACTTTTTTTAGGTTTTTTGCTTTTGTGATTTTTTTT
TGATACTTGCCTAACATGCATGTGCTGTAAAAATAGTTAACAAGGAAATAACTTGAGATGATGGCTAGCTTTGTT
TAATGTCTTATGAAATGTTCGTGGATAATCCAAGCATAATTGTTAAGAACACGTGTATTAAATTCATGTAAGTGG
AATAAAAGTTTTATGAATGGACTTTTCAACTACTTTCTCTACAGCTTTTCGTGTAAATTAGTCTTTTGGTTCTGA
AATTTCTCTAAAGGAAATTGTACATTTTTGAAATTTATTCCTTATTCCCTCTTGGCAGCTAATGGGCTTTTAGTA
AGTTTAAACAAAAAATTTATCATAACAACAAAAAATACTACTAATATAACTACTGTTTCCATGTCCCATGATCCC
GTCTCTTCCTCCCCACCCTGAAAAAAATGAGTTCCTATTTTTTCTGGGAGAGGGGAGATTAATTGGAAAAAAATG
TTAATATGTTCCATTTAAAATTTTGGTATATGGCATTTTCTAACTTAAGAAGCCACAATGTTCTTGGCCCATCAT
GACAATGGGTAGCATTAACTATAAGTTTTGTGCTTCCAAATCACTTTTCGGTTTTTAAGAATTTCTTGATACTCC
TACAGCCTGCCTTCGATTTTGATCCTTTATTCTGTTTGTCAGGTGCACAAGATTACCTTCCTTTTTTAGCCATCT
GTCTTGTCACCAACCATTCCTACTTGGTGGCCATGTACTTGGAAAAAGGCCGCATGATCTTTCTGGCTCCACTCA
ATGTCTAAGGCACCCTGCTTCCTTTGCTTGCATCCCACAGACTATTTCCCTCATCCTATTTACTGCAGCAATTGT
CTCCTTAGTTGACGAGATTGTGTTTATCTCCCTTTAAAACCCTACCTATCCTGAATGATCTGTCATTGTCTGCCT
TTAAAATCCTTCCTCTTTCTTCCTTCTCTATTCTCTAAATAATGATGGGGCTAAATTATACCCAAAGCTCACTTT
ACAAAATATTTCCTCAGTACTTTGCAGAAAACACCAAACAAAAATGCCATTTTAAAAGAGGTGTATTTTTTCTTT
TAGAATGTTAGAATGTAAGCTCCTCAAAAGCAGGGACAATGTTTTCCGTATGTTCTACTGTGCCTAGTATACTGT
AAATGCTCAATAAATACTGATGATGGGAGGCAGTGAGTCTTGATGATAAGGGTGAGAAACCGAAATCCC

FIGURE 858

GATGACATGGCAGCCTGCATGAAGTCTGTAACTAAGCAAGGAGCTGAATTATCCAATGAGGAGAGGAATCTTCTC
TCAGTTGCTTATAAAAATGTTGTAGGAGCCCGTAAGTCATCTTGGAGGGTCGTCTCAAGTATTGAACAAAAAACG
GAAGGTGCTGAGAAAAAACAGCAGATGGCTCGAGAACACAGAGAGAAAATTGAGACGGAGCTAAGAGATATCTGT
AATGATGTATTGTCTCTTTTGGAAAAGTTCTTGATCCCCAATGCTTCACAAGCAGAGAGCAAAGTCTTCTATTTG
AAAATGAAAGGAGATTACTACCGTTACTTGACTGAGGTTACTGCTGGTGATGACAAGATAGGGATTGTGGATCAG
TCACAACAAGCATACCAAGAAGCTTTTGAAATCAGCAAAAAAGAAATGCAACCAACACATCCTGTCAGATTGGGT
CTGGCCCTTAACTTCTGTGTTCTATTATGAGATTCTGAACTCCCCAGAGAAAGCCTGCTGTCTTGCAAAGACCGC
TTTTGATGAAGCCATTGCTGAACTTGATACATTAAGTGAAGAGTCATACAAAGACAGCATGCTAATAATGCAATT
ACTGAGAGACAACTTGACAATGTGGTTTTTATGTTTAATATTAAGGGAGTAGAGCCAGTCAACATTTAGGGAGGT
ATCTGTTTTCATCTTGAGGTGGCCAATATTGGGATGTGGAATTTTTATACAAGTTATAAATGTTTGGCATAGTAC
TTTTG

FIGURE 859A

TTTTCGGCGCCGTGGCGGAATGGCGGCTTCCATCTCTGAGGCGAGCGACGCTATGGATCCCACAGTGGTTTGCTA
AGAAGGCCATTTTCAACTCTCCACTGGAGGCTGCTATGGCGTTCCCTCACCTGCAGCAGCCCAGCTTTCTACTGG
CTAGCCTGAAAGCTGACTCTATAAATAAGCCCTTTGCACAGCAGTGCCAAGACTTGGTTAAAGTCATTGAGGACT
TTCCAGCAAAGGAGCTGCACACCATCTTCCCATGGCTGGTAGAAAGCATTTTTGGCAGCCTAGATGGTGTCCTCG
TTGGCTGGAACCTCCGCTGCTTACAGGGGCGCGTGAATCCTGTGGAGTACAGCATCGTGATGGAATTTCTCGACC
CTGGTGGCCCAATGATGAAGTTGGTTTATAAGCTTCAAGCTGAAGACTATAAGTTCGACTTTCCTGTCTCCTACT
TGCCTGGTCCTGTGAAGGCGTCCATCCAGGAGTGCATCCTCCCTGACAGTCCTCTGTACCACAACAAGGTCCAGT
TCACCCCTACTGGGGGCCTTGGTCTGAACTTGGCCCTGAATCCGTTCGAGTATTACATATTCTTCTTTGCCTTGA
GCCTCATCACTCAGAAGCCACTTCCTGTGTCCCTCCACGTCCGTACTTCAGACTGTGCCTATTTCATCCTGGTGG
ACAGGTACCTGTCATGGTTCCTGCCCACCGAAGGCAGTGTGCCCCCACCACTCTCCTCCAGCCCAGGGGGGACCA
GCCCCTCACCACCTCCCAGGACACCAGCCATACCCTTTGCTTCCTATGGCCTCCACCACACTAGCCTCCTAAAGC
GACACATCTCTCATCAGACGTCTGTGAATGCAGACCCCGCCTCCCACGAGATCTGGAGGTCAGAAACTCTGCTCC
AGGTTTTTGTTGAAATGTGGCTTCATCACTATTCCTTGGAGATGTATCAAAAAATGCAGTCCCCTCATGCCAAGG
AGTCGTTCACGCCTACTGAGGAGCATGTGTTGGTGGTGCGCCTGCTGCTGAAGCACCTGCACGCCTTTGCCAACA
GCCTGAAGCCAGAGCAGGCCTCACCCTCCGCCCACTCCCACGCCACCAGCCCCCTGGAGGAGTTCAAACGGGCTG
CTGTCCCGAGGTTCGTCCAGCAGAAACTCTACCTCTTCTTGCAGCATTGCTTTGGCCACTGGCCCCTGGACGCAT
CGTTCAGAGCTGTCCTGGAGATGTGGCTGAGCTACCTGCAGCCGTGGCGGTACGCGCCTGACAAGCAGGCTCCGG
GCAGCGACTCCCAGCCCCGGTGTGTGTCGGAGAAATGGGCACCCTTTGTCCAGGAGAACCTGCTGATGTACACCA
AGTTGTTTGTGGGCTTTCTGAACCGCGCGCTCCGCACAGACCTGGTCAGCCCCAAGCACGCGCTCATGGTGTTCC
GAGTGGCCAAAGTCTTTGCCCAGCCCAACCTGGCTGAGATGATTCAGAAAGGTGAGCAGCTATTCCTGGAGCCAG
AGCTGGTCATCCCCCACCGCCAGCACCGACTCTTCACGGCCCCCACATTCACTGGGAGCTTCCTGTCACCCTGGC
CACCAGCGGTCACTGATGCCTCCTTCAAGGTGAAGAGCCACGTCTACAGCCTGGAGGGCCAGGACTGCAAGTACA
CCCCGATGTTTGGGCCCGAGGCCCGCACCCTGGTCCTGCGCCTCGCTCAGCTCATCACACAGGCCAAACACACAG
CCAAGTCCATCTCCGACCAGTGTGCGGAGAGCCCGGCTGGCCACTCCTTCCTCTCATGGCTGGGCTTTAGCTCCA
TGGACACCAATGGCTCCTACACAGCCAACGACCTGGACGAGATGGGGCAAGACAGTGTCCGGAAGACAGATGAAT
ACCTGGAGAAGGCCCTGGAGTACCTGCGCCAGATATTCCGGCTCAGCGAAGCGCAGCTCAGGCAGTTCACACTCG
CCTTGGGCACCACCCAGGATGAGAATGGAAAAAAGCAACTCCCCGACTGCATCGTGGGTGAGGACGGACTCATCC
TTACGCCCCTGGGGCGGTACCAGATCATCAATGGGCTGCGAAGGTTTGAAATTGAGTACCAGGGGGACCCGGAGC
TGCAGCCCATCCGGAGCTATGAGATCGCCAGCTTGGTCCGCACACTCTTTAGGCTGTCGTCTGCCATCAACCACA
GATTTGCAGGACAGATGGCGGCTCTGTGTTCCCGGGATGACTTCCTCGGCAGCTTCTGTCGCTACCACCTCACAG
AACCTGGGCTGGCCAGCAGGCACCTGCTGAGCCCTGTGGGGCGGAGGCAGGTGGCCGGCCACACCCGCGGCCCCA
GGCTCAGCCTGCGCTTCCTGGGCAGTTACCGGACGCTGGTCTCGCTGCTGCTGGCCTTCTTCGTGGCCTCTCTGT
TCTGCGTCGGGCCCCTCCCATGCACGCTGCTGCTCACCCTGGGCTATGTCCTCTACGCCTCTGCCATGACACTGC
TGACCGAGCGGGGGAAGCTGCACCAGCCCTGAAGGTGTCAGCTGCCTTCAGAGCAGGCTGGAGGGATTTGCCACA
CAGCCCCACCCTTGGGCTGAGAGGACCTGGGAAGCCCCTCCAGGAGGGAACACGGTCATCCTCGGGCTTCTGGAG
CGGGGTTCCTGCAGCCGCAGAGGCATCTGGAGGAAACGCAACCAAGAAAGGAAGGCAGGTGGGCCCCAGCAAAGG
AGTAGCTGCCAGGGCTCAACAGCTACGCTCTGTGACAGCGCAGAGCTCAGCGGCGGCCTTTCCCTCCCTCCGCCA
AGGACTCACGGCCAAGCCAGCTCTCGGGGCCTTTTTTCCACTGCCCATTTGGCTACTCTGCTGCACCAAGCTTGG
GAGCCAGCCTGCCAACAGCCACCTGGGCCTGGCCTCCCCACTGGCTGGCCTTGAGGTTGGCAGAGTGGGTTGTGG
CGCTTCCTCTCTCTGTGTGGGACCAGGACAGTGGCTTAAGTCTCCACTCCAGGAAAGAATCAAAGTTTCTAGAGT
TGTGAGAAAACCAGAGAGTGGCTGTCCTGATTCTTCACTGTGAGGGGCGTTCTTCATGTTCTCCCAGCTGTTCCA
AGACTGGGCCGTAGAATTCCATGTTTCAGGAGCCTAAGACCCTCCCAGAGCCCAGGGGCTTCACCGCAGACCCCA
AGCCATTGAGCACATCACCCAAAGCAGTGGCCAACATCGCGGACCCCTGTGCCTTGTCACAGATGGGTGCTGGTC
CTCAGGCGTTGGGGACACTGCTGGGTCGATGGGGTCGGATTCTGCCAGTTTCTGCTCTGCAGCCAAAGATGGTCA
GAAGCATTGTCACTTCAGTAACATCAAGTGCTCAAAGACATGGCAACCGTTCAGTGGTACTTAAGTATTCAAAAT
ATACAACTACAGATTCTCTGACAGAAACCAGCACGGGGTCTTCACCTTCATTCACCCCACAGGCGACATGCGAGG
GAGAACAGCATCTCAGTGGTGATTTCCAAACCAAGCCTTTGTTTTCGGTGTGGGGTTTTGGGGGTTTGCTTTAAT
GTTTTTGAAATTGTAAATGTTGGGCTTTGTATTTTGATGTAAACTGAGCATAATGGCATTTTAGGGCCTGTGACC

FIGURE 859B

AAAATGAAGCTTGTAACGACCCATGGATCTGAATAAACATGTCCTTGCTTCTGAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAA

FIGURE 860

MAFPHLQQPSFLLASLKADSINKPFAQQCQDLVKVIEDFPAKELHTIFPWLVESIFGSLDGVLVGWNLRCLQGRV
NPVEYSIVMEFLDPGGPMMKLVYKLQAEDYKFDFPVSYLPGPVKASIQECILPDSPLYHNKVQFTPTGGLGLNLA
LNPFEYYIFFFALSLITQKPLPVSLHVRTSDCAYFILVDRYLSWFLPTEGSVPPPLSSSPGGTSPSPPPRTPAIP
FASYGLHHTSLLKRHISHQTSVNADPASHEIWRSETLLQVFVEMWLHHYSLEMYQKMQSPHAKESFTPTEEHVLV
VRLLLKHLHAFANSLKPEQASPSAHSHATSPLEEFKRAAVPRFVQQKLYLFLQHCFGHWPLDASFRAVLEMWLSY
LQPWRYAPDKQAPGSDSQPRCVSEKWAPFVQENLLMYTKLFVGFLNRALRTDLVSPKHALMVFRVAKVFAQPNLA
EMIQKGEQLFLEPELVIPHRQHRLFTAPTFTGSFLSPWPPAVTDASFKVKSHVYSLEGQDCKYTPMFGPEARTLV
LRLAQLITQAKHTAKSISDQCAESPAGHSFLSWLGFSSMDTNGSYTANDLDEMGQDSVRKTDEYLEKALEYLRQI
FRLSEAQLRQFTLALGTTQDENGKKQLPDCIVGEDGLILTPLGRYQIINGLRRFEIEYQGDPELQPIRSYEIASL
VRTLFRLSSAINHRFAGQMAALCSRDDFLGSFCRYHLTEPGLASRHLLSPVGRRQVAGHTRGPRLSLRFLGSYRT
LVSLLLAFFVASLFCVGPLPCTLLLTLGYVLYASAMTLLTERGKLHQP

FIGURE 861

GGCGCCGAGTAGCCGGGCCGGGCCGGAGCGCGGGCGGCGGCGGAGGCAGCTGCGCCCGCGCCTCCTGCCCTCCCA
GGCCCCGCGCCCCGCGCCCGGGCCCCGGCGATGGTGACACATGCGGCGGCGGCGCCGGCGGCAGGACCATGGT
TGAGCGCGCCAGCAAGTTCGTGCTGGTGGTGGCGGGCTCGGTGTGCTTCATGCTCATCTTGTACCAGTACGCGGG
CCCAGGACTGAGCCTGGGCGCGCCCGGCGGCCGCGCGCCGCCCGACGACCTGGACCTGTTCCCCACGCCCGACCC
CCACTACGAGAAGAAGTACTACTTCCCGGTCCGCGAGCTGGAGCGCTCGCTGCGCTTCGACATGAAGGGCGACGA
CGTGATCGTCTTCCTGCACATCCAGAAGACGGGCGGCACCACCTTCGGCCGCCACCTCGTGCAGAACGTACGCCT
CGAGGTGCCGTGCGACTGCCGGCCCGGCCAGAAGAAGTGCACCTGCTACCGGCCCAACCGCCGCGAGACTTGGCT
CTTCTCCCGCTTCTCCACCGGCTGGAGCTGCGGGCTGCACGCCGACTGGACCGAGCTCACCAACTGCGTGCCCGG
CGTGCTGGACCGCCGCGACTCCGCCGCGCTGCGCACGCCCAGGAAGTTCTACTACATCACCCTGCTACGAGACCC
CGTGTCCCGCTACCTGAGCGAGTGGCGGCATGTGCAGAGGGGTGCCACGTGGAAGACGTCGTTGCATATGTGTGA
TGGGCGCACGCCCACGCCTGAGGAGCTGCCGCCCTGCTACGAGGGCACGGACTGGTCGGGCTGCACGCTACAGGA
GTTCATGGACTGCCCGTACAACCTGGCCAACAACCGCCAGGTGCGCATGCTGGCCGACCTGAGCCTGGTGGGCTG
CTACAACCTGTCCTTCATCCCCGAGGGCAAGCGGGCCCAGCTGCTGCTCGAGAGCGCCAAGAAGAACCTGCGGGG
CATGGCCTTCTTCGGCCTGACCGAGTTCCAGCGCAAGACGCAGTACCTGTTCGAGCGGACGTTCAACCTCAAGTT
CATCCGGCCCTTCATGCAGTACAATAGCACGCGGGCGGGCGGCGTGGAGGTGGATGAAGACACCATCCGGCGCAT
CGAGGAGCTCAACGACCTGGACATGCAGCTGTACGACTACGCCAAGGACCTCTTCCAGCAGCGCTACCAGTACAA
GCGGCAGCTGGAGCGCAGGGAGCAGCGCCTGAGGAGCCGCGAGGAGCGTCTGCTGCACCGGGCCAAGGAGGCACT
GCCGCGGGAGGATGCCGACGAGCCGGGCCGCGTGCCCACCGAGGACTACATGAGCCACATCATTGAGAAGTGGTA
GTGGCGGTGGTGGCCACGGGGAGGCCTCTTGGGGGGTGTGGGGGATAAAACAGGACAGACGACAGGTCCACCCAA
GACTGTCAAGGGATGAGCATCCCAAACCTGCTCCACAGAGGTAGCTGCGTCCTGAAAAAAAACAGAGCAGGGATG
TAGTGGGGCTGGGCAGGGATGGGGGCTTGAGAAATCAACAGGTGCAGCCCAGTGGGTCAGAGGAAAGCGTGCTCG
AAGGATGCCATGGTCAGGGCAGGGCCTCCAGAGCAGGTGTTGTGCCTGGAGCTGCTCTCCTGGCCTCCTTGGATT
TATCGCAAAAACTGAAGGTTTGCGCAAGAGACGAGGACAGCGGAAAGTGGACCTGCCAGGCCGGGAGTGTGTCCC
TCACCAACTATGCACACAGCACTCGCTCTTAGCTCCTCTGTCCGGGCTACTAGGAGTGAGACCAGCTTCTGGCAA
CTGCCCCAGCTCCAGGCCATCCCATAGCCCCTCCTCTTCTGGCTGCCCCCAATGCCCCGAGGCCTGGGGAGCCCC
CAGCTCACCCATCTGTAGCTCCCTCAAAGTCAGGGCCCACCCCATCTGAGGCAGAGAAGACTCGAGTCCAGCCCC
CAGGAAGCCTGCTCCCCTCTCTGGCCCATGGTCCTGCTTCATGCTTTGGGTCAGGAGGCCAAAGCTGATGTTCAG
GCCCCACCCACTCCCTACAGTCCTCAGACC

FIGURE 862

GACTGCCCGTACAACCTGGCCAACAACCGCCAGGTGCGC**ATG**CTGGCCGACCTGAGCCTGGTGGGCTGCTACAAC
CTGTCCTTCATCCCCGAGGGCAAGCGGGCCCAGCTGCTGCTCGAGAGCGCCAAGAAGAACCTGCGGGGCATGGCC
TTCTTCGGCCTGACCGAGTTCCAGCGCAAGACGCAGTACCTGTTCGAGCGGACGTTCAACCTCAAGTTCATCCGG
CCCTTCATGCAGTACAATAGCACGCGGGCGGGCGGCGTGGAGGTGGATGAAGACACCATCCGGCGCATCGAGGAG
CTCAACGACCTGGACATGCAGCTGTACGACTACGCCAAGGACCTCTTCCAGCAGCGCTACCAGTACAAGCGGCAG
CTGGAGCGCAGGGAGCAGCGCCTGAGGAGCCGCGAGGAGCGTCTGCTGCACCGGGCCAAGGAGGCACTGCCGCGG
GAGGATGCCGACGAGCCGGGCCGCGTGCCCACCGAGGACTACATGAGCCACATCATTGAGAAGTGG**TAG**TGGCGG
TGGTGGCCACGGGGAGGCCTCTTGGGGGGTGTGGGGGATAAAACAGGACAGACGACAGGTCCACCCAAGACTGTC
AAGGGATGAGCATCCCAAACCTGCTCCACAGAGGTAGCTGCGTCCTGAAAAAAAACAGAGCAGGGATGTAGTGGG
GCTGGGCAGGGATGGGGGCTTGAGAAATCAACAGGTGCAGCCCAGTGGGTCAGAGGAAAGCGTGCTCGAAGGATG
CCATGGTCAGGGCAGGGCCTCCAGAGCAGGTGTTGTGCCTGGAGCTGCTCTCCTGGCCTCCTTGGATTTATCGCA
AAAACTGAAGGTTTGCGCAAGAGACGAGGACAGCGGAAAGTGGACCTGCCAGGCCGGGAGTGTGTCCCTCACCAA
CTATGCACACAGCACTCGCTCTTAGCTCCTCTGTCCGGGCTACTAGGAGTGAGACCAGCTTCTGGCAACTGCCCC
AGCTCCAGGCCATCCCATAGCCCCTCCTCTTCTGGCTGCCCCCAATGCCCCGAGGCCTGGGGAGCCCCCAGCTCA
CCCATCTGTAGCTCCCTCAAAGTCAGGGCCCACCCCATCTGAGGCAGAGAAGACTCGAGTCCAGCCCCCAGGAAG
CCTGCTCCCCTCTCTGGCCCATGGTCCTGCTTCATGCTTTGGGTCAGGAGGCCAAAGCTGATGTTCAGGCCCCAC
CCACTCCCTACAGTCCTCAGACCAAGGAGGGGTTTGGGTAGTAGGCCCGAGCTGCATTGCCGGCCTTCCTCGGGC
CAACTGGCAGCCCAGGAGTGGGGAGGCTTTGGCCAGGGATGCTGCCACTTGTGCGTGAGTCCGCGGCTGGCCCTT
GGAGGTGACCATCCAGGCAGGCCTGGCTCAGACTGGAAGGGCTGGGGACCGAGGGCTCCCCTGCCTCTGTTCTCC
TTTCTGACCCACTGGGATTTGCTAGCAGGCTGCCCCAGCCCCATCACCGAAACACATACTCAAGAGCTCAAATAC
CACTGCTCCCACCAGCGTACGGATTAAGTTCATCAGGCTTCCATCGGCTGGAGCATGGACCATAGCCCCTGCCC
AGGAGCCGTACCCTCGGACCACAGTGGCTCTGTATGGCCAGGAACTGGGACTCGAGCTTTCAGATTCTCAACTAG
CCTTGGCAAAACAGCTGTAGGTGGCCTCCCTGACAACAGACACTCAGCCCTCCCCACCCTGGCTCTCCTTGCATT
TCCCCATGCTCCCCACCCCCTGGCAAAAGGCTGGCCATGCTCTGTTCCCAGCAGCCGCGCAGGTTTCCCCACTGG
CTGCAATGGCCCTACCAAAAGCCATGTTGCATATCCGTTGTAAGCACGTGCCCTGTGCCCTGTCCCCATTCCTTA
TGCCCTAGGAGGCCAAGCTGGTGTCTCTAGGAGGGCCCACACAGGCACCCTGGATCCCCCAGAGAGTAGATTGGT
GTGCTCAGGCCGCAGGCTGACTCAGAGGTAGGGCAGTGGGCTCTGCAGGCCACCTGGCTGGGGTTGGTGGGGGTC
CTCTCTCCTGCCCCAGCTTCCACTCAGCCACCACAGTTGCCACACCATGGGGTGGAGACGTGGGTCACCACGGGC
TTGGGAGCAAGCGCCTTCTGCAGCACAGGAAGCCGAAGCTGGGGTCAGGTGAGGTCGCTACCCCTGGAGGTCTGG
CATAAGGGCCCCACCCTCAGGTCTCCTACACTGGCCCCATTTTACTTTGGGGTCCAAGGACAGGATGGTCAACAG
GGCAGGGTGGACAGCGTGCCAGCGCCGCGCAGGGCCACCTCCCTGGGTGGATGCATCACACTAAGGAAGTGAGTG
CCAAGGGGATTTAGTGGTGTGGTTCTTTCAAAGGGAGGTCAGGGTCAATGGGAATCTGCTCGGACACTCAACATG
GGGGTGGGTGCACTCCTTGGAGGAGGAGGAACACGTTCAGGGGATTGTGAGGTCTTGCACAAGCCACGTGGGGCA
CCTTGGCTTCCCGGCAGGAGGTGGACACCCAGCCAGAGGCCTGGCTCAAGGTGACCTCACCTTCACCATGGGCTT
CCTGGGTGCGCGGGCCTGAGCGCAGGTTGTTTTGTACATATTGGAATATGTGTTAACTTATGCCCCGCATCCCAA
CTCACACGGAAGCACGGGTCTTGTCTCAGTCTCTTCGCTGCATTTGGAAAGCAGTCTCCTCTCGGGCCAGCGCCG
GGCTGAGGTGTCCAGAGGCGGCGGCAGCTGGCAGTGCCCTCAGCCCCCAAGTGTCCAGCCTGGCACTTCCCATTC
AGGCCACCTGCTTTGGGTCAACAGTTCCTTTGCCAGCAGCATCTCCTAAATTGTAAGGACTCTGTCCACCGGGGC
CCTCCCAGGGCTGTGAGGACGGAAACAGGCAGGGAGTGGAGCTAACAGCTTAGTCACCAGGACCCCCAGACCTGC
AAACGTCCCCTCCTGGAAGGGGAAGCCAGGAACAGCAGAACTGCCCACAAAACAAGGCTGTGAACTTTTCGGGAA
CTGGAACTGTTTAACTTGAACCCAGGATTGTTTAAAGCTTTATTTATTTATAGCTTCTTCTTAAAAAAAAGTGTT
GAAGAAATTTTTTGGTTATTCATACAAAAAAATGAGTTGATGATGGAAAAGCAAGTCATAATCATCTAATTGTTT
TTGTCTAGGTCGAGAATGAATGTTAGCTGATGAAATAAACCCTGACAAGG

FIGURE 863

MLADLSLVGCYNLSFIPEGKRAQLLLESAKKNLRGMAFFGLTEFQRKTQYLFERTFNLKFIRPFMQYNSTRAGGV
EVDEDTIRRIEELNDLDMQLYDYAKDLFQQRYQYKRQLERREQRLRSREERLLHRAKEALPREDADEPGRVPTED
YMSHIIEKW

FIGURE 864

GGAAAAAAGCGACTTGTGGCGGTCGAGCGTGGCGCAGGCGAATCCTCGGCACTAAGCAAATATGGACCTCGCGGC
GGCAGCGGAGCCGGGCGCCGGCAGCCAGCACCTGGAGGTCCGCGACGAGGTGGCCGAGAAGTGCCAGAAACTGTT
CCTGGACTTCTTGGAGGAGTTTCAGAGCAGCGATGGAGAAATTAAATACTTGCAATTAGCAGAGGAACTGATTCG
TCCTGAGAGAAACACATTGGTTGTGAGTTTTGTGGACCTGGAACAATTTAACCAGCAACTTTCCACCACCATTCA
AGAGGAGTTCTATAGAGTTTACCCTTACCTGTGTCGGGCCTTGAAAACATTCGTCAAAGACCGTAAAGAGATCCC
TCTTGCCAAGGATTTTTATGTTGCATTCCAAGACCTGCCTACCAGACACAAGATTCGAGAGCTCACCTCATCCAG
AATTGGTTTGCTCACTCGCATCAGTGGGCAGGTGGTGCGGACTCACCCAGTTCACCCAGAGCTTGTGAGCGGAAC
TTTTCTGTGCTTGGACTGTCAGACAGTGATCAGGGATGTAGAACAGCAGTTCAAATACACACAGCCAAACATCTG
CCGAAATCCAGTTTGTGCCAACAGGAGGAGATTCTTACTGGATACAAATAAATCAAGATTTGTTGATTTTCAAAA
GGTTCGTATTCAAGAGACCCAAGCTGAGCTTCCTCGAGGGAGTATCCCCCGCAGTTTAGAAGTAATTTTAAGGGC
TGAAGCTGTGGAATCAGCTCAAGCTGGTGACAAGTGTGACTTTACAGGGACACTGATTGTTGTGCCTGACGTCTC
CAAGCTTAGCACACCAGGAGCACGTGCAGAAACTAATTCCCGTGTCAGTGGTGTTGATGGATATGAGACAGAAGG
CATTCGAGGACTCCGGGCCCTTGGTGTTAGGGACCTTTCTTATAGGCTGGTCTTTCTTGCCTGCTGTGTTGCGCC
AACCAACCCAAGGTTTGGGGGGAAAGAGCTCAGAGATGAGGAACAGACAGCTGAGAGCATTAAGAACCAAATGAC
TGTGAAAGAATGGGAGAAAGTGTTTGAGATGAGTCAAGATAAAAATCTATACCACAATCTTTGTACCAGCCTGTT
CCCTACTATACATGGCAATGATGAAGTAAAACGGGGTGTCCTGCTGATGCTCTTTGGTGGCGTTCCAAAGACAAC
AGGAGAAGGGACCTCTCTTCGAGGGGACATAAATGTTTGCATTGTTGGTGACCCAAGTACAGCTAAGAGCCAATT
TCTCAAGCACGTGGAGGAGTTCAGCCCCAGAGCTGTCTACACCAGTGGTAAAGCGTCCAGTGCTGCTGGCTTAAC
AGCAGCTGTTGTGAGAGATGAAGAATCTCATGAGTTTGTCATTGAGGCTGGAGCTTTGATGTTGGCTGATAATGG
TGTGTGTTGTATTGATGAATTTGATAAGATGGACGTGCGGGATCAAGTTGCTATTCATGAAGCTATGGAACAGCA
GACCATATCCATCACTAAAGCAGGAGTGAAGGCTACTCTGAACGCCCGGACGTCCATTTTGGCAGCAGCAAACCC
AATCAGTGGACACTATGACAGATCAAAATCATTGAAACAGAATATAAATTTGTCAGCTCCCATCATGTCCCGATT
CGATCTCTTCTTTATCCTTGTGGATGAATGTAATGAGGTTACAGATTATGCCATTGCCAGGCGCATAGTAGATTT
GCATTCAAGAATTGAGGAATCAATTGATCGTGTCTATTCCCTCGATGATATCAGAAGATATCTTCTCTTTGCAAG
ACAGTTTAAACCCAAGATTTCCAAAGAGTCAGAGGACTTCATTGTGGAGCAATATAAACATCTCCGCCAGAGAGA
TGGTTCTGGAGTGACCAAGTCTTCATGGAGGATTACAGTGCGACAGCTTGAGAGCATGATTCGTCTCTCTGAAGC
TATGGCTCGGATGCACTGCTGTGATGAGGTCCAACCTAAACATGTGAAGGAAGCTTTCCGGTTACTGAATAAATC
AATCATCCGTGTGGAAACACCTGATGTCAATCTAGATCAAGAGGAAGAGATCCAGATGGAGGTAGATGAGGGTGC
TGGTGGCATCAATGGTCATGCTGACAGCCCTGCTCCTGTGAACGGGATCAATGGCTACAATGAAGACATAAATCA
AGAGTCTGCTCCCAAAGCCTCCTTAAGGCTGGGCTTCTCTGAGTACTGCCGAATCTCTAACCTTATTGTGCTTCA
CCTCAGAAAGGTGGAAGAAGAAGAGGACGAGTCAGCATTAAAGAGGAGCGAGCTTGTTAACTGGTACTTGAAGGA
AATCGAATCAGAGATAGACTCTGAAGAAGAACTTATAAATAAAAAAAGAATCATAGAGAAAGTTATTCATCGACT
CACACACTATGATCATGTTCTAATTGAGCTCACCCAGGCTGGATTGAAAGGCTCCACAGAGGGAAGTGAGAGCTA
TGAAGAAGATCCCTACTTGGTAGTTAACCCTAACTACTTGCTCGAAGATTGAGATAGTGAAAGTAACTGACCAGA
GCTGAGGAACTGTGGCACAGCACCTCGTGGCCTGGAGCCTGGCTGGAGCTCTGCTAGGGACAGAAGTGTTTCTGG
AAGTGATGCTTCCAGGATTTGTTTTCAGAAACAAGAATTGAGTTGATGGTCCTATGTGTCACATTCATCACAGGT
TTCATACCAACACAGGCTTCAGCACTTCCTTTGGTGTGTTTCCTGTCCCAGTGAAGTTGGAACCAAATAATGTGT
AGTCTCTATAACCAATACCTTTGTTTTCATGTGTAAGAAAAGGCCCATTACTTTTAAGGTATGTGCTGTCCTATT
GAGCAAATAACTTTTTTTCAATTGCCAGCTACTGCTTTTATTCATCAAAATAAAATAACTTGTTCTG

FIGURE 865

MDLAAAAEPGAGSQHLEVRDEVAEKCQKLFLDFLEEFQSSDGEIKYLQLAEELIRPERNTLVVSFVDLEQFNQQL
STTIQEEFYRVYPYLCRALKTFVKDRKEIPLAKDFYVAFQDLPTRHKIRELTSSRIGLLTRISGQVVRTHPVHPE
LVSGTFLCLDCQTVIRDVEQQFKYTQPNICRNPVCANRRRFLLDTNKSRFVDFQKVRIQETQAELPRGSIPRSLE
VILRAEAVESAQAGDKCDFTGTLIVVPDVSKLSTPGARAETNSRVSGVDGYETEGIRGLRALGVRDLSYRLVFLA
CCVAPTNPRFGGKELRDEEQTAESIKNQMTVKEWEKVFEMSQDKNLYHNLCTSLFPTIHGNDEVKRGVLLMLFGG
VPKTTGEGTSLRGDINVCIVGDPSTAKSQFLKHVEEFSPRAVYTSGKASSAAGLTAAVVRDEESHEFVIEAGALM
LADNGVCCIDEFDKMDVRDQVAIHEAMEQQTISITKAGVKATLNARTSILAAANPISGHYDRSKSLKQNINLSAP
IMSRFDLFFILVDECNEVTDYAIARRIVDLHSRIEESIDRVYSLDDIRRYLLFARQFKPKISKESEDFIVEQYKH
LRQRDGSGVTKSSWRITVRQLESMIRLSEAMARMHCCDEVQPKHVKEAFRLLNKSIIRVETPDVNLDQEEEIQME
VDEGAGGINGHADSPAPVNGINGYNEDINQESAPKASLRLGFSEYCRISNLIVLHLRKVEEEEDESALKRSELVN
WYLKEIESEIDSEEELINKKRIIEKVIHRLTHYDHVLIELTQAGLKGSTEGSESYEEDPYLVVNPNYLLED

FIGURE 866

CCGGGATCTCGAGATAGCCGCAGCTCTCGCGATCTTTCTGGAGCCGCACCTCCACGCGGAGTCCGAGCGCGTGTG
CTGAGACCCCAGGGTCGGGAGGGCGGAGACTGGGAGGGAGGGAGAAGCCCCTTTGGCCTGCCTTACGGAAGCCTG
CGAGGGAGGGTGGTGTCCACTGCCCAGTTCCGTGTCCCGATGCCCAGCGCCAGCGCCAGCCGCAAGAGTCAGGAG
AAGCCGCGGGAGATCATGGACGCGGCGGAAGATTATGCTAAAGAGAGATATGGAATATCTTCAATGATACAATCA
CAAGAAAAACCAGATCGAGTTTTGGTTCGGGTTAGAGACTTGACAATACAAAAAGCTGATGAAGTTGTTTGGGTA
CGTGCAAGAGTTCATACAAGCAGAGCTAAAGGGAAACAGTGCTTCTTAGTCCTACGTCAGCAGCAGTTTAATGTC
CAGGCTCTTGTGGCGGTGGGAGACCATGCAAGCAAGCAGATGGTTAAATTTGCTGCCAACATCAACAAAGAGAGC
ATTGTGGATGTAGAAGGTGTTGTGAGAAAAGTGAATCAGAAAATTGGAAGCTGTACACAGCAAGACGTTGAGTTA
CATGTTCAGAAGATTTATGTGATCAGTTTGGCTGAACCCCGTCTGCCCCTGCAGCTGGATGATGCTGTTCGGCCT
GAGGCAGAAGGAGAAGAGGAAGGAAGAGCTACTGTTAACCAGGATACAAGATTAGACAACAGAGTCATTGATCTT
AGGACATCAACTAGTCAGGCAGTCTTCCGTCTCCAGTCTGGCATCTGCCATCTCTTCCGAGAAACTTTAATTAAC
AAAGGTTTTGTGGAAATCCAAACTCCTAAAATTATTTCAGCTGCCAGTGAAGGAGGAGCCAATGTTTTTACTGTG
TCATATTTTAAAAATAATGCATACCTGGCTCAGTCCCCACAGCTATATAAGCAAATGTGCATTTGTGCTGATTTT
GAGAAGGTTTTCTCTATTGGACCAGTATTCAGAGCGGAAGACTCTAATACCCATAGACATCTAACTGAGTTTGTT
GGTTTGGACATTGAAATGGCTTTTAATTACCATTACCACGAAGTTATGGAAGAAATTGCTGACACCATGGTACAA
ATATTCAAAGGACTTCAAGAAAGGTTTCAGACTGAAATTCAAACAGTGAATAAACAGTTCCCATGTGAGCCATTC
AAATTTTTGGAGCCAACTCTAAGACTAGAATATTGTGAAGCATTGGCTATGCTTAGGGAAGCTGGAGTCGAAATG
GGAGATGAAGACGATCTGAGCACACCAAATGAAAAGCTGTTGGGTCATTTGGTAAAGGAAAAGTATGATACAGAT
TTTTATATTCTTGATAAATATCCATTGGCTGTAAGACCTTTCTATACCATGCCTGACCCAAGAAATCCCAAACAG
TCCAACTCTTACGATATGTTCATGAGAGGAGAAGAAATATTGTCAGGAGCTCAAAGAATACATGATCCTCAACTG
CTAACAGAGAGAGCTTTACATCATGGAATTGATTTGGAGAAAATTAAGGCTTACATTGATTCCTTCCGCTTTGGA
GCCCCTCCTCATGCTGGTGGAGGCATTGGATTGGAACGAGTTACTATGCTGTTTCTGGGATTGCATAATGTTCGT
CAGACCTCCATGTTCCCTCGTGATCCCAAACGACTCACTCCTTAAATTCACACTTTGCCACTTAACTCCAGTGTG
GATGACAGAGCGAGACCCTGCCTCAAAAAAAAAAAAAAAAAAAGAAAGCCACACTTATTCTTTTCAGTAACCTGC
TAGTGCACAGGCTGTACTTTAGGTACTTAAAATATGCACTAGAATAAATTTGCAAGGCCCTAAAATATCACTGTT
ATTTTTGGAGTAATTCAGTATAGGTTCGTTTAAAAGAGATTTTTATAACTTCAGACATGCATCAGTAGGAAATAA
CTTGAGAAATTCATATGGTTATGTTACAAATTCATATTCTGTTACTACAGTAAACGTTAAGAGTTTTAAACAGTT
AAGATTGTACAATTTTTCTTCTTTTCTATATTACAAGGGCCCCAGTGTTAATGTCTTAGATTTTCAGTATTTGAA
CTTATTTTTTTAAATTCTGTCATTGAGATAAGAATAATTCAGGTAGCATCTGAAATTTTAATGAATGTATAATTG
GCATATCATGGAAAATTAACCAGAAAGTATCAGTTCTTAAAAGTTATGCCTAGAAATTATGTAAAGCTAAACTAC
TGGTTAGAAAGTATTCAGTGTAATATTGTATTAATTTGTTAAATTCTAAACTTGAATTTCAATAAAATTTTAAAG
CT

FIGURE 867

ATGACAAAGAAAAATGCCTGCATGGGCCTTGTTTTCCAGATTCAATCAAGGCTCAAAGCTTTTATCTTGTTCTTA
ATAGCACCTTGCACCGATAGAGCCCGGCAAGGCTTTGCGGGCCTTAATTATTTCCCCAAGATCGATGAGACCCCT
CAGCCCCCTGGGCAGCAGCATCCCACGGCAGTTTTCCAGATGGATGAGCTGCGTCGAAAGCTGCAGAGCAGACAG
GGATGCAGACAAGGTCCAGCACGCCCAGCAGAGCCTGCGGCCTGCGGGTTCCTCGGGCGGATGGCACTGCAAAAT
TCAGCCCTTAATTCAATCAATATGTGCCTTCGAGGAGTTTATAGTCATGGTTTGGTATGGTTGGTATGTGATGCA
CACAAAGCAGAGACAGCTGCATGTAGAAGGGCAGGGGAGCATGGAGGCCCCAGTACAGCCAGGAGGCCCCTGGAG
CTTCAGGCAGCAGGACATGGGTCTGGATCTGTAGTCAGAGGGGAGGTCAGGAAAGAGCTTGTACACCAGCAAAAG
ATTGGATCCTGTGGTTCTCAAACCCTTATTAGTCCTGGAGCTGTGTTTCAAGGAAATTCTGCAGAAGAACAGCAG
TTCCCTTGCAAGGATGACCCCAGGGCCCCTGGTTCCCAGCAGCTCCAAGATGAGATGGCAGAAAGGGAGAGGGGG
AACCAAGGAGAGGGAAGGAGGAAATATATTCAGTGCAGCTGCCCCAACGTCCCTCAAGGACAAGCACAAAGGGGT
GGTGTGGACAAGCATAATGCAATTGGCCCAGGGACAGGCCATAGACCCCACTTCCAAACCCCATTTCTCCTCACA
GCCCAGGGCCTGAAGGGAACCCGCTGGATGCAAAGCCGAGGTCACCCAGAGATGGAGGTGGACAGACAGTGTGGG
ATGGCCCTGCACCCTGAAACTCCCAGGCACTACCTTGCATTGTCAGTTTCTAATTTTACACACACTGGGGAGAGG
TCTGCTGTGGGCCAGGCTGGCCACCAGCGCTGGGTAAGTAGGGACTGGCCTAGCCACAGGCCTCAAGGATGCCGA
AGTCTGGTGGGGGAGACAAGCATGGAGAGAGACAGAGATGGCAGAGGCCAGGACAGGAAGCCTCTGGGCATCCTG
GCTGAGGACAGGGTGGCACACCCAGAGGAGAGTGAATCGTGGAAATGCCGAAAGCTAAAGAGAAGATTCCCACCA
GAGATCACAGAGCAGAACATGCAAAAGTATAAAATTGCCCAACCACCGTCACTCACGGACCCCTTTGTCCCCTTC
TCTTCCCCTCCACCCCATAGAAGTTTGGCTGACAACCACGGGTTCATACCACATTTCCACATATGGGAAGAATCT
GTGGCCCAGAGTGGTTACATTAGAGCACCTCCTCCCCTGAGAGCCACACAAGGGCCCATACCACCTTCCAGTTCA
TGGCTCCACCTTTGTCCTGCTCTCACAACCTTCCCAGACCTGGCCTATACCCACATGTTATTAAATAATCTTCTA
GATATGCCTTTAGGATTTGCTGCAAAGACACTTGAGATAAAGTATCTGTCAGAACCAACCTGGGATGTAGCCAAA
GCTAAGGAATATGTCCTGTTCTGTGGAGAGCAGATGATCAATAGGTGGTTCCCAGCTAATGGAGTGACTGGAGCA
AGGCTCATAGGCCTTTCAGTTCCATCAAAGGAAGATAAGTCCCCACTCATTGTCCCTGGAGGAAACTGTGAGGTC
TTCTTATATTTGCATGTATGTGCCAAAGAGAGACATGTAAAAACCAGAGCCCGGAGACATAGAGAAGATCATTCA
AAAGCACATGCCAAGCTAAAGACAATACCAGGGACAGGACCTCATCTTCTGACTCTTGGTCCAGTTCTCCCTCCA
ACTCAGCAAACAGCCTTTGGATTCCACTTGGGAAATATGGAAACTGAACAGCCAGAAGAAACCTTCCCTAACACT
GAAACCAGTGGTGAATTTGGTAAACGCCCTGCAGAAGATATGGAAGAGGAACAAGCATTTAAAAGATCTAGAAAC
ACTGATGAGATGGTTGAATTACCCATTCTGCTTCAGAGCAAGAATGCTGGAGCAGTGACTGGAAAAGGAGGCAAG
AATATTAAGGCTCTCCATACAGACTACAACGCCAGCATTTCAGTTCTAGACAGCAGTGGCCCCCAGCATATATTG
CATATCAGTGCTGATATCGAAACAATTGGAGAAATTCTGAAGAAAATCATCACTACCTTGGAAGAGGGCCCGCAG
TTGCCATCACCCACTGCAACCAGCCAGCTCCCGCTCGAATCTGATGCTGTGGAATACTTAAATTACCAACAATAT
AAAGGAAGGGACTTTGACTGCGAGTTGAGGCTGTTGATTCATCAGAGTCTAGCAGGAGGAATTATTGGGGAATGT
TGTCCTCATTTCACTGATAGAGTTGTTCTTATTGGAGGAAAACCCAATAGGGTTGTAGAGTGCATAAAGATCATC
CTTGATCTTATTTCTGAGTCTCCCATCAAAGGACATGCACAGCCTTATGATCCCAATTTTTACGATGAAACCTAT
GATTATGGTGGTTTTACAATGGTGTTTGCTGACGACCGTGGACGCCCAGGGGGAGACCTCATGACCTATAACAGA
AAAGGGAGACCTGGAAACCGTTACGACGGCGTGGTTGATTTCAGTGCTGATGAAACTTGGGGCTCTGCAATAGAT
ACATGGAACGCATCAGAATGGCAGATGGCTTATGAACCACAGGGTGGCTCCAGATATGATTATTCCTATGCAGGG
TGTCATGGCTCATATGGTGATCTTGGTGGACCTATTATTACTACACAAGGAGCTTTGATCAAAATTGATGAGCCT
TTAGAAGGATCCGAAGATCGGATCATTACCATTACAGGAACACAGGACCAGATACAGAATGCACAGTATTTGCCG
CAGAATAGTGTGAAGCAGTATTCTGGAAAGTTTTTC**TAA**

FIGURE 868

MTKKNACMGLVFQIQSRLKAFILFLIAPCTDRARQGFAGLNYFPKIDETPQPPGQQHPTAVFQMDELRRKLQSRQ
GCRQGPARPAEPAACGFLGRMALQNSALNSINMCLRGVYSHGLVWLVCDAHKAETAACRRAGEHGGPSTARRPLE
LQAAGHGSGSVVRGEVRKELVHQQKIGSCGSQTLISPGAVFQGNSAEEQQFPCKDDPRAPGSQQLQDEMAERERG
NQGEGRRKYIQCSCPNVPQGQAQRGGVDKHNAIGPGTGHRPHFQTPFLLTAQGLKGTRWMQSRGHPEMEVDRQCG
MALHPETPRHYLALSVSNFTHTGERSAVGQAGHQRWVSRDWPSHRPQGCRSLVGETSMERDRDGRGQDRKPLGIL
AEDRVAHPEESESWKCRKLKRRFPPEITEQNMQKYKIAQPPSLTDPFVPFSSPPPHRSLADNHGFIPHFHIWEES
VAQSGYIRAPPPLRATQGPIPPSSSWLHLCPALTTFPDLAYTHMLLNNLLDMPLGFAAKTLEIKYLSEPTWDVAK
AKEYVLFCGEQMINRWFPANGVTGARLIGLSVPSKEDKSPLIVPGGNCEVFLYLHVCAKERHVKTRARRHREDHS
KAHAKLKTIPGTGPHLLTLGPVLPPTQQTAFGFHLGNMETEQPEETFPNTETSGEFGKRPAEDMEEEQAFKRSRN
TDEMVELPILLQSKNAGAVTGKGGKNIKALHTDYNASISVLDSSGPQHILHISADIETIGEILKKIITTLEEGPQ
LPSPTATSQLPLESDAVEYLNYQQYKGRDFDCELRLLIHQSLAGGIIGECCPHFTDRVVLIGGKPNRVVECIKII
LDLISESPIKGHAQPYDPNFYDETYDYGGFTMVFADDRGRPGGDLMTYNRKGRPGNRYDGVVDFSADETWGSAID
TWNASEWQMAYEPQGGSRYDYSYAGCHGSYGDLGGPIITTQGALIKIDEPLEGSEDRIITITGTQDQIQNAQYLP
QNSVKQYSGKFF

FIGURE 869

ATGAAGCAGTTAATTACCCCTGCTAAACAGCAGGAAGCATTTGAGCAAAAACTCTGCTCACCTTCCTCAATCAGA
GGACATTTCTGCTCATCAGTCAAGCAGGCAGACCACAGGACTCTCAGACAAAGGCTGAGAGGTAGACTGATGAGG
AGGAGACTGTCAGTGAGCACAAAGGCCTTAAGATTAGCGACTGAAGGCTCCTGGAATGAGTATGTGGTTAGAGAC
TGGAACTACTCAGGAGTTTCCCTAGGTCTGCTCCAAATAGCACAAGCAATGGATGATGAAGGATCCATGTTAATA
GCAGTGGATCCACAGTGCAGATTTTCAGGTGATCTGCTCCCCTACGACTCACTAATTGGAGTCCCATTGGCCCCC
CATGTGACCCTCTTGGATAAAAATCAAAATGGCTCTCGTCTTGTTTGTTTCTCCTGTTTGCCCCCAGTCAGGGCT
GGCACAGAGTGGCAGCTCTCTGCTCTCCACAGGGCTCCCCGCTCCACCCAGCCCGATAAAGCATGCCGACTGGGC
TACAAAGCCAAGCAAGGTTACATTATATATAGGATTTGTGTTCGCCGTGAGGAGCAAGCTGGACACCACTGTGGG
GCTCTAAGAGTCCTGAATTCGTACTGGGTTGGTGAAGATTCCACATACAAATTTTTTGAGGTTATCCTCATTGAT
CCATTCCATAAAGCTATCAGAAGAAATCCTGACACCCAGTGGATCACCAAACCAGTCCACAAGCACAGGGAAATG
CGTGGGCTGACATCTGCAGGC**TGA**

FIGURE 870

MKQLITPAKQQEAFEQKLCSPSSIRGHFCSSVKQADHRTLRQRLRGRLMRRRLSVSTKALRLATEGSWNEYVVRD
WNYSGVSLGLLQIAQAMDDEGSMLIAVDPQCRFSGDLLPYDSLIGVPLAPHVTLLDKNQNGSRLVCFSCLPPVRA
GTEWQLSALHRAPRSTQPDKACRLGYKAKQGYIIYRICVRREEQAGHHCGALRVLNSYWVGEDSTYKFFEVILID
PFHKAIRRNPDTQWITKPVHKHREMRGLTSAG

FIGURE 871

ATGTGGGGCGACCTCTGGCTCCTCCCGCCTGCCTCTGCCAATCCGGGCACTGGGACAGAGGCTGAGTTTGAGAAA
GCTGCAGAGGAGGTTAGGCACCTTAAGACCAAGCCATCGGATGAGGAGATGCTGTTCATCTATGGCCACTACAAA
CAAGCAACTGTGGGCGACATAAATACAGAACGGCCCGGGATGTTGGACTTCACGGGCAAGGCCAAGTGGGATGCC
TGGAATGAGCTGAAAGGGACTTCCAAGGAAGATGCCATGAAAGCTTACATCAACAAAGTAGAAGAGCTAAAGAAA
AAATACGGGATA**TGA**GAGACTGGATTTGGTTACTGTGCCATGTGTTTATCCTAAACTGAGACAATGCCTTGTTTT
TTTCTAATACCGTGGATGGTGGGAATTCGGGAAAATAACCAGTTAAACCAGCTACTCAAGGCTGCTCACCATACG
GCTCTAACAGATTAGGGGCTAAAACGATTACTGACTTTCCTTGAGTAGTTTTTATCTGAAATCAATTAAAAGTGT
ATTTGTTACTTT

FIGURE 872

MWGDLWLLPPASANPGTGTEAEFEKAAEEVRHLKTKPSDEEMLFIYGHYKQATVGDINTERPGMLDFTGKAKWDA
WNELKGTSKEDAMKAYINKVEELKKKYGI

FIGURE 873

GTTTAGGGGCTGGTACAAAGGATGAATTGCACATTGTTGAAGTAGAGGCA**ATG**AATTACAAAGGCAGTCCAATTA
AAGTAACACTGGCAACTTTGAAAATGTCTGTACAGCCAAAGGATTCCCTTGGAGGCTTTGAAATCACACCACCAG
TGGTCTTACGGTTGAAGTGTGGTTCAGGGCCAGTGCATATTAGTGGACAGCACTTAGTAGCTGTGGAGGAAGATG
CAGAGTCAGAAGATGAAGAGGAGGAGGATGTGAAACTCTTAAGTGTATCTGGAAAGCGGTCGGCCCGTGGAGGTG
GTAGCAAGATTCCACAGAAAAAAGTAAAAGTTGCTGCTGATGAAGATGAAGATGATGATGATGAGGATTTTGATG
ATGGGGAAGCTGAAGAAAAAGCGCCGGTGAAGAAATCCATACGAGATACTCCAGCCAAAAATGCACAAAAGTCAA
ATCAGAATGGAAAAGACTCAAAACCGTCAACACCAAGATCAAAAGGACAAGACTCCTTCAAAAAAACAGGAAAAA
ACTTC**TAA**AACACCGAAAGGACCTAGTTCCATAGAAGACATTAAAGCGAAAATGCAAGCAAGTATAGAAAAAGCG
CATTGAACAGTCCTGGGCACTGCTGGTAAATTAAGCCCAAAGATGGGGAGAAAGGAAAAGGAGAGACAAATATAG
TCCATACTGAG

FIGURE 874

MNYKGSPIKVTLATLKMSVQPKDSLGGFEITPPVVLRLKCGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSVS
GKRSARGGGSKIPQKKVKVAADEDEDDDDEDFDDGEAEEKAPVKKSIRDTPAKNAQKSNQNGKDSKPSTPRSKGQ
DSFKKTGKNF

FIGURE 875

AGCGGGTTTGCGGGAGCGCCGCGTGGTTAGCGTCGGCGGCTTTTGGC**ATG**GCGACTTTTTCTGGCCCGGCTGGGC
CAATCCTGTCGCTTAATCCGCAGGAAGATGTCGAGTTCAAAAGGAGGTGGCGCAGGTTCGCAAGCGCATAACCC
AGCGAAAAAAACAAGAACAACTTACTCCTGGAGTAGTCTATGTGCGCCACCTACCTAACCTACTTGACGAAACCC
AGATCTTTTCATATTTCTCCCAGTTTGGCACTGTGACACGGTTCAGGCTGTCCAGAAGTAAAAGGACTGGAAATA
GCAAAGGCTATGCATTTGTGGAGTTTGAGTCTGAGGATGTTGCCAAAATAGTTGCTGAAACAATGAACAACTACC
TGTTTGGTGAAAGACTCTTGGAGTGTCATTTTATGCCACCTGAAAAAGTACATAAAGAACTCTTTAAAGACTGGA
ATATTCCATTTAAGCAGCCATCATATCAATCAGTGAAACGGTATAATCGGAATCGGACACTAACACAAAAGCTAC
GGATGGAGGAGCGATTTAAAAAGAAAGAAAGATTACTCAGGAAGAAATTAGCTAAAAAAGGAATTGACTATGATT
TTCCTTCTTTGATTTTACAGAAAACGGAAAGTATTTCAAAAACTAATCGTCAGACGTCTACAAAAGGCCAGGTTT
TACGTAAGAAGAAGAAAAAAGTTTCAGGTACTCTTGACACTCCTGAGAAGACTGTGGATAGCCAGGGCCCCACAC
CAGTTTGTACACCAACATTTTTGGAGAGGCGAAAATCTCAAGTGGCTGAACTGAATGATGATGATAAAGATGATG
AAATAGTTTTCAAACAGCCCATATCCTGTGTAAAAGAAGAAATACAAGAGACTCAAACACCTACACATTCACGGA
AAAAAAGACGAAGAAGCAGCAATCAG**TGA**TTTTCAATGTATTATATTTCTTTTGAAAAATATAATATTTTTATGA
GAGTGGACTTTGTATTTCACTAGGTACAATGGAATACAACCTTTGACAAGATTTTCAGAGGAAAAATACACTGTT
TGGTCAAGTTAAGGAAAGCAGTGTGTAATTTTGGATTGCCTGCCCTTGGCTGAAATACAGGGGTGCATACCATCT
TGCAGTGGCTTGGCTGACATTGCCTCTTTGTCCTGGCCTCTAGTTTTCTTTTGATATTTCATAGCTCTCCTTAGT
TTACTCTGCCTGGATAGAAAGTTGACCACTAACTGCAGGTTTAAGTACTAAACTGCAGCCTTTTCTGTCGCCAGC
AATTAAAGACCACCAATCTTGTTTGTCCATCTACATGGTTTGTCGGGGACATTTAACTCATGGAGGTGCTTTAGA
TTTCAACATCAGATGGTTGAAGCTGGAAGTTTAATTATATGTAGAGTGAGAAGGCAGTTCCAGTTTTAGCACAGA
TTTGTTTATGTGTTCAGATTTTAATAGAGATTCAAAAATGACTCATTTTTACCAATAATGTTAAATTAGTTTTGG
TTGTGCTAGCATGAATTAATAACCACCATTTTATACCAGTATCATCAGTGAAGAATTGTATTTCAAGATTCAAAC
AATAACCAGCAATTAAACTTTTTTCTACAATGTATTTGTTTGCGAGTAGGACTTGGGAGTCATTGGAAAAAAAAA
ATAATAAATTTTCCCCTTCATTAACAAAAAAAAAAAAAAAA

FIGURE 876

MATFSGPAGPILSLNPQEDVEFQKEVAQVRKRITQRKKQEQLTPGVVYVRHLPNLLDETQIFSYFSQFGTVTRFR
LSRSKRTGNSKGYAFVEFESEDVAKIVAETMNNYLFGERLLECHFMPPEKVHKELFKDWNIPFKQPSYQSVKRYN
RNRTLTQKLRMEERFKKKERLLRKKLAKKGIDYDFPSLILQKTESISKTNRQTSTKGQVLRKKKKKVSGTLDTPE
KTVDSQGPTPVCTPTFLERRKSQVAELNDDDKDDEIVFKQPISCVKEEIQETQTPTHSRKKRRRSSNQ

FIGURE 877

CCGCGGCGTCCACACTCGCCGCGCGCGCGGCGGCCGGGCTGGACCTTGCTGGCCCGCGGCGCCATGAGCCGCAGC
CTGGACTCGGCGCGGAGCTTCCTGGAGCGGCTGGAAGCGCGGGGCGGCCGGGAGGGGGCAGTCCTCGCCGGCGAG
TTCAGCGACATCCAGGCCTGCTCGGCCGCCTGGAAGGCTGACGGCGTGTGCTCCACCGTGGCCGGCAGTCGGCCA
GAGAACGTGAGGAAGAACCGCTACAAAGACGTGCTGCCTTATGATCAGACGCGAGTAATCCTCTCCCTGCTCCAG
GAAGAGGGACACAGCGACTACATTAATGGCAACTTCATCCGGGGCGTGGATGGAAGCCTGGCCTACATTGCCACG
CAAGGACCCTTGCCTCACACCCTGCTAGACTTCTGGAGACTGGTCTGGGAGTTTGGGGTCAAGGTGATCCTGATG
GCCTGTCGAGAGATAGAGAATGGGCGGAAAAGGTGTGAGCGGTACTGGGCCCAGGAGCAGGAGCCACTGCAGACT
GGGCTTTTCTGCATCACTCTGATAAAGGAGAAGTGGCTGAATGAGGACATCATGCTCAGGACCCTCAAGGTCACA
TTCCAGAAGGAGTCCCGTTCTGTGTACCAGCTACAGTATATGTCCTGGCCAGACCGTGGGGTCCCCAGCAGTCCT
GACCACATGCTCGCCATGGTGGAGGAAGCCCGTCGCCTCCAGGGATCTGGCCCTGAACCCCTCTGTGTCCACTGC
AGTGCGGGTTGTGGGCGAACAGGCGTCCTGTGCACCGTGGATTATGTGAGGCAGCTGCTCCTGACCCAGATGATC
CCACCTGACTTCAGTCTCTTTGATGTGGTCCTTAAGATGAGGAAGCAGCGGCCTGCGGCCGTGCAGACAGAGGAG
CAGTACAGGTTCCTGTACCACACGGTGGCTCAGATGTTCTGCTCCACACTCCAGAATGCCAGCCCCCACTACCAG
AACATCAAAGAGAATTGTGCCCCACTCTACGACGATGCCCTCTTCCTCCGGACTCCCCAGGCACTTCTCGCCATA
CCCCGCCCACCAGGAGGGGTCCTCAGGAGCATCTCTGTGCCCGGGTCCCCGGGCCACGCCATGGCTGACACCTAC
GCGGTGGTGCAGAAGCGCGGGGCTCCAGCGGGCGCCGGGAGTGGGACGCAGACGGGGACGGGGACGGGGACGGGG
GCGCGCAGCGCGGAGGAGGCGCCGCTCTACAGCAAGGTGACGCCGCGCGCCCAGCGACCCGGGGCGCACGCGGAG
GACGCGAGGGGGACGCTGCCTGGCCGCGTTCCTGCTGACCAAAGTCCTGCCGGATCTGGCGCCTACGAGGACGTG
GCGGGTGGAGCTCAGACCGGTGGGCTAGGTTTCAACCTGCGCATTGGGAGGCCGAAGGGTCCCCGGGACCCGCCT
GCTGAGTGGACCCGGGTGTAAGTCTAACGCCAGTTCCTGCCTGTTGCCTCTTGTGAGCTCGGACTGCTGATGCCC
CGGTGCTGCTGAGCGCCGTGCGCAGAATGGAAACAGTGGGCCTGGATCAAAGTTAAAGTTTCTCAGGGTGGGAAA
TGTGGGGGCTTTGCCCCAATGACTGTAGCATTCAAGGCTTGAGGCTGGAGGAGGTAGCTAGGGTATAGTGGCTGG
TGAGGCTGCACAGAGCAGATTCAAGAAAGAAGATCAGGAAGGGGCATGACCCCTGAGTTATGAAGGGGAGAAGGG
ACAGATGAGCTTCCGGAGACTGCTCTCCTCACCACACAGCACTAGTCCATCCTCAGCACCTGAGCCTCCCTCACT
TGGACACTCAGGGGACCACACAGAGAAGTGGATGGACACTTCGCCATCCAGGCAGAACTAAGCCAGGCATAACCA
CAGCCAAGCAGATTAACCCCAGGCAGACCGATAAAAAGACCTCCAGATAGGCAGACAGACAGATGGACCACCAAC
CTGGACAGACAGCCAAAGCTTCAGAGATACAGTCCACAGGTGGACAAAGGGATCCCCAGCCAGAGAGAGAGAGAC
CAGCCAACAGCTTGATAGACCAGTGCAGCCAGAGAGACCACCAAACAGAGCCCCCAAAAGACAGACATCTCTGCT
AGCTGGACAGCCAGGTGGACCCCCTAAGTTAGATTACTAGACAGATATAAACAGATCCCCTGCTGAACAGATACA
CAGAGTTCTCAGACCCCACCCCCACCCTCAGGTGGGCTGGCTGGCTGACAGACCTTCTGGCCAGACAGACTCCTA
ACCAACCAGATGGACTGCCAGACAGGCAGACATCAGCCACATGGAATCCTGACATCCCAGCCAGCCGGCCAGACT
CTCATCTTGATGTCTTGATGGATGGACCCCAGCTAGTCAGACATGATCCTCCAGATTGACAGACAAGTCCCCCAA
ATGAGTACACATCTCCAGCTATTCAGACAGATGGACCCCCAGCAAATCAGGACCTATCTAGGCAGACCCCAGCCA
GACCCCCGCCAGACAGACTCCCAACCAGACTGACCCCTTACTATTCACACAGCCTGCCGAGTAGCTGGGACTACA
GGTCTAATTTTTTTTTTTTTAAGAAATGAGTTTTTGCCATGTTGCCCAGACTGGTCTTGAACTCCCAACCTCAA
GCAATCCTCCTGCCTCAGCCTCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCAGGCTCAGCCCCCTAAGATTT
GAAACACTTTAAATGGCCCATGGTAGGGTTCCTGCTAGGATAAAACATTAAGCGGCTGTTAAAAGAAATAAAAGG
AGGACACGTCTCTGTGC

FIGURE 878

TGGAAGCGGCACTCAAG<u>ATG</u>CTGCGCCGCGAGGCCCGCCTGCGCCGCGAGTACCTGTACCGCAAGGCCCGGGAGG
AGGCGCAGCGCTCAGCCCAGGAGAGGAAGGAGCGGCTGCGGCGCGCTGGAAGAAAACCGCCTGATTCCCACTG
AGTTACGCCGAGAGGCTCTGGCCTTACAGGGGTCCCTGGAGTTTGATGATGCTGGAGGTGAAGGTGTGACCAGCC
ACGTGGATGATGAATACCGATGGGCAGGAGTCGAGGATCCCAAGGTTATGATCACTACCTCCCGAGACCCCAGTT
CCCGCCTCAAGATGTTTGCAAAGGAGCTGAAGCTGGTGTTCCCGGGCGCCCAGCGAATGAACCGAGGTCGACATG
AAGTGGGGGCACTGGTGCGAGCCTGCAAAGCCAACGGCGTCACCGATCTGCTGGTCGTTCACGAGCATCGGGGCA
CACCTGTGGGGCTCATCGTCAGCCACCTGCCCTTTGGTCCTACTGCCTACTTCACGCTGTGCAATGTGGTCATGC
GGCATGACATCCCAGACCTGGGCACCATGTCGGAGGCCAAGCCCCACCTCATCACACACGGCTTCTCCTCCCGCC
TGGGCAAGCGGGTCTCTGACATCCTCCGATACCTATTTCCCGTGCCCAAAGATGACAGCCACCGGGTCATCACCT
TCGCAAACCAGGACGACTACATATCATTCCGGCACCATGTGTATAAGAAGACAGACCACCGCAACGTGGAGCTCA
CTGAGGTCGGGCCCCGCTTTGAGCTGAAGCTGTACATGATCCGTCTGGGCACGCTGGAGCAGGAGGCCACAGCAG
ACGTGGAGTGGCGCTGGCACCCTTACACCAATACCGCACGCAAGAGAGTCTTCCTGAGCACCGAG<u>TGA</u>GCACACT
CACCACTCAGTCAGGACATGGACTTGGAACTCAGGATGGGGCTGTCATAGACAGACCCACCAGTAGGAACTGTCA
CAGAATGGCCTGCTGAACTGGGATGTGGAACTGTGGCGGGTGGAGAGGTCTGAATAAACCGTCTGTGTCATGGCA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 879

MLRREARLRREYLYRKAREEAQRSAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGVTSHVDDEY
RWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGAQRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLI
VSHLPFGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRVSDILRYLFPVPKDDSHRVITFANQDD
YISFRHHVYKKTDHRNVELTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVFLSTE

FIGURE 880

GGCGGCGGCAGCGGGTTCGGTTGCGCGTGACGCACGGGGTGGGAGCGGAGCCCAGGCCGGGAGCAGGCGCCTCTG
CCAGAGACCATGGGGAACGTGTTGGCCGCCAGGTCGCCGCCCGCAGGGCCGCCACCGCCGCCTGCGCCGGCCCTC
GTGGAGCTGCCGCCACCTCCGCCCTCGCCGCCGGGCTTCACGCTGCCGCCGCTGGGAGGCGGCCTGGGCGCCGGC
ACCAGTACGAGTCGAGGTTCGGAACTGACCCCCGGGGCTGCAACTGCCAGCGCCTCAGGGGCCGCCGAGGATGGG
GCCTGCGGCTGCCTGCCCAACCCGGGCACATTCGGGGAGTGCCACCGGAAGTGCAAGGAGCTGTTTCCCATTCAG
ATGGAGGGTGTCAAGCTCATAGTCAACAAAGGGTTGAGTAACCATTTCCAGGTGAACCACACAGTAGCCCTCAGC
ACAATCAGGGAGTCCAGCTACCACTTCGGGGTCACGTATGTGGGGACAAAGCAGCTGAGTCCCACAGAGGCGTTC
CTTGTATTGGTGGGTGACATGGACAACAGCGGCAGTCTCAACGCTCAGGTCATTCACCAGCTGGGCCCCCGCCTC
AGGTCCAAGATGGCCATCCAGACCCAGCAGTCGAAGTTTGTGAACTGGCAGGTGGACGGGGAGTATCGGGGCTCT
GACTCACAGCAGCCGTAACCCTGGGGAAACCCAGACGTCCTCGTGGGTTCAGGAATCCTCGTAGCCCACTACCTC
CAGAGCATCACGCCTTGCCTGGCCCTGGGCAGAATGCTGGTCTACCACCAGCAGCCTGGGGAGGAGGGCACTGTC
ATGTCTCTAGCTGGGAAATACACATTGAACAACTGGTTGGCAACGGTAACGTTGGGCCAGGCGGGCATGCACGCA
ACATACTACCACAAAGCCAGTGACCAGCTGCAGGTGGGTGTGGAGTTTGAGGCCAGCACAAGGATGCAGGACACC
AGCGTCTCCTTCGGGTACCAGCTGGACCTGCCCAAGGCCAAAGGCTCTGTGGATAGCAACTGGATCGTGTGTGCC
ACGTTGGAGAAGAAGCTCCCGCCCCTGCCCCTGACACTGGCCCTTGGGGCCTTCCTGAATCAC

FIGURE 881

AAGAACTGGCCTGTACATTTTCAAGGAATTCTTGAGAGGTTCTTGGAGAGATTCTGGGAGCCAAACACTCCATTG
GGATCCTAGCTGTTTTAGAGAACAACTTGTAATGGAGCCTTCATCTCTTGAGCTGCCGGCTGACACAGTGCAGCG
CATTGCGGCTGAACTCAAATGCCACCCAACGGATGAGAGGGTGGCTCTCCACCTAGATGAGGAAGATAAGCTGAG
GCACTTCAGGGAGTGCTTTTATATTCCCAAAATACAGGATCTGCCTCCAGTTGATTTATCATTAGTGAATAAAGA
TGAAAATGCCATCTATTTCTTGGGAAATTCTCTTGGCCTTCAACCAAAAATGGTTAAAACATATCTTGAAGAAGA
ACTAGATAAGTGGGCCAAAATAGCAGCCTATGGTCATGAAGTGGGGAAGCGTCCTTGGATTACAGGAGATGAGAG
TATTGTAGGCCTTATGAAGGACATTGTAGGAGCCAATGAGAAAGAAATAGCCCTAATGAATGCTTTGACTGTAAA
TTTACATCTTCTAATGTTATCATTTTTAAGCCTACGCCAAAACGATATAAAATTCTTCTAGAAGCCAAAGCCTT
CCCTTCTGATCATTATGCTATTGAGTCACAACTACAACTTCACGGACTTAACATTGAAGAAAGTATGCGGATGAT
AAAGCCAAGAGAGGGGGAAGAAACCTTAAGAATAGAGGATATCCTTGAAGTAATTGAGAAGGAAGGAGACTCAAT
TGCAGTGATCCTGTTCAGTGGGGTGCATTTTTACACTGGACAGCACTTTAATATTCCTGCCATCACAAAAGCTGG
ACAAGCGAAGGGTTGTTATGTTGGCTTTGATCTAGCACATGCAGTTGGAAATGTTGAACTCTACTTACATGACTG
GGGAGTTGATTTTGCCTGCTGGTGTTCCTACAAGTATTTAAATGCAGGAGCAGGAGGAATTGCTGGTGCCTTCAT
TCATGAAAAGCATGCCCATACGATTAAACCTGCATTAGTGGGATGGTTTGGCCATGAACTCAGCACCAGATTTAA
GATGGATAACAAACTGCAGTTAATCCCTGGGGTCTGTGGATTCCGAATTTCAAATCCTCCCATTTTGTTGGTCTG
TTCCTTGCATGCTAGTTTAGAGATCTTTAAGCAAGCGACAATGAAGGCATTGCGGAAAAAATCTGTTTTGCTAAC
TGGCTATCTGGAATACCTGATCAAGCATAACTATGGCAAAGATAAAGCAGCAACCAAGAAACCAGTTGTGAACAT
AATTACTCCGTCTCATGTAGAGGAGCGGGGGTGCCAGCTAACAATAACATTTTCTGTTCCAAACAAAGATGTTTT
CCAAGAACTAGAAAAAAGAGGAGTGGTTTGTGACAAGCGGAATCCAAATGGCATTCGAGTGGCTCCAGTTCCTCT
CTATAATTCTTTCCATGATGTTTATAAATTTACCAATCTGCTCACTTCTATACTTGACTCTGCAGAAACAAAAAA
TTAGCAGTGTTTCTAGAACAACTTAAGCAAATTATACTGAAAGCTGCTGTGGTTATTTCAGTATTATTCGATTT
TTAATTATTGAAAGTATGTCACCATTGACCACATGTAACTAACAATAAATAATATACCTTAC

FIGURE 882

MEPSSLELPADTVQRIAAELKCHPTDERVALHLDEEDKLRHFRECFYIPKIQDLPPVDLSLVNKDENAIYFLGNS
LGLQPKMVKTYLEEELDKWAKIAAYGHEVGKRPWITGDESIVGLMKDIVGANEKEIALMNALTVNLHLLMLSFFK
PTPKRYKILLEAKAFPSDHYAIESQLQLHGLNIEESMRMIKPREGEETLRIEDILEVIEKEGDSIAVILFSGVHF
YTGQHFNIPAITKAGQAKGCYVGFDLAHAVGNVELYLHDWGVDFACWCSYKYLNAGAGGIAGAFIHEKHAHTIKP
ALVGWFGHELSTRFKMDNKLQLIPGVCGFRISNPPILLVCSLHASLEIFKQATMKALRKKSVLLTGYLEYLIKHN
YGKDKAATKKPVVNIITPSHVEERGCQLTITFSVPNKDVFQELEKRGVVCDKRNPNGIRVAPVPLYNSFHDVYKF
TNLLTSILDSAETKN

FIGURE 883

GTGTACGGTCCGCAGCGGCAGGTGAAGTCTAGCAGAGGACGCGGCCAGGCGATTCGGTGAAGCGATTCCTGCAGG
CGTTGGTTCCCCTCTTTGACCTGGTAAATGCAGGCTTTTATGCGAGAGGATTTGAATTTGTTGAAATGAGCAGTC
GTAAATCAAAGAGTAACAGCTTAATTCACACAGAGTGCCTTTCACAGGTACAAAGAATTTTACGTGAAAGATTTT
GTCGTCAGAGTCCACATAGTAACCTATTTGGAGTGCAAGTACAATACAAACACTTAAGTGAGCTGCTGAAAAGAA
CTGCTCTCCATGGAGAGAGTAACTCTGTCCTTATTATCGGACCCCGAGGATCAGGAAAAACTATGTTAATAAATC
ATGCTTTGAAAGAACTCATGGAAATAGAAGAAGTGAGTGAAAATGTATTACAAGTTCACTTAAATGGACTGCTGC
AGATCAATGACAAAATCGCCCTAAAGGAAATCACAAGGCAGTTAAATCTGGAAAATGTAGTTGGAGATAAAGTTT
TTGGAAGCTTTGCTGAAAACCTTTCATTTCTTCTGGAAGCTTTAAAAAAAGGTGACCGAACTAGCAGTTGCCCAG
TGATCTTCATATTAGATGAATTTGATCTTTTTGCTCATCATAAAAACCAAACACTTCTCTATAATCTTTTTGACA
TTTCTCAGTCTGCACAGACCCCAATAGCAGTTATTGGTCTTACATGTAGATTGGATATTTTGGAACTCTTAGAAA
AAAGAGTGAAGTCAAGATTTTCTCACCGGCAGATACACTTAATGAATTCATTTGGTTTTCCACAGTATGTTAAAA
TATTTAAAGAACAGTTATCTCTACCTGCAGAGTTTCCAGACAAGGTTTTTGCTGAGAAGTGGAATGAAAATGTTC
AGTATCTCTCAGAAGATAGAAGTGTGCAAGAAGTACTACAGAAGCATTTCAATATCAGCAAAAACCTGCGGTCAT
TACACATGCTATTGATGCTTGCTTTAAATCGAGTAACAGCATCGCACCCATTTATGACTGCCGTAGATCTAATGG
AAGCAAGCCAACTGTGTAGCATGGACTCGAAAGCAAATATTGTACATGGTCTATCAGTCTTGGAAATCTGTCTTA
TAATAGCAATGAAACATTTAAATGACATCTATGAGGAAGAGCCATTTAATTTTCAAATGGTCTATAATGAGTTTC
AGAAGTTTGTTCAAAGGAAAGCACATTCCGTTTATAATTTTGAAAAACCTGTTGTCATGAAGGCTTTTGAACACT
TGCAGCAATTAGAATTAATAAAGCCCATGGAAAGAACTTCAGGAAATTCACAGAGAGAGTACCAGCTGATGAAAC
TGCTTTTGGATAATACTCAAATTATGAATGCTCTGCAGAAATATCCCAACTGTCCTACAGATGTGAGGCAGTGGG
CAACATCCTCACTAAGCTGGTTATGAATATAACCAGTGACTTCAACTTTGGCATTTCATTCATACTTCTGTAGAG
AACGGAAAACTATTGTCCATTAACATGATATGCTAAACATTCTATAAACATTCTTGTATTTATGTGAGACTTGCC
CATCTACTGTCTTGGCTGTGTCTTGCCTTTTAATCATGAACAGTTACATGATTTATAATTTCACTGATTGAGATT
ACTTTGTAAGTAGCTGTTCAGAAGAATAAAATATGACTGTTTTAGGGACTAGACCATGTGCTTTTTTAACACTTA
TATATATAATGGTCTATTTGAAGAGCTCACTTCAACCTAACAGCTAGATGTCTTTACAAACCTTAAACCAAAGGA
GTAAAAAAAACAATGGTAAGCACTGAAGTATAATAAGTAACCTTTGGTACAGCAGGTTTGCTGCAGTGTTTTTTT
CTGTCCACATGCAAATTTTGGATTCTATCCCAGACCCAGGTTTTCTAGTTCAGAAGACTAACCAGCTTAGTCAGA
AGATGGTTCCATGGAAGAAAAAGGCCAAGGAGTTTGAAGATTTTTCTTCTAGACATCTCAAAATGTGGTACTCAT
ACCATCCACATCAGAATCCCTTGTAGGATTTTCTAAAATTACAGATTGTTGAGCCTACCATAGGTCAAAAGGACT
GGAATTTTCCTTCTTAACAAGTATAGTCATGGCACCACGTAACATTTTGGTCAATGACATTGTATAAAGGGTGGT
CTCATAAGATTATACCATATTTTACTGTACCTTTTCTATGTCTAAATATACAAATGTTTTACCATTG

FIGURE 884

MSSRKSKSNSLIHTECLSQVQRILRERFCRQSPHSNLFGVQVQYKHLSELLKRTALHGESNSVLIIGPRGSGKTM
LINHALKELMEIEEVSENVLQVHLNGLLQINDKIALKEITRQLNLENVVGDKVFGSFAENLSFLLEALKKGDRTS
SCPVIFILDEFDLFAHHKNQTLLYNLFDISQSAQTPIAVIGLTCRLDILELLEKRVKSRFSHRQIHLMNSFGFPQ
YVKIFKEQLSLPAEFPDKVFAEKWNENVQYLSEDRSVQEVLQKHFNISKNLRSLHMLLMLALNRVTASHPFMTAV
DLMEASQLCSMDSKANIVHGLSVLEICLIIAMKHLNDIYEEEPFNFQMVYNEFQKFVQRKAHSVYNFEKPVVMKA
FEHLQQLELIKPMERTSGNSQREYQLMKLLLDNTQIMNALQKYPNCPTDVRQWATSSLSWL

FIGURE 885

ATTCGGCACCGCAGCGTAGGTGCTACCACCGCTGCCGTCGCCGCCGCCATTTTGATGGCAGGAAGAGTCCGGTTC
TGGGACAGCTGGAGACAGTGGTGGTGACTGAAATAACTTTACCAAAGGAAAGCTATTTTGCGAACTATCTTCTCC
AGCGGAG**ATG**GCCAATGTGCTTTGTAACAGAGCCAGACTGGTTTCCTATCTCCCAGGATTTTGCTCTTTAGTTAA
AAGGGTTGTCAATCCCAAAGCCTTTTCGACTGCAGGATCATCAGGTTCGGATGAGTCTCATGTGGCTGCTGCACC
TCCAGATATATGCTCTCGAACAGTGTGGCCTGATGAAACTATGGGACCCTTTGGACCTCAAGATCAGAGGTTCCA
GCTTCCTGGGAACATAGGTTTTGATTGTCACCTCAATGGGACTGCTTCACAGAAGAAAAGCCTGGTTCATAAAAC
TTTGCCTGATGTTCTAGCAGAACCTTTATCAAGTGAAAGACATGAGTTTGTGATGGCACAATATGTGAATGAATT
TCAGGGTAATGATGCACCTGTTGAACAAGAAATTAACAGTGCAGAAACTTACTTTGAAAGTGCCAGAGTAGAGTG
TGCAATACAAACATGTCCAGAATTGCTGCGAAAAGATTTTGAATCACTGTTTCCAGAAGTAGCTAATGGCAAACT
AATGATTCTGACTGTAACACAAAAAACTAAGAATGATATGACTGTTTGGAGTGAAGAAGTAGAAATTGAAAGAGA
AGTGCTCTTAGAAAAGTTCATCAATGGTGCTAAGGAAATTTGCTATGCTCTTCGAGCTGAGGGTTATTGGGCTGA
CTTTATTGACCCATCATCTGGTTTGGCATTTTTTGGACCATATACAAACAACACTCTTTTTGAAACTGATGAACG
CTACCGACATTTAGGATTCTCTGTTGATGACCTTGGATGCTGTAAAGTGATTCGTCATAGTCTCTGGGGTACCCA
TGTAGTTGTAGGGAGTATCTTCACTAATGCAACACCAGACAGCCATATTATGAAGAAATTAAGTGGAAAT**TAG**CA
GAAATATCCATTCATTTGCTGTACTATTTGTATGTAATATTTGGGTTGATCTATAAACACTGTCAGACTAAAGTT
TTTAAAATATACTTATTTCTAAGTATTTATTTCAGCATTTATGAATTTGCAACATTGGCAAGTGATTTGGGATTT
TAAAATTGCAAATGTTCATTTATTCATATCATTGAATACACGTTGAACACATCCACATTGTATAGGATGTGGTAA
TTAGCTTGTAACCAGGGTATGATCTGCTATTGTTATTTCTCCTCTTTATTGGAAAAAGGCCTCAGTTTTAATTAT
TTTCTTCCCAAAATAAATCACACATTTGGTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 886

MANVLCNRARLVSYLPGFCSLVKRVVNPKAFSTAGSSGSDESHVAAAPPDICSRTVWPDETMGPFGPQDQRFQLP
GNIGFDCHLNGTASQKKSLVHKTLPDVLAEPLSSERHEFVMAQYVNEFQGNDAPVEQEINSAETYFESARVECAI
QTCPELLRKDFESLFPEVANGKLMILTVTQKTKNDMTVWSEEVEIEREVLLEKFINGAKEICYALRAEGYWADFI
DPSSGLAFFGPYTNNTLFETDERYRHLGFSVDDLGCCKVIRHSLWGTHVVVGSIFTNATPDSHIMKKLSGN

FIGURE 887

TATCGCAAGCAGCAGTCTCTGGTCCCAGCCCACCCC**ATG**GCCCCTCCCAGTCCCAGCACCACCAGCAGTAATAAC
AACAGTAGCAGCAGTAGCAACTCAGGATGGGATCAGCTCAGCAAAACGAACCTCTATATCCGAGGACTGCCTCCC
CACACCACCGACCAGGACCTGGTGAAGCTCTGTCAACCATATGGGAAAATAGTCTCCACAAAGGCAATTTTGGAT
AAGACAACGAACAAATGCAAAGGTTATGGTTTTGTCGACTTTGACAGCCCTGCAGCAGCTCAAAAAGCTGTGTCT
GCCCTGAAGGCCAGTGGGGTTCAAGCTCAAATGGCAAAGCAACAGGAACAAGATCCTACCAACCTCTACATTTCT
AATTTGCCACTCTCCATGGATGAGCAAGAACTAGAAAATATGCTCAAACCATTTGGACAAGTTATTTCTACAAGG
ATACTACGTGATTCCAGTGGTACAAGTCGTGGTGTTGGCTTTGCTAGGATGGAATCAACAGAAAAATGTGAAGCT
GTTATTGGTCATTTTAATGGAAAATTTATTAAGACACCACCAGGAGTTTCTGCCCCCACAGAACCTTTATTGTGT
AAGTTTGCTGATGGAGGACAGAAAAAGAGACAGAACCCAAACAAATACATCCCTAATGGAAGACCATGGCATAGA
GAAGGAGAGGTGAGACTTGCTGGAATGACACTTACTTACGACCCAACTACAGCTGCTATACAGAACGGATTTTAT
CCTTCACCATACAGTATTGCTACAAACCGAATGATCACTCAAACTTCTATTACACCCTATATTGCATCTCCTGTA
TCTGCCTACCAGGTGCAAAGTCCTTCGTGGATGCAACCTCAACCATATATTCTACAGCACCCTGGTGCCGTGTTA
ACTCCCTCAATGGAGCACACCATGTCACTACAGCCCGCATCAATGATCAGCCCTCTGGCCCAGCAGATGAGTCAT
CTGTCACTAGGCAGCACCGGAACATACATGCCTGCAACGTCAGCTATGCAAGGAGCCTACTTGCCACAGTATGCA
CATATGCAGACGACAGCGGTTCCTGTTGAGGAGGCAAGTGGTCAACAGCAGGTGGCTGTCGAGACGTCTAATGAC
CATTCTCCATATACCTTTCAACCTAATAAG**TAA**CTGTGAGATGTACAGAAAGGTGTTCTTACATGAAGAAGGGTG
TGAAGGCTGAACAATCATGGATTTTTCTGATCAATTGTGCTTTAGGAAATTATTGACAGTTTTGCACAGGTTCTT
GAAAACGTTATTTATAATGAAATCAACTAAAACTATTTTTGCTATAAGTTCTATAAGGTGCATAAAACCCTTAAA
TTCATCTAGTAGCTGTTCCCCCGAACAGGTTTATTTAGTAAAAAAAAAAAA

FIGURE 888

MAPPSPSTTSSNNNSSSSSSNSGWDQLSKTNLYIRGLPPHTTDQDLVKLCQPYGKIVSTKAILDKTTNKCKGYGFV
DFDSPAAAQKAVSALKASGVQAQMAKQQEQDPTNLYISNLPLSMDEQELENMLKPFGQVISTRILRDSSGTSRGV
GFARMESTEKCEAVIGHFNGKFIKTPPGVSAPTEPLLCKFADGGQKKRQNPNKYIPNGRPWHREGEVRLAGMTLT
YDPTTAAIQNGFYPSPYSIATNRMITQTSITPYIASPVSAYQVQSPSWMQPQPYILQHPGAVLTPSMEHTMSLQP
ASMISPLAQQMSHLSLGSTGTYMPATSAMQGAYLPQYAHMQTTAVPVEEASGQQQVAVETSNDHSPYTFQPNK

FIGURE 889

AGACTTGGAAACCCCAAAGTGTCCGCGACCCTGCACGGCAGCTCCCTTCCAGCTTCATGGGCAAAGTGTGGAAAC
AGCAGATGTACCCTCAGTACGCCACCTACTATTACCCCCAGTATCTGCAAGCCAAGTTTGGAAGGCATTCGGGAA
TACCAAGTGAAAAGGAAGAGTGAAGAACAGAAAAATGTTAGTGGGATGGCAAACACTGTGAACATTGCTGTTTCT
AGTGGGCCAGAAAAATCAGTCTCTGGTCCCAGCCCACCCC**ATG**GCCCCTCCCAGTCCCAGCACCACCAGCAGTAA
TAACAACAGTAGCAGCAGTAGCAACTCAGGATGGGATCAGCTCAGCAAAACGAACCTCTATATCCGAGGACTGCC
TCCCCACACCACCGACCAGGACCTGGTGAAGCTCTGTCAACCATATGGGAAAATAGTCTCCACAAAGGCAATTTT
GGATAAGACAACGAACAAATGCAAAGGTTATGGTTTTGTCGACTTTGACAGCCCTGCAGCAGCTCAAAAAGCTGT
GTCTGCCCTGAAGGCCAGTGGGGTTCAAGCTCAAATGGCAAAGCAACAGGAACAAGATCCTACCAACCTCTACAT
TTCTAATTTGCCACTCTCCATGGATGAGCAAGAACTAGAAAATATGCTCAAACCATTTGGACAAGTTATTTCTAC
AAGGATACTACGTGATTCCAGTGGTACAAGTCGTGGTGTTGGCTTTGCTAGGATGGAATCAACAGAAAAATGTGA
AGCTGTTATTGGTCATTTTAATGGAAAATTTATTAAGACACCACCAGGAGTTTCTGCCCCCACAGAACCTTTATT
GTGTAAGTTTGCTGATGGAGGACAGAAAAAGAGACAGAACCCAAACAAATACATCCCTAATGGAAGACCATGGCA
TAGAGAAGGAGAGGTGAGACTTGCTGGAATGACACTTACTTACGACCCAACTACAGCTGCTATACAGAACGGATT
TTATCCTTCACCATACAGTATTGCTACAAACCGAATGATCACTCAAACTTCTATTACACCCTATATTGCATCTCC
TGTATCTGCCTACCAGGTGGCAAAGGAAACCAGAGAAAACAAGTATCGGGGCTCTGCTATCAAGGTGCAAAGTCC
TTCGTGGATGCAACCTCAACCATATATTCTACAGCACCCTGGTGCCGTGTTAACTCCCTCAATGGAGCACACCAT
GTCACTACAGCCCGCATCAATGATCAGCCCTCTGGCCCAGCAGATGAGTCATCTGTCACTAGGCAGCACCGGAAC
ATACATGCCTGCAACGTCAGCTATGCAAGGAGCCTACTTGCCACAGTATGCACATATGCAGACGACAGCGGTTCC
TGTTGAGGAGGCAAGTGGTCAACAGCAGGTGGCTGTCGAGACGTCTAATGACCATTCTCCATATACCTTTCAACC
TAATAAG**TAA**CTGTGAGATGTACAGAAAGGTGTTCTTACATGAAGAAGGGTGTGAAGGCTGAACAATCATGGATT
TTTCTGATCAATTGTGCTTTAGGAAATTATTGACAGTTTTGCACAGGTTCTTGAAAACGTTATTTATAATGAAAT
CAACTAAAACTATTTTTGCTATAAGTTCTATAAGGTGCATAAAACCCTTAAATTCATCTAGTAGCTGTTCCCCCG
AACAGGTTTATTTTAGTAAAAAAAAAAAA

FIGURE 890

MAPPSPSTTSSNNNSSSSSNSGWDQLSKTNLYIRGLPPHTTDQDLVKLCQPYGKIVSTKAILDKTTNKCKGYGFV
DFDSPAAAQKAVSALKASGVQAQMAKQQEQDPTNLYISNLPLSMDEQELENMLKPFGQVISTRILRDSSGTSRGV
GFARMESTEKCEAVIGHFNGKFIKTPPGVSAPTEPLLCKFADGGQKKRQNPNKYIPNGRPWHREGEVRLAGMTLT
YDPTTAAIQNGFYPSPYSIATNRMITQTSITPYIASPVSAYQVAKETRENKYRGSAIKVQSPSWMQPQPYILQHP
GAVLTPSMEHTMSLQPASMISPLAQQMSHLSLGSTGTYMPATSAMQGAYLPQYAHMQTTAVPVEEASGQQQVAVE
TSNDHSPYTFQPNK

FIGURE 891

GGCTAATGTAACATACTCTACCACTTGGTCTGAAGCCCAGCAGTATCTGATGGATAATCCAACTTTTGCAGAAGA
TGAGGAGTTACAAAATATGGACAAAGAAGATGCATTAATTTGCTTTGAAGAACACATTCGGGCTTTAGAAAAGGA
GGAAGAAGAAGAAAAACAGAAGAGTTTGCTGAGAGAAAGGAGACGACAGCGAAAAAATAGGGAATCTTTCCAGAT
ATTTTTAGATGAATTACATGAACATGGACAACTGCATTCTATGTCATCTTGGATGGAATTGTATCCAACTATTAG
TTCTGATATTAGATTCACTAATATGCTTGGTCAGCCTGGATCAACTGCACTTGATCTTTTCAAGTTTTATGTTGA
GGATCTTAAAGCACGTTATCATGACGAGAAGAAGATAATAAAAGACATTCTAAAGGATAAAGGATTTGTAGTTGA
AGTAAACACTACTTTTGAAGATTTTGTGGCGATAATCAGTTCAACTAAAAGATCAACTACATTAG<u>ATG</u>CTGGAAA
TATCAAATTGGCTTTCAATATTACTAGAAAAGGCAGAAGCCCGTGAACGTGAAAGAGAAAAAGAAGAGGCTCGGA
AGATGAAACGAAAAGAATCTGCATTTAAGAGTATGTTAAAACAAGCTGCTCCTCCGATAGAATTGGATGCTGTCT
GGGAAGATATCCGTGAGAGATTTGTAAAAGAGCCAGCATTTGAGGACATAACTCTAGAATCTGAAAGAAAACGAA
TATTTAAAGATTTTATGCATGTGCTTGAGCATGAATGTCAGCATCATCATTCAAAGAACAAGAAACATTCTAAGA
AATCTAAAAAACATCATAGGAAACGTTCCCGCTCTCGATCGGGGTCAGATTCAGATGATGATGATAGCCATTCAA
AGAAAAAAAGACAGCGATCAGAGTCTCGTTCTGCTTCAGAACATTCTTCTAGTGCAGAGTCTGAGAGAAGTTATA
AAAAGTCAAAAAAGCATAAGAAGAAAAGTAAGAAGAGGAGACATAAATCTGACTCTCCAGAATCCGATGCTGAGC
GAGAGAAGGATAAAAAAGAAAAAGATCGGGAAAGTGAAAAAGACAGAACTAGACAAAGATCAGAATCAAAACACA
AATCGCCTAAGAAAAAGACTGGAAAGGATTCTGGTAATTGGGATACTTCTGGCAGCGAACTGAGTGAAGGGGAAT
TGGAAAAGCGCAGAAGAACCCTTTTGGAGCAACTGGATGATGATCAA<u>TAA</u>ATTATACCAAATATATGTTTACAGT
ATGATTTAAAGTCTGATTCAGACCAGGGACTCTATTTTAAGTTCAACTGAAATAACACTGGGTTTTAATTATATC
ACAGGAAAAAAAAAGTGCATTTAAGTATTGTTATCGTGGACTTTATAAAAGCAAAGGAAATTGAAAGTAACTTTT
GATTCTGTATCAAGAATCATATTTTCATACAGTCATAACTGTCTTTCTGTGACCCTTTCACAGGGCACTGTAGGA
TGGATTAAAGGTGGCAATTTACTGATAACTGCAGATGTCTCTACTTTGTTCTAAAATCTAAGTCATGAGGTGATT
TGATTTACTTTATAGAAGCTGGATTTTGAAGATCTAATGAAAAATTTTTTGATAATATAGTAGTACAAAAAAAGC
ACCAGCAACTGATAAAAATTGCTTTTTTGTGCGCTACCCAACTGGTTAAAGCCAATGTGATCTTTTATGGTGAAA
CTCCTAAGAAACAGGTGGTTTTGCTGGAAACTTGGTAGACCCTTAATTATAGTGGTGCTAATGAGCACTACTGTA
ATATAAAGCCACCATTATTTTTTATCAAACATCTGAATACATTTTACAAAGGCTATTGTGAGGCATTATTTTGA
GCATCTATTTTGAGGTGATGTTTAAAAAAACTTTAACATCAAATCAAATTGTAAATTAATTTAAATATATTGCCT
TAAGGACCTACTAAAGAATGTGCCACCAGACTTTAAGTGATAGTTGCAATATCCTTGTCTAAAAAAAAAAAAAAA
GTTGACTTAAACATTTTCTTTAACAGTTGTCTTTTTTTTCTAAATTCAGTCTTTCTCTTGCTTTTTTTTCCCTGC
TATTGAGGAAGTATTTTGCCTTCCCTACTCACTGAGAAGTATTGACTTCGTGGTACACATTCTAAAGCATTTCTG
ATTTGAATATTTTTGTACATTTTTATCAATTATTAAACCTTCTCTTCTAGTG

FIGURE 892

MLEISNWLSILLEKAEARERERЕKEEARKMKRKESAFKSMLKQAAPPIELDAVWEDIRERFVKEPAFEDITLESE
RKRIFKDFMHVLEHECQHHHSKNKKHSKKSKKHHRKRSRSRSGSDSDDDDSHSKKKRQRSESRSASEHSSSAESE
RSYKKSKKHKKKSKKRRHKSDSPESDAEREKDKKEKDRESEKDRTRQRSESKHKSPKKKTGKDSGNWDTSGSELS
EGELEKRRRTLLEQLDDDQ

FIGURE 893

CCAGCACGCGGCCGCTCTGGCCCAGGGAAGTCCCTGTCCTTACCTTCAGCAGGAGCCGGTTCCCTGTGTGTGTGT
CCGCTCGCCCTCTGCTCCGTCCTGCGGCTGCCCACTGCCCTCCTACGGTCCACCATGGCCCTGCTGCACTCCGGC
CGCGTCCTCCCCGGGATCGCCGCCGCCTTCCACCCGGGCCTCGCCGCCGCGGCCTCTGCCAGAGCCAGCTCCTGG
TGGACCCATGTGGAAATGGGACCTCCAGATCCCATTCTGGGAGTCACTGAAGCCTTTAAGAGGGACACCAATAGC
AAAAAGATGAATCTGGGAGTTGGTGCCTACCGGGATGATAACGGAAAGCCTTACGTGCTGCCTAGCGTCCGCAAG
GCAGAGGCCCAGATTGCCGCAAAAAATTTGGACAAGGAATACCTGCCCATTGGGGGACTGGCTGAATTTTGCAAG
GCATCTGCAGAACTAGCCCTGGGTGAGAACAGCGAAGTCTTGAAGAGTGGCCGGTTTGTCACTGTGCAGACCATT
TCTGGAACTGGAGCCTTAAGGATCGGAGCCAGTTTTCTGCAAAGATTTTTAAGTTCAGCCGAGATGTCTTTCTG
CCCAAACCAACCTGGGGAAACCACACACCCATCTTCAGGGATGCTGGCATGCAGCTACAAGGTTATCGGTATTAT
GACCCCAAGACTTGCGGTTTTGACTTCACAGGCGCTGTGGAGGATATTTCAAAAATACCAGAGCAGAGTGTTCTT
CTTCTGCATGCCTGCGCCCACAATCCCACGGGAGTGGACCCGCGTCCGGAACAGTGGAAGGAAATAGCAACAGTG
GTGAAGAAAAGGAATCTCTTTGCGTTCTTTGACATGGCCTACCAAGGCTTTGCCAGTGGTGATGGTGATAAGGAT
GCCTGGGCTGTGCGCCACTTCATCGAACAGGGCATTAATGTTTGTCTCTGCCAATCATATGCCAAGAACATGGGC
TTATATGGTGAGCGTGTAGGAGCCTTCACTATGGTCTGCAAAGATGCGGATGAAGCCAAAAGGGTAGAGTCACAG
TTGAAGATCTTGATCCGTCCCATGTATTCCAACCCTCCCCTCAATGGGGCCCGGATTGCTGCTGCCATTCTGAAC
ACCCCAGATTTGCGAAAACAATGGCTGCAAGAAGTGAAAGGCATGGCTGACCGCATCATTGGCATGCGGACTCAA
CTGGTCTCCAACCTCAAGAAGGAGGGTTCCACCCACAATTGGCAACACATCACCGACCAAATTGGCATGTTCTGT
TTCACAGGGCTAAAGCCTGAACAGGTGGAGCGGCTGATCAAGGAGTTCTCCATCTACATGACAAAAGATGGCCGC
ATCTCTGTGGCAGGGGTCACCTCCAGCAACGTGGGCTACCTTGCCCATGCCATTCACCAGGTCACCAAGTAATGT
CCCTGGTGCGAGGAAACAGAGACAACCTTTCTGTCTTCAGCCTCTGCTATTGAGAGCTTCACACAGACAATGAGA
GAGGGTGGATGGTGGTGAGTGGATCATTTCTTTCAGCCACAGTGTGTAACACTCAGCATTTGAATGTTTCTCAGA
AAAGAACATGTAGTGACACAGGGCAGAGGCATCCATGGCTGGCGTCTGGAATATTAAACCAAACTCTCCCCGGTC
CTTTTTTCTCCAACTTTTCTCAAAGAGTTTACATGTGCAAGAAAGTCATCGCACCAAAAAAACCTGTCAATTATGC
CATTGCAATATTTCAGAAGCTTTAACTGAAGTGTCAGGTTCCTCGTGAGAAACAGCACACGTTAGAGGCTTTGAG
AGAAGGCCTAGTTCTGTCATGAGTAGTCGGCCTCGTGTCTGTCCTCCCATCTTGGAACAACCTTATCAACAGGCC
GCACTGCAGAAATGATGTTTTATGAAAACCAATGAGGCTGCTGCCACTCCAGCAAGGGAAATAATGCAGTTTCCT
GTCTTATTTAAGAAAAAGAGAAGGCTCTCTTTTCTCCCTTGTCATTGCCGTTCTTTTCCTTACACGCAAAGATTT
TTTAACTATTGCAGATTTTCATCCCATTCTACTGCTTGATTGACCATCAACTCCATCCTATCGAGATTTATTTAA
GAATGAAGAACATAATTTTCTGCTGATGCCGTACCCTCACCCTTTTCAGCAAAGAATAGTGGAGAGTAGGAAACT
GTACTTTATCTCGGCATCCTCTTGAATGATAGTGCAAGTTTCTCCAGTTGGGATGTTGTCTCTGCCCGGTTGGAC
CTCCTCCCTTTGTTGAATGTGGTGTGCAGCCTCTCATCTCACACTGTGAGTCCAGCGGCGCAGGGTGGTACCAGG
AAAGAGGATATTCTAGGCTTTGCGTGCTGCTAGCTGGGTTCAGGCTTCACCCACTGGAAAGAACCACCATCTGCT
CTAACCATGTAGACTTATTGCGGCCTGGTTTCTCTGTTACAATAAAATTACTGTAGACCC

FIGURE 894

GAGTGACTCCACCGCCCGGAGCAGCGGTGCAGGACGCGCGTCTCCGCCGCCCGCGGTGACTTCTGCCTGCGCTCC
TTCTCTGAACGCTCACTTCCGAGGAGACGCCGACGATGAAGACACCGTGGAAGGTTCTTCTGGGACTGCTGGGTG
CTGCTGCGCTTGTCACCATCATCACCGTGCCCGTGGTTCTGCTGAACAAAGGCACAGATGATGCTACAGCTGACA
GTCGCAAAACTTACACTCTAACTGATTACTTAAAAAATACTTATAGACTGAAGTTATACTCCTTAAGATGGATTT
CAGATCATGAATATCTCTACAAACAAGAAAATAATATCTTGGTATTCAATGCTGAATATGGAAACAGCTCAGTTT
TCTTGGAGAACAGTACATTTGATGAGTTTGGACATTCTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTA
TTCTCTTAGAATACAACTACGTGAAGCAATGGAGGCATTCCTACACAGCTTCATATGACATTTATGATTTAAATA
AAAGGCAGCTGATTACAGAAGAGAGGATTCCAAACAACACACAGTGGGTCACATGGTCACCAGTGGGTCATAAAT
TGGCATATGTTTGGAACAATGACATTTATGTTAAAATTGAACCAAATTTACCAAGTTACAGAATCACATGGACGG
GGAAAGAAGATATAATATATAATGGAATAACTGACTGGGTTTATGAAGAGGAAGTCTTCAGTGCCTACTCTGCTC
TGTGGTGGTCTCCAAACGGCACTTTTTTAGCATATGCCCAATTTAACGACACAGAAGTCCCACTTATTGAATACT
CCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAGGCAGGAGCTGTGAATC
CAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCTCAGCTCAGTCACCAATGCAACTTCCATACAAATCACTG
CTCCTGCTTCTATGTTGATAGGGGATCACTACTTGTGTGATGTGACATGGGCAACACAAGAAAGAATTTCTTTGC
AGTGGCTCAGGAGGATTCAGAACTATTCGGTCATGGATATTTGTGACTATGATGAATCCAGTGGAAGATGGAACT
GCTTAGTGGCACGGCAACACATTGAAATGAGTACTACTGGCTGGGTTGGAAGATTTAGGCCTTCAGAACCTCATT
TTACCCTTGATGGTAATAGCTTCTACAAGATCATCAGCAATGAAGAAGGTTACAGACACATTTGCTATTTCCAAA
TAGATAAAAAAGACTGCACATTTATTACAAAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCAGTGATT
ATCTATACTACATTAGTAATGAATATAAAGGAATGCCAGGAGGAAGGAATCTTTATAAAATCCAACTTAGTGACT
ATACAAAAGTGACATGCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTCAGTACTATTCTGTGTCATTCAGTAAAG
AGGCGAAGTATTATCAGCTGAGATGTTCCGGTCCTGGTCTGCCCCTCTATACTCTACACAGCAGCGTGAATGATA
AAGGGCTGAGAGTCCTGGAAGACAATTCAGCTTTGGATAAAATGCTGCAGAATGTCCAGATGCCCTCCAAAAAAC
TGGACTTCATTATTTTGAATGAAACAAAATTTTGGTATCAGATGATCTTGCCTCCTCATTTTGATAAATCCAAGA
AATATCCTCTACTATTAGATGTGTATGCAGGCCCATGTAGTCAAAAAGCAGACACTGTCTTCAGACTGAACTGGG
CCACTTACCTTGCAAGCACAGAAAACATTATAGTAGCTAGCTTTGATGGCAGAGGAAGTGGTTACCAAGGAGATA
AGATCATGCATGCAATCAACAGAAGACTGGGAACATTTGAAGTTGAAGATCAAATTGAAGCAGCCAGACAATTTT
CAAAAATGGGATTTGTGGACAACAAACGAATTGCAATTTGGGGCTGGTCATATGGAGGGTACGTAACCTCAATGG
TCCTGGGATCGGGAAGTGGCGTGTTCAAGTGTGGAATAGCCGTGGCGCCTGTATCCCGGTGGGAGTACTATGACT
CAGTGTACACAGAACGTTACATGGGTCTCCCAACTCCAGAAGACAACCTTGACCATTACAGAAATTCAACAGTCA
TGAGCAGAGCTGAAAATTTTAAACAAGTTGAGTACCTCCTTATTCATGGAACAGCAGATGATAACGTTCACTTTC
AGCAGTCAGCTCAGATCTCCAAAGCCCTGGTCGATGTTGGAGTGGATTTCCAGGCAATGTGGTATACTGATGAAG
ACCATGGAATAGCTAGCAGCACAGCACACCAACATATATATACCCACATGAGCCACTTCATAAAACAATGTTTCT
CTTTACCTTAGCACCTCAAAATACCATGCCATTTAAAGCTTATTAAAACTCATTTTTGTTTTCATTATCTCAAAA
CTGCACTGTCAAGATGATGATGATCTTTAAAATACACACTCAAATCAAGAAACTTAAGGTTACCTTTGTTCCCAA
ATTTCATACCTATCATCTTAAGTAGGGACTTCTGTCTTCACAACAGATTATTACCTTACAGAAGTTTGAATTATC
CGGTCGGGTTTTATTGTTTAAAATCATTTCTGCATCAGCTGCTGAAACAACAAATAGGAATTGTTTTTATGGAGG
CTTTGCATAGATTCCCTGAGCAGGATTTTAATCTTTTTCTAACTGGACTGGTTCAAATGTTGTTCTCTTCTTTAA
AGGGATGGCAAGATGTGGGCAGTGATGTCACTAGGGCAGGGACAGGATAAGAGGGATTAGGGAGAGAAGATAGCA
GGGCATGGCTGGGAACCCAAGTCCAAGCATACCAACACGAGCAGGCTACTGTCAGCTCCCCTCGGAGAAGAGCTG
TTCACAGCCAGACTGGCACAGTTTTCTGAGAAAGACTATTCAAACAGTCTCAGGAAATCAAATATGCAAAGCACT
GACTTCTAAGTAAAACCACAGCAGTTGAAAAGACTCCAAAGAAATGTAAGGGAAACTGCCAGCAACGCAGGCCCC
CAGGTGCCAGTTATGGCTATAGGTGCTACAAAAACACAGCAAGGGTGATGGGAAAGCATTGTAAATGTGCTTTTA
AAAAAAAATACTGATGTTCCTAGTGAAAGAGGCAGCTTGAAACTGAGATGTGAACACATCAGCTTGCCCTGTTAA
AAGATGAAAATATTTGTATCACAAATCTTAACTTGAAGGAGTCCTTGCATCAATTTTTCTTATTTCATTTCTTTG
AGTGTCTTAATTAAAAGAATATTTTAACTTCCTTGGACTCATTTTAAAAAATGGAACATAAAATACAATGTTATG
TATTATTATTCCCATTCTACATACTATGGAATTTCTCCCAGTCATTTAATAAATGTGCCTTCATTTTTTC

FIGURE 895

MKTPWKVLLGLLGAAALVTIITVPVVLLNKGTDDATADSRKTYTLTDYLKNTYRLKLYSLRWISDHEYLYKQENN
ILVFNAEYGNSSVFLENSTFDEFGHSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPN
NTQWVTWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEEVFSAYSALWWSPNGTFLAY
AQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSSVTNATSIQITAPASMLIGDHYL
CDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWNCLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKII
SNEEGYRHICYFQIDKKDCTFITKGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELN
PERCQYYSVSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDFIILNETKFW
YQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASFDGRGSGYQGDKIMHAINRRLGT
FEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGYVTSMVLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPT
PEDNLDHYRNSTVMSRAENFKQVEYLLIHGTADDNVHFQQSAQISKALVDVGVDFQAMWYTDEDHGIASSTAHQH
IYTHMSHFIKQCFSLP

FIGURE 896

GTTTGAAATCGGAAAGTTGGCGGGGCTGCGGGAGCTGAGCCTAGAGTCCGGCTGTTGGCTAGAGTGGGCGCGGAT
CTGGTGTGGGGAAGGCGGCGGGACTCAGGCCTGCCTGCGAAGCATTGTCCTACATA<u>ATG</u>GTAGAGGACGAACTGG
CACTTTTCGATAAAAGCATAAATGAATTTTGGAATAAATTCAAAAGTACGGACACCTCCTGTCAGATGGCGGGAC
TAAGAGATACCTACAAGGATTCCATCAAAGCATTTGCAGAAAAGCTGTCTGTGAAATTAAAGGAAGAAGAACGAA
TGGTTGAGATGTTTCTGGAATATCAAAATCAGATCAGCAGGCAAAATAAGCTCATTCAAGAAAAAAAGGATAACT
TGTTAAAATTGATTGCTGAAGTAAAAGGCAAAAAGCAGGAATTGGAAGTACTGACTGCAAATATCCAGGATCTTA
AGGAAGAATATTCTAGGAAGAAGGAAACTATTTCTACTGCTAATAAAGCGAATGCAGAGAGGTTGAAAAGGCTGC
AGAAATCTGCAGACTTGTATAAAGATCGACTTGGACTAGAAATTCGAAAAATTTATGGTGAGAAATTGCAGTTTA
TTTTCACTAATATTGACCCTAAGAATCCTGAGAGCCCATTTATGTTTTCCTTACATCTCAATGAAGCAAGGGACT
ATGAAGTGTCAGATAGTGCCCCTCATCTTGAGGGCCTAGCAGAATTTCAAGAGAATGTAAGGAAGACCAACAATT
TTTCAGCTTTTCTTGCCAATGTTCGGAAAGCTTTTACTGCCACGGTTTATAAT**<u>TAA</u>**CATACAAATAGTGTATATA
AAAACGGTTTATTTTTCTTCTCTATTACATATCTCTTTTTTTTCTTGTTTTTATTATTACTATACTTTAAGTTTT
AGGGTACATGTGCACAATGTGCAGGTTTGTTACATATGTATACATGTGCCATATTGGTGTGCTGCACCCATTAAC
TCGTCATTTCATTAGGTATATCTCCTAATGCTATCCCTCCCCCCTCCCCCAACCCACAACAGTCCCCGTTGTGTG
ATGTTCCCCTTCCTGTGTCCATGTGTTCTCATTGTTCAATTCCCACCTAGGAGTGAGAATATGTGGTGTTTGGTT
TTTTGTCCTTTCGATAGTTTGCTGAGAATGATGGTTTCCAGCTTCATCCATGTTCCTACAAAGGACATGAACTCA
TCCTTTTTTATGGCTGCATAGTATTCCATGGTGTATATGTGCCACATTTTCTTAATCCAGTCTATCATTGTTGGA
CATTTGGGTTGGTTCCAAGTCTTTGCTATTGTGAATAGTGCCGAAATAAACATACGTGTGCATGTGTCTCCAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 897

MVEDELALFDKSINEFWNKFKSTDTSCQMAGLRDTYKDSIKAFAEKLSVKLKEEERMVEMFLEYQNQISRQNKLI
QEKKDNLLKLIAEVKGKKQELEVLTANIQDLKEEYSRKKETISTANKANAERLKRLQKSADLYKDRLGLEIRKIY
GEKLQFIFTNIDPKNPESPFMFSLHLNEARDYEVSDSAPHLEGLAEFQENVRKTNNFSAFLANVRKAFTATVYN

FIGURE 898

AAGCACAGGCCACCACTCTGCCCTGGTCCACACAAGCTCCGGTAGCCC**ATG**GAGCCCTGGCCTCTCCTCCTGCTC
TTTAGCCTTTGCTCAGCTGGCCTCGTCCTGGGCTCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGAC
TACAGCAGCGTGGTGCGGCCAGTGGAAGACCACCGCCAGGTCGTGGAGGTCACCGTGGGCCTGCAGCTGATACAG
CTCATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGCAATGGGTGGATTACAAC
CTAAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAAATTCACATTCCTTCAGAAAAGATCTGGCGCCCAGAC
CTTGTTCTCTATAACAATGCAGATGGTGACTTTGCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGC
CACATCACGTGGACACCTCCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAA
CAGAACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCGTGGCCATCAACCCGGAAAGCGACCAG
CCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGGAGTCCCGGGGCTGGAAGCACTCCGTGACC
TATTCCTGCTGCCCCGACACCCCCTACCTGGACATCACCTACCACTTCGTCATGCAGCGCCTGCCCCTCTACTTC
ATCGTCAACGTCATCATCCCCTGCCTGCTCTTCTCCTTCTTAACTGGCCTGGTATTCTACCTGCCCACAGACTCA
GGGGAGAAGATGACTCTGAGCATCTCTGTCTTACTGTCTTTGACTGTGTTCCTTCTGGTCATCGTGGAGCTGATC
CCCTCCACGTCCAGTGCTGTGCCCTTGATTGGAAAATACATGCTGTTCACCATGGTGTTCGTCATTGCCTCCATC
ATCATCACTGTCATCGTCATCAACACACACCACCGCTCACCCAGCACCCATGTCATGCCCAACTGGGTGCGGAAG
GTTTTTATCGACACTATCCCAAATATCATGTTTTTCTCCACAATGAAAAGACCATCCAGAGAAAAGCAAGACAAA
AAGATTTTTACAGAAGACATTGATATCTCTGACATTTCTGGAAAGCCAGGGCCTCCACCCATGGGCTTCCACTCT
CCCCTGATCAAACACCCCGAGGTGAAAAGTGCCATCGAGGGCATCAAGTACATCGCAGAGACCATGAAGTCAGAC
CAGGAGTCTAACAATGCGGCGGCAGAGTGGAAGTACGTTGCAATGGTGATGGACCACATACTCCTCGGAGTCTTC
ATGCTTGTTTGCATCATCGGAACCCTAGCCGTGTTTGCAGGTCGACTCATTGAATTAAATCAGCAAGGA**TGA**GCA
GAAAATGAGCTGAGCTTAGCTCTGCCCTGGAACCTACCAGAGCAGAGAAGGGCAGGAGAGGAAGATTTGTCTACT
TGCTCCACTCGCACTTATCAAACGTGTTATATTCCATACTTATTATTGATGATAAGATTTACCTTTATGTAAGTT
TATGGCCTTGAAGTGTTTTCATATTGCTTCTCCCTTTAGTTCTGCTGTCTCCCTGAAGAGTGAACCCTCTTTAGT
AAATGAAACTAATCACT

FIGURE 899

MEPWPLLLLFSLCSAGLVLGSEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTVGLQLIQLINVDEVNQIVTTNVR
LKQQWVDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTPPAIFKSYCEI
IVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKESRGWKHSVTYSCCPDTPYLDITYHF
VMQRLPLYFIVNVIIPCLLFSFLTGLVFYLPTDSGEKMTLSISVLLSLTVFLLVIVELIPSTSSAVPLIGKYMLF
TMVFVIASIIITVIVINTHHRSPSTHVMPNWVRKVFIDTIPNIMFFSTMKRPSREKQDKKIFTEDIDISDISGKP
GPPPMGFHSPLIKHPEVKSAIEGIKYIAETMKSDQESNNAAAEWKYVAMVMDHILLGVFMLVCIIGTLAVFAGRL
IELNQQG

FIGURE 900

GTTCGCAGCCGCCGCCGCGCCGCCGTCGCTCTCCAACGCCAGCGCCGCCTCTCGCTCGCCGAGCTCCAGCCGAAG
GAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACTGCCCGCAAATCGACCGGTGGT
AAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGCAAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCT
CATCGTTACAGGCCTGGTACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTCGC
AAACTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAAACAGATCTGCGCTTCCAGAGCGCAGCT
ATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGACACCAACCTGTGTGCTATCCAT
GCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTAGCACGCCGCATACGTGGAGAACGTGCTTAAGAATCC
ACTATGATGGGAAACATTTCATTCTCAAAAAAAAAAAAAAAATTTCTCTTCTTCCTGTTATTGGTAGTTCTGAAC
GTTAGATATTTTTTTTCCATGGGGTCAAAAGGTACCTAAGTATATGATTGCGAGTGGAAAAATAGGGGACAGAAA
TCAGGTATTGGCAGTTTTTCCATTTTCATTTGTGTGTGAATTTTTAATATAAATGCGGAGACGTAAAGCATTAAT
GCAAGTTAAAATGTTTCAGTGAACAAGTTTCAGCGGTTCAACTTTATAATAATTATAAATAAACCTGTTAAATTT
TTCTGGACAATGCCAGCATTTGGATTTTTTTAAAACAAGTAAATTTCTTATTGATGGCAACTAAATGGTGTTTGT
AGCATTTTTATCATACAGTAGATTCCATCCATTCACTATACTTTTCTAACTGAGTTGTCCTACATGCAAGTACAT
GTTTTTAATGTTGTCTGTCTTCTGTGCTGTTCCTGTAAGTTTGCTATTAAAATACATTAAACTAT

FIGURE 901

CGCCGAGCTCCAGCCGAAGGAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACTGC
CCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGCAAGAGTGCGCCCTCTAC
TGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTC
CACTGAACTTCTGATTCGCAAACTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAAACAGATCT
GCGCTTCCAGAGCGCAGCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGACAC
CAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTAGCACGCCGCATACGTGG
AGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTCATTCTCTCCATGGGGTCAAAAGGTACCTAAGTATAT
GATTGCGAGTGGAAA

FIGURE 902

MARTKQTARKSTGGKAPRKQLATKAARKSAPSTGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREI
AQDFKTDLRFQSAAIGALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA

FIGURE 903

CAGCCGTTGAGGGGACGGGCCTGCGTTCTCTCCTCCTTCCTCCCCGCCTCCAGCTGCCGGCAGGACCTTTCTCTC
GCTGCCGCTGGGACCCCGTGTCATCGCCCAGGCCGAGCACG**ATG**CCCCCTAAAAAGGGAGGTGATGGAATTAAAC
CACCCCCAATCATTGGAAGATTTGGAACCTCACTGAAAATTGGTATTGTTGGATTGCCAAATGTTGGGAAATCTA
CTTTCTTCAATGTGTTAACCAATAGTCAGGCTTCAGCAGAAAACTTCCCGTTCTGCACTATTGATCCTAATGAGA
GCAGAGTACCTGTGCCAGATGAAAGGTTTGACTTTCTTTGTCAATACCACAAACCAGCAAGCAAAATTCCTGCCT
TTCTAAATGTGGTGGATATTGCTGGCCTTGTGAAAGGAGCTCACAATGGGCAGGGCCTGGGGAATGCTTTTTTAT
CTCATATTAGTGCCTGTGATGGCATCTTTCATCTAACACGTGCTTTTGAAGATGATGATATCACGCACGTTGAAG
GAAGTGTAGATCCTATTCGAGATATAGAAATAATACATGAAGAGCTTCAGCTTAAAGATGAGGAAATGATTGGGC
CCATTATAGATAAACTAGAAAAGGTGGCTGTGAGAGGAGGAGATAAAAAACTAAAACCTGAATATGATATAATGT
GCAAAGTAAAATCCTGGGTTATAGATCAAAAGAAACCTGTTCGCTTCTATCATGATTGGAATGACAAAGAGATTG
AAGTGTTGAATAAACACTTATTTTTGACTTCAAAACCAATGGTCTACTTGGTTAATCTTTCTGAAAAAGACTACA
TTAGAAAGAAAAACAAATGGTTGATAAAAATTAAAGAGTGGGTGGACAAGTATGACCCAGGTGCTTTGGTCATTC
CTTTTAGTGGGGCCTTGGAACTCAAGTTGCAAGAATTGAGTGCTGAGGAGAGACAGAAGTATCTGGAAGCGAACA
TGACACAAAGTGCTTTGCCAAAGATCATTAAGGCTGGGTTTGCAGCACTCCAACTAGAATACTTTTTCACTGCAG
GCCCAGATGAAGTGCGTGCATGGACCATCAGGAAAGGGACTAAGGCTCCTCAGGCTGCAGGAAAGATTCACACAG
ATTTTGAAAAGGGATTCATTATGGCTGAAGTAATGAAATACGAAGATTTTAAAGAGGAAGGTTCTGAAAATGCAG
TCAAGGCTGCTGGAAAGTACAGACAACAAGGCAGAAATTATATTGTTGAAGATGGAGATATTATCTTCTTCAAAT
TTAACACACCTCAACAACCGAAGAAGAAA**TAA**AATTTAGTTATTGCTCAGATAAACATACAACTTCCAAAAGGCA
TCTGATTTTTAAAAAATTAAAATTTCTGAAAACCAATGCGACAAATAAAGTTGGGGAGATGGGAATCTTTGACAA
ACAAATTATTTTTATTTGTTTTAAAATTAAAATACTGTGTACCCCCCCCCCCCCCATGAAATGCAGGTTCACTAAA
TGTGAACAGCTTTGCTTTTCACGTGATTAAGACCCTACTCCAAATTGTAGAAGCTTTTCAGGAACCATATTACTC
TCATGATACTTCATTAATCTCCATCATGTATGCCAAGCCTGACACATTTGACAGTGAGGACAATGTGGCTTGCTC
CTTTTTGAATCTACAGATAATGCATGTTTTACAGTACTCCAGATGTCTACACTCAATAAAACATTTGACAAAACC
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 904

MPPKKGGDGIKPPPIIGRFGTSLKIGIVGLPNVGKSTFFNVLTNSQASAENFPFCTIDPNESRVPVPDERFDFLC
QYHKPASKIPAFLNVVDIAGLVKGAHNGQGLGNAFLSHISACDGIFHLTRAFEDDDITHVEGSVDPIRDIEIIHE
ELQLKDEEMIGPIIDKLEKVAVRGGDKKLKPEYDIMCKVKSWVIDQKKPVRFYHDWNDKEIEVLNKHLFLTSKPM
VYLVNLSEKDYIRKKNKWLIKIKEWVDKYDPGALVIPFSGALELKLQELSAEERQKYLEANMTQSALPKIIKAGF
AALQLEYFFTAGPDEVRAWTIRKGTKAPQAAGKIHTDFEKGFIMAEVMKYEDFKEEGSENAVKAAGKYRQQGRNY
IVEDGDIIFFKFNTPQQPKKK

FIGURE 905

CTGCCAGCCGCGCTGCTGCTGCTCCTCCTGCTGTGGGACCGCTGACCGCGCGGCTGCTCCGCTCTCCCCGCTCCA
AGCGCCGATCTGGGCACCCGCCACCAGCATGGACGCTCGCCGCGTGCCGCAGAAAGATCTCAGAGTAAAGAAGAA
CTTAAAGAAATTCAGATATGTGAAGTTGATTTCCATGGAGACCTCGTCATCCTCTGATGACAGTTGTGACAGCTT
TGCTTCTGATAATTTTGCAAACACGAAACCTAAATTCAGGTCAGATATCAGTGAAGAACTGGCAAGTGTTTTTTA
TGAGGACTCTGATAATGAATCTTTCTGCGGCTTTTCAGAAAGTGAGGTGCAAGATGTATTAGACCATTGTGGATT
TTTACAGAAACCAAGGCCAGATGTCACTAACGAACTGGCCGGTATTTTTCATGCCGACTCTGACGATGAATCATT
TTGCGGTTTCTCAGAGAGTGAGATACAAGATGGAATGAGGCTGCAGTCAGTTCGGGAAGGCTGTAGGACCCGCAG
CCAGTGCAGGCACTCTGGACCTCTCAGGGTGGCGATGAAGTTTCCAGCGCGGAGTACCAGGGGAGCAACCAACAA
AAAAGCAGAGTCCCGCCAGCCCTCAGAGAATTCTGTGACTGATTCCAACTCCGATTCAGAAGATGAAAGTGGAAT
GAATTTTTTGGAGAAAAGGGCTTTAAATATAAAGCAAAACAAAGCAATGCTTGCAAAACTCATGTCTGAATTAGA
AAGCTTCCCTGGCTCGTTCCGTGGAAGACATCCCCTCCCAGGCTCCGACTCACAATCAAGGAGACCGCGAAGGCG
TACATTCCCGGGTGTTGCTTCCAGGAGAAACCCTGAACGGAGAGCTCGTCCTCTTACCAGGTCAAGGTCCCGGAT
CCTCGGGTCCCTTGACGCTCTACCCATGGAGGAGGAGGAGGAAGAGGATAAGTACATGTTGGTGAGAAAGAGGAA
GACCGTGGATGGCTACATGAATGAAGATGACCTGCCCAGAAGCCGTCGCTCCAGATCATCCGTGACCCTTCCGCA
TATAATTCGCCCAGTGGAAGAAATTACAGAGGAGGAGTTGGAGAACGTCTGCAGCAATTCTCGAGAGAAGATATA
TAACCGTTCACTGGGCTCTACTTGTCATCAATGCCGTCAGAAGACTATTGATACCAAAACAAACTGCAGAAACCC
AGACTGCTGGGGCGTTCGAGGCCAGTTCTGTGGCCCCTGCCTTCGAAACCGTTATGGTGAAGAGGTCAGGGATGC
TCTGCTGGATCCGAACTGGCATTGCCCGCCTTGTCGAGGAATCTGCAACTGCAGTTTCTGCCGGCAGCGAGATGG
ACGGTGTGCGACTGGGGTCCTTGTGTATTTAGCCAAATATCATGGCTTTGGGAATGTGCATGCCTACTTGAAAAG
CCTGAAACAGGAATTTGAAATGCAAGCATAATATCTGGAAAATTTGCTGCCTGCCTTCTACTTCTCAAATCTTTC
TTGTAAAAGTTTCCAATTTTTTCACTGAAACCTGAGTTAAAAATCTTGATGATCAGCCTGTTTCATAAGAAACTC
CAATCAAGTTAATCTTAGCAGACATGTGTTTCTGGAGCATCACAGAAGGTATATTGCTAGTTACACTTTGCCCTC
CTGCAGTTTCTTCTCTGCTCCCAACCCCCATCTCATAGCATCCCCCTCTATTTCCAATGCTCCTCTCCAACCGCT
TAGTTTCTGAATTTCTTTTAAATTACAGTTTTATGAAAGCATATTTTATTTACTTGGTGTTGAAATAGCCCTCAT
AAAACCTAAGCACTTGGAAACACAATAATAGTATTAACTAACTAGATCTATTGAATTTCAGAGAAGAGCCTTCTA
ACTTGTTTACACAAAAACGAGTATGATTTAGCATTCATACTAGTTGAAATTTTTAATAGAATCAAGGCACAAAAG
TCTTAAAACCATGTGGAAAAATTAGGTAATTATTGCAGATTGATGTCTCTCAATCCCATGTATTGCGCTTATGTT
ACAAGTTGTTGTCACAGTTGAGACTTAATTTCTCCTAATTTCTTCTGCCCGAAGGGTAAGTGGTGCGTCCAGCTT
ACACAATCATAATTCAAAGGTTGGTGGGCAATGTAATACTTAATTAAAATAATGATGGAAGAGCTATCTGGAGAT
TATGAGTAAGCTGATTTGAATTTTCAGTATAAAACTTTAGTATAATTGTAGTTTGCAAAGTTTATTTCAGTTCAC
ATGTAAGGTATTGCAAATAAATTCTTGGACAATTTTGTATGGAAACTTGATATTAAAAACTAGTCTGTGGTTCTT
TGCAGTTTCTTGTAAATTTATAAACCAGGCACAAGGTTCAAGTTTAGATTTTAAGCACTTTTATAACAATGATAA
GTGCCTTTTTGGAGATGTAACTTTTAGCAGTTTGTTAACCTGACATCTCTGCCAGTCTAGTTTCTGGCAGGTTT
CCTGTGTCAGTATTCCCCCTCCTCTTTGCATTAATCAAGGTATTTGGTAGAGGTGGAATCTAAGTGTTTGTATGT
CCAATTTACTTGCATATGTAAACCATTGCTGTGCTATTCAATGTTTGATGCATAATTGGACCTTGAATCGATAAG
TGTAAATACAGCTTTTGATCTGTAATGCTTTTATACAAAAGTTTATTTTAATAATAAAATGTTTGTTCT

FIGURE 906

MDARRVPQKDLRVKKNLKKFRYVKLISMETSSSSDDSCDSFASDNFANTKPKFRSDISEELASVFYEDSDNESFC
GFSESEVQDVLDHCGFLQKPRPDVTNELAGIFHADSDDESFCGFSESEIQDGMRLQSVREGCRTRSQCRHSGPLR
VAMKFPARSTRGATNKKAESRQPSENSVTDSNSDSEDESGMNFLEKRALNIKQNKAMLAKLMSELESFPGSFRGR
HPLPGSDSQSRRPRRRTFPGVASRRNPERRARPLTRSRSRILGSLDALPMEEEEEEDKYMLVRKRKTVDGYMNED
DLPRSRRSRSSVTLPHIIRPVEEITEEELENVCSNSREKIYNRSLGSTCHQCRQKTIDTKTNCRNPDCWGVRGQF
CGPCLRNRYGEEVRDALLDPNWHCPPCRGICNCSFCRQRDGRCATGVLVYLAKYHGFGNVHAYLKSLKQEFEMQA

FIGURE 907

GCAAG**ATG**GCAGAAGTAGAGCAGAAGAAGAAGCGGACCTTCCGCAAGTTCACCTACCGCGGCGTGGACCTGGACC
AGCTGCTGGACATGTCCTACGAGCAGCTGGAGCAGCCGATGCAGCTGTACAGTGCGCGCCAGCGGCGGCGGCTGA
ACCGGGGCCTGCGGCGGAAGCAGCACTCCCTGCTGAAGCGCCTGCGCAAGGCCAAGAAGGAGGCGCCGCCCATGG
AGAAGCAGGAAGTGGTGAAGACGCACCTGCGGGACATGATCATCCTACCCGAGATGGTGGGCAGCATGGTGGGCG
TCTACAACGGCAAGACCTTCACCTACAAGCCCGTAAAGCACGGCCGGCCCGGCATCGGGGCCACCCACTCCTCCC
GCTTCATCCCTCTCAAG**TAA**TGGCTCAGCTAATAAAGGCGCACATGACTCC

FIGURE 908

MAEVEQKKKRTFRKFTYRGVDLDQLLDMSYEQLEQPMQLYSARQRRRLNRGLRRKQHSLLKRLRKAKKEAPPMEK
QEVVKTHLRDMIILPEMVGSMVGVYNGKTFTYKPVKHGRPGIGATHSSRFIPLK

FIGURE 909

GCTGAAATTAAAAGTACTGAGCTTACCAAGTGTTGATAAGGATGTAGAGGAACTGGAACTTTCATACACTGCTGG
TGGGAATATAAAATGGTATAACCATTTTGGAATACAACTTGGCAGTTTATTTGTTTGTTTAGGTTGTTTTTACTC
ACCACTATGCTAACGAGGAACTTGGCAGTTTCTTTAAAAGATAAACATATATCTCTGGTCCGTGCCTCCAAGATG
ACAAAGAAAAGAAGGAACAACGGTCATGCCAAAAAGGGCCGCGGCCACGTGCATCCTATTCGCTGCACTAACTGT
ACCCGATGCGTGCCCAAGGACAAGGCCATTAAGAAATTCGTCATTCGAAACGTAGTGGAGGCCGCAGCAGTCAGG
GACATTTCTGAAGTGAGCGTCTTCAATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTATATTACTGTGTGAGT
TGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCACAAAGACCGAACACCCCCACCCTGATTT
AGACCTGTGGGTGCTGCCCCACGTCCCCCACCAAAGCCCATGTAAGGAGCTGAGTTCTTAAAGACTGAAGACAGA
CTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTT

FIGURE 910

CTTTTATGTTAGATGAGGAAGGGGATACCCAAACAGAGGAAACCCGGCCTTCAGAAACAAAAGAAGTGGAGCCAG
AGCCAACTGAGGACAAAGATTTGGAAGCTGATGAAGAGGACACTAGGAAAAAAGATGCTTCTGATGATCTAGATG
ACTTGAACTTCTTTAATCAAAAGAAAAAGAAGAAAAAAACTAAAAAGATATTTGATATTGATGAAGCTGAAGAAG
GTGTAAAGGATCTTAAGATTGAAAGTGATGTTCAAGAACCAACTGAACCAGAGGATGACCTTGACATTATGCTTG
GCAATAAAAAGAAGAAAAAGAAGAATGTTAAGTTCCCAGATGAGGATGAAGCTCTAGAAGATGAAGACAACAAAA
AAGATGATGGTATCTCATTCAGTAATCAGACAGGCCCTGCTTGGGCAGGCTCAGAAAGAGACTACACATACGAGG
AGCTGCTGAATCGAGTGTTCAACATCATGAGGGAAAAGAATCCAGATATGGTTGCTGGGGAGAAAAGGAAATTTG
TCATGAAACCTCCACAAGTCGTCCGAGTAGGAACCAAGAAAACTTCTTTTGTCAACTTTACAGATATCTGTAAAC
TTGGTTCTATAGATGGTAATAACCAACTTGTAATCAAAGGAAGATTCCAACAGAAACAGATAGAAAATGTCTTGA
GAAGATATATCAAGGAGTATGTCACTTGTCACACATGCCGATCACCGGACACAATCCTGCAGAAGGACATGCGAC
TCTATTTCCTACAGTGCGAAACTTGTCATTCTAGATGTTCTGTTGCCATTATCAAAATTGGCTTCCAGGCTGTCA
TGGGCAAGCGAGCACAGCTCCGTGCCAAAGCTAACTAATTTGCTAATCACTGATTTTGCAAAGCTTGTTGTGGAG
ATGTGGCTGGACAGGTTTGCCATCAGAGTGGATATACCATTGTATTAAAAACAAGATAAAAAAGCTGCCAAGATT
TTTGGCGAGTGGTTGGTTGGTCTGAAGTCCTTGCAAGACGCTGATGCTCAAGCTGTTGACATACTCATTGCCTAC
TTTAACACCTGTCAGAGAAACGTGATATGGGGTAAGGAGGTGCTTTTTTAAAATAGTTCATAGACTTCTGTAAAA
TGCAAGATAAATTAAAGTTATTATAACAGTGA

FIGURE 911

GGTGGGAGAGGTATCGGCAGGGGCAGCGCTGCCGCCGGGGCCTGGGGCTGACCCGTCTGACTTCCCGTCCGTGCC
GAGCCCACTCGAGCCGCAGCCATGTCTGGGGACGAGATGATTTTTGATCCTACTATGAGCAAGAAGAAAAAGAAG
AAGAAGAAGCCTTTTATGTTAGATGAGGAAGGGGATACCCAAACAGAGGAAACCCGGCCTTCAGAAACAAAAGAA
GTGGAGCCAGAGCCAACTGAGGACAAAGATTTGGAAGCTGATGAAGAGGACACTAGGAAAAAAGATGCTTCTGAT
GATCTAGATGACTTGAACTTCTTTAATCAAAAGAAAAAGAAGAAAAAAACTAAAAAGATATTTGATATTGATGAA
GCTGAAGAAGGTGTAAAGGATCTTAAGATTGAAAGTGATGTTCAAGAACCAACTGAACCAGAGGATGACCTTGAC
ATTATGCTTGGCAATAAAAAGAAGAAAAAGAAGAATGTTAAGTTCCCAGATGAGGATGAAGCTCTAGAAGATGAA
GACAACAAAAAAAGATGATGGTATCTCATTCAGTAATCAGACAGGCCCTGCTTGGGCAGGCTCAGAAAGAGACTAC
ACATACGAGGAGCTGCTGAATCGAGTGTTCAACATCATGAGGGAAAAGAATCCAGATATGGTTGCTGGGGAGAAA
AGGAAATTTGTCATGAAACCTCCACAAGTCGTCCGAGTAGGAACCAAGAAAACTTCTTTTGTCAACTTTACAGAT
ATCTGTAAACTATTACATCGTCAACCCAAACATCTCCTTGCATTTTTATTGGCTGAATTGGGTACAAGTGGTTCT
ATAGATGGTAATAACCAACTTGTAATCAAAGGAAGATTCCAACAGAAACAGATAGAAAATGTCTTGAGAAGATAT
ATCAAGGAGTATGTCACTTGTCACACATGCCGATCACCGGACACAATCCTGCAGAAGGACATGCGACTCTATTTC
CTACAGTGCGAAACTTGTCATTCTAGATGTTCTGTTGCCATTATCAAAATTGGCTTCCAGGCTGTCATGGGCAAG
CGAGCACAGCTCCGTGCCAAAGCTAACTAATTTGCTAATCACTGATTTTGCAAAGCTTGTTGTGGAGATGTGGCT
GGACAGGTTTGCCATCAGAGTGGATATACCATTGTATTAAAAACAAGATAAAAAAGCTGCCAAGATTTTTGGCGA
GTGGTTGGTTGGTCTGAAGTCCTTGCAAGACGCTGATGCTCAAGCTGTTGACATACTCATTGCCTACTTTAACAC
CTGTCAGAGAAACGTGATATGGGGTAAGGAGGTGCTTTTTTAAAATAGTTCATAGACTTCTGTAAAATGCAAGAT
AAATTAAAGTTATTATAACAGTGA

FIGURE 912

CGAGTTGGAAGAGGCGAGTCCGGTCTCAAAATGGAGGTAAAACCGCCGCCCGGTCGCCCCCAGCCCGACTCCGGC
CGTCGCCGTCGCCGCCGGGGGGAGGAGGGCCATGATCCAAAGGAACCAGAGCAGTTGAGAAAACTGTTTATTGGT
GGTCTGAGCTTTGAAACTACAGATGATAGTTTACGAGAACATTTTGAGAAATGGGGCACACTCACAGATTGTGTG
GTAATGAGAGACCCCCAAACAAAACGTTCCAGGGGCTTTGGTTTTGTGACTTATTCTTGTGTTGAAGAGGTGGAT
GCAGCAATGTGTGCTCGACCACACAAGGTTGATGGGCGTGTAGTGGAACCAAAGAGAGCTGTTTCTAGAGAGGAT
TCTGTAAAGCCTGGTGCCCATC**TAA**CAGTGAAGAAAATTTTTGTTGGTGGTATTAAAGAAGATACAGAAGAATAT
AATTTGAGAGACTACTTTGAAAAGTATGGCAAGATTGAAACCATAGAAGTTATGGAAGACAGGCAGAGTGGAAAA
AAGAGAGGATTTGCTTTTGTAACTTTTGATGATCATGATACAGTTGATAAAATTGTTGTTCAGAAATACCACACT
ATTAATGGGCATAATTGTGAAGTGAAAAAGGCCCTTTCTAAACAAGAGATGCAGTCTGCTGGATCACAGAGAGGT
CGTGGAGGTGGATCTGGCAATTTTATGGGTCGCGGAGGGAACTTTGGAGGTGGTGGAGGTAATTTTGGCCGTGGT
GGAAACTTTGGTGGAAGAGGTAGGCTATGGTGGTGGAGGTGGTGGCAGCAGAGGTAGTTATGGAGGAGGTGATGG
TGGATATAATGGATTTGGAGGTGATGGTGGCAACTATGGCGGTGGTCCTGGTTATAGTAGTAGAGGGGGCTATGG
TGGTGGTGGACCAGGATATGGAAACCAAGGTGGTGGATATGGTGGAGGTGGAGGATATGATGGTTACAATGAAGG
AGGAAATTTTGGCGGTGGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTATAGTGGACAACAGCA
ATCAAATTATGGACCCATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAGTCCCTATGGTGGTGGTTATGG
ATCTGGTGGTGGAAGTGGTGGATATGGTAGCAGAAGGTTCTAAAAACAGCAGAAAAGGGCTACAGTTCTTAGCAG
GAGAGAGAGCGAGGAGTTGTCAGGAAAGCTGCAGGTTACTTTGAGACAGTCGTCCCAAATGCATTAGAGGAACTG
TAAAAATCTGCCACAGAAGGAACGATGATCCATAGTCAGAAAAGTTACTGCAGCTTAAACAGGAAACCCTTCTTG
TTCAGGACTGTCATAGCCACAGTTTGCAAAAAGTGCAGCTATTGATTAATGCAATGTAGTGTCAATTAGATGTAC
ATTCCTGAGGTCTTTTATCTGTTGTAGCTTTGTCTTTTTCTTTTTCTTTTCATTACATCAGGTATATTGCCCTGT
AAATTGTGGTAGTGGTACCAGGAATAAAAAATTAAGGAATTTTTAACTTTTCAATATTTGTGTAGTTCAGTTTTT
CTACATTTTAGTACAGAAACTTTAACAAAATGCAGTTTCGAAGGTGTTTCCTTGTGAGTTAACAAGTAAAGAAGA
TCATTGTTAATTACTATTTTGTATGAATTTTGCTAAAGTTAACTGTAAAGAAACACCTGCTGACTTGCAGTTTAA
GGGGAATCTATTCTCCCCATTTCCAAACCATGATATGAATGGGCGCTGACATGTGGAGAGAATAGATAATTTGTG
TGTTTGCAATGTGTGTTTTAGATAAATAGGATTGGGTATTTAAATTAGCATTTGTGAATTTAATAGCATTAAGAT
TACCTTCAAATGAAAAAAAATCTCAAAATTTCTATTTGGTTTTTGTGCATTTTCTTTTAAAATGTAATCATATGA
TTTTAGTGTGTTAGACTTGCTGAGTCCTAGCTGTGTTTAGAACATCTCTATTCTACATTTACCTTGGTCAAATTT
GAACTGCTGCCATAGG

FIGURE 913

MEGHDPKEREQLRKPFIGGLSFETTDDGLREHFEKWVTLTDCVVMRDPQTKCSRGFGFVTYSYIEEVDAAMCAPP
HKVDGCVVEPKRAVSREDFVKPGAHLTVKKIFVGGIKIQKNII

FIGURE 914

CTTCATCCTGCGACTAGCACCGCGTCCGGCAGCGCCTGCCCTACACTCGCCCGTGCCATGGCCTCCGTCTCCAAG
CTCGCCTGCATCTACTCGGCCCTCATTCTGCACGACGATGAGGTGACAGTCACGGAGGATAAGATCAATGCCCTC
ATTAAAGCAGCCGGTGTAAATGTTGAACCTTTTTGGCCTGGCTTGTTTGCAAAGGCCCTGGCCAACGTCAACATT
GGGAGCCTCATCTGCAATGTAGGGGCTGGTGGACCTGCTCCAGCTGAGGAGAAGAAAGTGGAAGCAAAGAAAGAA
GAATCCAAGGAGTCTGATGATGACATGGGCCTTGGTCTTTTTGACTAAACCTCTTTTATAACGTGTTCAATAAAA
AGCTGAACTT

FIGURE 915

MASVSKLACIYSALILHDDEVTVTEDKINALIKAAGVNVEPFWPGLFAKALANVNIGSLICNVGAGGPAPAEEKK
VEAKKEESKESDDDMGLGLFD

FIGURE 916

ACGGGGCCTGGGCGGSAGGGGCGGTGGCTGGAGCTCGGTAAAGCTCGTGGGACCCCATTGGGGGAATTTGATCCA
AGGAAGCGGTGATTGCCGGGGGAGGAGAAGCTCCCAGATCCTTGTGTCCACTTGCAGCGGGGGAGGCGGAGACGC
GGAGCGGGCCTTTTGGCGTCCACTGCGCGGCTGCACCCTGCCCCATCCTGCCGGGATC**ATG**GTCTGCGGCAGCCC
GGGAGGGATGCTGCTGCTGCGGGCCGGGCTGCTTGCCCTGGCTGCTCTCTGCCTGCTCCGGGTGCCCGGGGCTCG
GGCTGCAGCCTGTGAGCCCGTCCGCATCCCCCTGTGCAAGTCCCTGCCCTGGAACATGACTAAGATGCCCAACCA
CCTGCACCACAGCACTCAGGCCAACGCCATCCTGGCCATCGAGCAGTTCGAAGGTCTGCTGGGCACCCACTGCAG
CCCCGATCTGCTCTTCTTCCTCTGTGCCATGTACGCGCCCATCTGCACCATTGACTTCCAGCACGAGCCCATCAA
CCCCTGTAAGTCTGTGTGCGAGCGGGCCCGGCAGGGCTGTGAGCCCATACTCATCAAGTACCGCCACTCGTGGCC
GGAGAACCTGGCCTGCGAGGAGCTGCCAGTGTACGACAGGGGCGTGTGCATCTCTCCCGAGGCCATCGTTACTGC
GGACGGAGCTGATTTTCCTATGGATTCTAGTAACGGAAACTGTAGAGGGGCAAGCAGTGAACGCTGTAAATGTAA
GCCTATTAGAGCTACACAGAAGACCTATTTCCGGAACAATTACAACTATGTCATTCGGGCTAAAGTTAAAGAGAT
AAAGACTAAGTGCCATGATGTGACTGCAGTAGTGGAGGTGAAGGAGATTCTAAAGTCCTCTCTGGTAAACATTCC
ACGGGACACTGTCAACCTCTATACCAGCTCTGGCTGCCTCTGCCCTCCACTTAATGTTAATGAGGAATATATCAT
CATGGGCTATGAAGATGAGGAACGTTCCAGATTACTCTTGGTGGAAGGCTCTATAGCTGAGAAGTGGAAGGATCG
ACTCGGTAAAAAAGTTAAGCGCTGGGATATGAAGCTTCGTCATCTTGGACTCAGTAAAAGTGATTCTAGCAATAG
TGATTCCACTCAGAGTCAGAAGTCTGGCAGGAACTCGAACCCCCGGCAAGCACGCAAC**TAA**ATCCCGAAATACAA
AAAGTAACACAGTGGACTTCCTATTAAGACTTACTTGCATTGCTGGACTAGCAAAGGAAAATTGCACTATTGCAC
ATCATATTCTATTGTTTACTATAAAAATCATGTGATAACTGATTATTACTTCTGTTTCTCTTTGGTTTCTGCTT
CTCTCTTCTCTCAACCCCTTTGTAATGGTTTGGGGGCAGACTCTTAAGTATATTGTGAGTTTTCTATTTCACTAA
TCATGAGAAAAACTGTTCTTTTGCAATAATAATAAATTAAACATGCTGTTA

FIGURE 917

MVCGSPGGMLLLRAGLLALAALCLLRVPGARAAACEPVRIPLCKSLPWNMTKMPNHLHHSTQANAILAIEQFEGL
LGTHCSPDLLFFLCAMYAPICTIDFQHEPINPCKSVCERARQGCEPILIKYRHSWPENLACEELPVYDRGVCISP
EAIVTADGADFPMDSSNGNCRGASSERCKCKPIRATQKTYFRNNYNYVIRAKVKEIKTKCHDVTAVVEVKEILKS
SLVNIPRDTVNLYTSSGCLCPPLNVNEEYIIMGYEDEERSRLLLVEGSIAEKWKDRLGKKVKRWDMKLRHLGLSK
SDSSNSDSTQSQKSGRNSNPRQARN

FIGURE 918

<u>**ATG**</u>TCCATCAGGACGACCCAGAAGTCCTACAGGGTGTCCACTTCTGGCCCCCGGGCCTTCAGCAGCCATTTCTAC
ACAAGTGGGCCTGGTGCCTCCATCAGCTCCTCGAGCTTCTCCCAAGTGGGCAGCAGCAGCTTCCGGGGTGGCCTG
GGAGGAGGCTACGGTGGGGCCAGTGGCATGGGAGGCATCACCACCGTCACTGTCAACCAGAGCCTGCTGAGCCCC
CTTAACCTGGAGGTGGACCCACACATCCAGGCAGTGCACACTCAGAAGAAGGAGCAGATCAAGACCCTCAACACT
AAGTTTGCCACCTTCATATACAAGAGTTACATCAACAACCTTAGGCAGCAGCTGGAGACTCTGGGCCAGGAAAAG
CTGAAGCTGGAGGCGGAGCTTGGCAACATGCAGGGGCTGGTGGAGGACTTCAAGAACAAGTATGAGGATGAGATC
AATAAGCGTACAGAGATGGAGAATGAATTTGTCCTCATCAAGAAGGATGTGGATGAAGCTTACCTGAACAAGGTA
GAGCTGGAGTCTCGCCTGGAAGGGCTGACTGACGAAATCAACTTCCTCAGGCAGCTGTATGAAGAGGATATCCCG
GAGCTGCAGTCCCAGATCTCAGACACGTCTGTGGTGCTGCCCATGGACAACAGCCACTCCCTGGACATGGACAGC
ATCATCAATGAGGTCAAGCGCAGTACGAGATCACCAACCGCAGCCAGCTGGCTCCAGGCAGAGATTGAGGGTCTC
AAAGGCCAGAGGGCTTCCCTGGAGGCCGCCATCGCAGATGCGGAGCAGCGCGGGGAGTTGGCCGTTAAGGATGCC
AGCGCCAAGCTGTCTGAGCTGGAGGCCGCCCTGCAGCAAACCAAGCAGGACGTGGAGCTGATGAACGACAAGCTG
GCCCTGGACATTGAGATCGCCACCTACAGGCAGCTGCTGGAGGGCGAGGAGAGCTGGCTGGAGTCTGGGATGCAG
AGCATGAGTATCCATACAAAGACCATCAGCAGCTATGCAGGTGGTCTGAGCTCGGCCTATGGGGGCCTCACAAGC
CCCGGCCTCAGCTGTGGACTGGGCTCCAGCTTTGGCTCTGGCGCGGGCTCCAGTTCCTTCAGCTGCATCAGCTAC
ACCAGGGCCGTGGTTGTGAAGAAGATTGAGACCCGTGATGGGACGCTGGTGTCAGAGTTCTCTGACGTCCTGCCC
AAG<u>**TGA**</u>

FIGURE 919

MSIRTTQKSYRVSTSGPRAFSSHFYTSGPGASISSSSFSQVGSSSFRGGLGGGYGGASGMGGITTVTVNQSLLSP
LNLEVDPHIQAVHTQKKEQIKTLNTKFATFIYKSYINNLRQQLETLGQEKLKLEAELGNMQGLVEDFKNKYEDEI
NKRTEMENEFVLIKKDVDEAYLNKVELESRLEGLTDEINFLRQLYEEDIPELQSQISDTSVVLPMDNSHSLDMDS
IINEVKRSTRSPTAASWLQAEIEGLKGQRASLEAAIADAEQRGELAVKDASAKLSELEAALQQTKQDVELMNDKL
ALDIEIATYRQLLEGEESWLESGMQSMSIHTKTISSYAGGLSSAYGGLTSPGLSCGLGSSFGSGAGSSSFSCISY
TRAVVVKKIETRDGTLVSEFSDVLPK

FIGURE 920

ACGCAACCCCATAAGGTAGCACGCCGTTACCCGTGGGGAGCGTTTCCGCCATTTTTGAAAATTAATTGGGAAGGT
ACTGGTTTTAAGTGTAGTTGCCGACGCAATGGCAGCCTTTGCAGTGGAACCTCAGGGGCCCGCGTTAGGATCTGA
ACCAATGATGCTGGGTTCACCCACATCTCCAAAGCCAGGAGTTAATGCCCAGTTCTTACCTGGATTTTTAATGGG
GGATTTGCCAGCTCCGGTGACTCCACAACCTCGATCAATTAGTGGCCCTTCAGTAGGAGTAATGGAAATGAGATC
ACCTTTACTTGCAGGTGGGTCACCACCACAACCAGTTGTACCAGCTCATAAAGATAAAAGTGGCGCTCCACCAGT
TAGAAGTATATATGATGACATTTCTAGCCCAGGACTTGGATCAACACCTTTAACTTCAAGAAGACAGCCAAACAT
TTCAGTAATGCAGAGTCCTCTTGTTGGAGTTACATCTACTCCTGGAACAGGGCAAAGTATGTTTAGTCCAGCAAG
TATCGGTCAGCCACGAAAGACGACATTATCTCCTGCCCAGTTGGATCCTTTTTATACTCAAGGAGATTCTTTGAC
TTCAGAAGATCACCTCGATGACTCTTGGGTGACTGTATTTGGGTTTCCTCAAGCATCTGCTTCCTACATATTACT
ACAATTTGCACAGTATGGGAATATCTTAAAACATGTGATGTCTAATACAGGAAATTGGATGCATATTCGTTATCA
ATCTAAACTGCAGGCTCGGAAAGCCTTAAGCAAAGATGGGAGGATTTTTGGAGAATCCATCATGATTGGTGTAAA
ACCATGTATTGACAAAAGTGTTATGGAAAGCAGTGACAGATGTGCTTTATCATCTCCATCTTTAGCCTTTACACC
ACCAATCAAAACTCTAGGTACACCAACACAACCTGGAAGTACTCCTAGGATTTCTACCATGAGACCTCTTGCTAC
AGCATACAAAGCCTCTACTAGTGATTATCAGGTTATTTCTGACAGACAAACGCCAAAAAAAGATGAAAGTCTTGT
ATCCAAAGCAATGGAGTACATGTTTGGCTGGTAGTAGAACACCAAGAAGGAGGTTGCTACACTAAAACAGAGTTA
GCAGAGTGCTGCTGGTTCCTTCGGTTAGTTATATAACTGTTCCTGCAGTATTGGATAGCTATCTCATACTTCTTT
TAGAAAGAAGCCTTTTTCATTAAGGATACAACCTATTTGTAGCTCGCACTTTAAAAGATGCTTGAGATACATTTT
AAAGAAAACTAAAAATCCCTGTAAATAGGATTTTGTGCTTTCTGTAACAGTGCATGCTTCAGCACAGAAAACTCA
GCATTGATTATTGTAAATTAAATAACTGAAATTGTGGTGAGACGTCATAGTCTTCATGAGAACGTGGGGGTGAAT
TTCATGAAGGGGAACTATAGTTATTTCTACCGACACAAATATTATAATTAGCAATTTGAATTATGGTCTTTTAAT
TTAGATAGTATTTAATATTTTAATTATCCTTGTTTGTATATGTCCTGTCACAGAGTGTCCTCTTGGTGTATTCTA
AAACGAGCATTCTTTTAAAAAACCTAAAGTTTCTTGATAATAAACATTGTCAATGAT

FIGURE 921A

GGCTGAGTTTTATGACGGGCCCGGTGCTGAAGGGCAGGGAACAACTTGATGGTGCTACTTTGAACTGCTTTTCTT
TTCTCCTTTTTGCACAAAGAGTCTCATGTCTGATATTTAGACATGATGAGCTTTGTGCAAAAGGGGAGCTGGCTA
CTTCTCGCTCTGCTTCATCCCACTATTATTTGGCACAACAGGAAGCTGTTGAAGGAGGATGTTCCCATCTTGGT
CAGTCCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATGCCAAATATGTGTCTGTGACTCAGGATCCGTTCTC
TGCGATGACATAATATGTGACGATCAAGAATTAGACTGCCCCAACCCAGAAATTCCATTTGGAGAATGTTGTGCA
GTTTGCCCACAGCCTCCAACTGCTCCTACTCGCCCTCCTAATGGTCAAGGACCTCAAGGCCCCAAGGGAGATCCA
GGCCCTCCTGGTATTCCTGGGAGAAATGGTGACCCTGGTATTCCAGGACAACCAGGGTCCCCTGGTTCTCCTGGC
CCCCCTGGAATCTGTGAATCATGCCCTACTGGTCCTCAGAACTATTCTCCCCAGTATGATTCATATGATGTCAAG
TCTGGAGTAGCAGTAGGAGGACTCGCAGGCTATCCTGGACCAGCTGGCCCCCCAGGCCCTCCCGGTCCCCCTGGT
ACATCTGGTCATCCTGGTTCCCCTGGATCTCCAGGATACCAAGGACCCCCTGGTGAACCTGGGCAAGCTGGTCCT
TCAGGCCCTCCAGGACCTCCTGGTGCTATAGGTCCATCTGGTCCTGCTGGAAAAGATGGAGAATCAGGTAGACCC
GGACGACCTGGAGAGCGAGGATTGCCTGGACCTCCAGGTATCAAAGGTCCAGCTGGGATACCTGGATTCCCTGGT
ATGAAAGGACACAGAGGCTTCGATGGACGAAATGGAGAAAAGGGTGAAACAGGTGCTCCTGGATTAAAGGGTGAA
AATGGTCTTCCAGGCGAAAATGGAGCTCCTGGACCCATGGGTCCAAGAGGGGCTCCTGGTGAGCGAGGACGGCCA
GGACTTCCTGGGGCTGCAGGTGCTCGGGGTAATGACGGTGCTCGAGGCAGTGATGGTCAACCAGGCCCTCCTGGT
CCTCCTGGAACTGCCGGATTCCCTGGATCCCCTGGTGCTAAGGGTGAAGTTGGACCTGCAGGGTCTCCTGGTTCA
AATGGTGCCCCTGGACAAAGAGGAGAACCTGGACCTCAGGGACACGCTGGTGCTCAAGGTCCTCCTGGCCCTCCT
GGGATTAATGGTAGTCCTGGTGGTAAAGGCGAAATGGGTCCCGCTGGCATTCCTGGAGCTCCTGGACTGATGGGA
GCCCGGGGTCCTCCAGGACCAGCCGGTGCTAATGGTGCTCCTGGACTGCGAGGTGGTGCAGGTGAGCCTGGTAAG
AATGGTGCCAAAGGAGAGCCCGGACCACGTGGTGAACGCGGTGAGGCTGGTATTCCAGGTGTTCCAGGAGCTAAA
GGCGAAGATGGCAAGGATGGATCACCTGGAGAACCTGGTGCAAATGGGCTTCCAGGAGCTGCAGGAGAAAGGGGT
GCCCCTGGGTTCCGAGGACCTGCTGGACCAAATGGCATCCCAGGAGAAAAGGGTCCTGCTGGAGAGCGTGGTGCT
CCAGGCCCTGCAGGGCCCAGAGGAGCTGCTGGAGAACCTGGCAGAGATGGCGTCCCTGGAGGTCCAGGAATGAGG
GGCATGCCCGGAAGTCCAGGAGGACCAGGAAGTGATGGGAAACCAGGGCCTCCCGGAAGTCAAGGAGAAAGTGGT
CGACCAGGTCCTCCTGGGCCATCTGGTCCCCGAGGTCAGCCTGGTGTCATGGGCTTCCCCGGTCCTAAAGGAAAT
GATGGTGCTCCTGGTAAGAATGGAGAACGAGGTGGCCCTGGAGGACCTGGCCCTCAGGGTCCTCCTGGAAAGAAT
GGTGAAACTGGACCTCAAGGACCCCCAGGGCCTACTGGGCCTGGTGGTGACAAAGGAGACACAGGACCCCCTGGT
CCACAAGGATTACAAGGCTTGCCTGGTACAGGTGGTCCTCCAGGAGAAAATGGAAAACCTGGGGAACCAGGTCCA
AAGGGTGATGCCGGTGCACCTGGAGCTCCAGGAGGCAAGGGTGATGCTGGTGCCCCTGGTGAACGTGGACCTCCT
GGATTGGCAGGGGCCCCAGGACTTAGAGGTGGAGCTGGTCCCCCTGGTCCCGAAGGAGGAAAGGGTGCTGCTGGT
CCTCCTGGGCCACCTGGTGCTGCTGGTACTCCTGGTCTGCAAGGAATGCCTGGAGAAAGAGGAGGTCTTGGAAGT
CCTGGTCCAAAGGGTGACAAGGGTGAACCAGGCGGCCCAGGTGCTGATGGTGTCCCAGGGAAAGATGGCCCAAGG
GGTCCTACTGGTCCTATTGGTCCTCCTGGCCCAGCTGGCCAGCCTGGAGATAAGGGTGAAGGTGGTGCCCCCGGA
CTTCCAGGTATAGCTGGACCTCGTGGTAGCCCTGGTGAGAGAGGTGAAACTGGCCCTCCAGGACCTGCTGGTTTC
CCTGGTGCTCCTGGACAGAATGGTGAACCTGGTGGTAAAGGAGAAAGAGGGGCTCCGGGTGAGAAAGGTGAAGGA
GGCCCTCCTGGAGTTGCAGGACCCCCTGGAGGTTCTGGACCTGCTGGTCCTCCTGGTCCCCAAGGTGTCAAAGGT
GAACGTGGCAGTCCTGGTGGACCTGGTGCTGCTGGCTTCCCTGGTGCTCGTGGTCTTCCTGGTCCTCCTGGTAGT
AATGGTAACCCAGGACCCCCAGGTCCCAGCGGTTCTCCAGGCAAGGATGGGCCCCCAGGTCCTGCGGGTAACACT
GGTGCTCCTGGCAGCCCTGGAGTGTCTGGACCAAAAGGTGATGCTGGCCAACCAGGAGAGAAGGGATCGCCTGGT
GCCCAGGGCCCACCAGGAGCTCCAGGCCCACTTGGGATTGCTGGGATCACTGGAGCACGGGGTCTTGCAGGACCA
CCAGGCATGCCAGGTCCTAGGGGAAGCCCTGGCCCTCAGGGTGTCAAGGGTGAAAGTGGGAAACCAGGAGCTAAC
GGTCTCAGTGGAGAACGTGGTCCCCCTGGACCCCAGGGTCTTCCTGGTCTGGCTGGTACAGCTGGTGAACCTGGA
AGAGATGGAAACCCTGGATCAGATGGTCTTCCAGGCCGAGATGGATCTCCTGGTGGCAAGGGTGATCGTGGTGAA
AATGGCTCTCCTGGTGCCCCTGGCGCTCCTGGTCATCCAGGCCCACCTGGTCCTGTCGGTCCAGCTGGAAAGAGT
GGTGACAGAGGAGAAAGTGGCCCTGCTGGCCCTGCTGGTGCTCCCGGTCCTGCTGGTTCCCGAGGTGCTCCTGGT
CCTCAAGGCCCACGTGGTGACAAAGGTGAAACAGGTGAACGTGGAGCTGCTGGCATCAAAGGACATCGAGGATTC
CCTGGTAATCCAGGTGCCCCAGGTTCTCCAGGCCCTGCTGGTCAGCAGGGTGCAATCGGCAGTCCAGGACCTGCA
GGCCCCAGAGGACCTGTTGGACCCAGTGGACCTCCTGGCAAAGATGGAACCAGTGGACATCCAGGTCCCATTGGA

FIGURE 921B

CCACCAGGGCCTCGAGGTAACAGAGGTGAAAGAGGATCTGAGGGCTCCCCAGGCCACCCAGGGCAACCAGGCCCT
CCTGGACCTCCTGGTGCCCCTGGTCCTTGCTGTGGTGGTGTTGGAGCCGCTGCCATTGCTGGGATTGGAGGTGAA
AAAGCTGGCGGTTTTGCCCCGTATTATGGAGATGAACCAATGGATTTCAAAATCAACACCGATGAGATTATGACT
TCACTCAAGTCTGTTAATGGACAAATAGAAAGCCTCATTAGTCCTGATGGTTCTCGTAAAAACCCCGCTAGAAAC
TGCAGAGACCTGAAATTCTGCCATCCTGAACTCAAGAGTGGAGAATACTGGGTTGACCCTAACCAAGGATGCAAA
TTGGATGCTATCAAGGTATTCTGTAATATGGAAACTGGGGAAACATGCATAAGTGCCAATCCTTTGAATGTTCCA
CGGAAACACTGGTGGACAGATTCTAGTGCTGAGAAGAAACACGTTTGGTTTGGAGAGTCCATGGATGGTGGTTTT
CAGTTTAGCTACGGCAATCCTGAACTTCCTGAAGATGTCCTTGATGTGCAGCTGGCATTCCTTCGACTTCTCTCC
AGCCGAGCTTCCCAGAACATCACATATCACTGCAAAAATAGCATTGCATACATGGATCAGGCCAGTGGAAATGTA
AAGAAGGCCCTGAAGCTGATGGGGTCAAATGAAGGTGAATTCAAGGCTGAAGGAAATAGCAAATTCACCTACACA
GTTCTGGAGGATGGTTGCACGAAACACACTGGGGAATGGAGCAAAACAGTCTTTGAATATCGAACACGCAAGGCT
GTGAGACTACCTATTGTAGATATTGCACCCTATGACATTGGTGGTCCTGATCAAGAATTTGGTGTGGACGTTGGC
CCTGTTTGCTTTTTA**TAA**ACCAAACTCTATCTGAAATCCCAACAAAAAAAATTTAACTCCATATGTGTTCCTCTT
GTTCTAATCTTGTCAACCAGTGCAAGTGACCGACAAAATTCCAGTTATTTATTTCCAAAATGTTTGGAAACAGTA
TAATTTGACAAAGAAAAATGATACTTCTCTTTTTTTGCTGTTCCACCAAATACAATTCAAATGCTTTTTGTTTTA
TTTTTTTACCAATTCCAATTTCAAAATGTCTCAATGGTGCTATAATAAATAAACTTCAACACTCTTTATGATAAC
AACACTGTGTTATATTCTTTGAATCCTAGCCCATCTGCAGAGCAATGACTGTGCTCACCAGTAAAAGATAACCTT
TCTTTCTGAAATAGTCAAATACGAAATTAGAAAAGCCCTCCCTATTTTAACTACCTCAACTGGTCAGAAACACAG
ATTGTATTCTATGAGTCCCAGAAGATGAAAAAAATTTTATACGTTGATAAAACTTATAAATTTCATTGATTAATC
TCCTGGAAGATTGGTTTAAAAAGAAAAGTGTAATGCAAGAATTTAAAGAAATATTTTTAAAGCCACAATTATTTT
AATATTGGATATCAACTGCTTGTAAAGGTGCTCCTCTTTTTTCTTGTCATTGCTGGTCAAGATTACTAATATTTG
GGAAGGCTTTAAAGACGCATGTTATGGTGCTAATGTACTTTCACTTTTAAACTCTAGATCAGAATTGTTGACTTG
CATTCAGAACATAAATGCACAAAATCTGTACATGTCTCCCATCAGAAAGATTCATTGGCATGCCACAGGGATTCT
CCTCCTTCATCCTGTAAAGGTCAACAATAAAAACCAAATTATGGGGCTGCTTTTGTCACACTAGCATAGAGAATG
TGTTGAAATTTAACTTTGTAAGCTTGTATGTGGTTGTTGATCTTTTTTTTCCTTACAGACACCCATAATAAAATA
TCATATTAAAATTC

FIGURE 922

MMSFVQKGSWLLLALLHPTIILAQQEAVEGGCSHLGQSYADRDVWKPEPCQICVCDSGSVLCDDIICDDQELDCP
NPEIPFGECCAVCPQPPTAPTRPPNGQGPQGPKGDPGPPGIPGRNGDPGIPGQPGSPGSPGPPGICESCPTGPQN
YSPQYDSYDVKSGVAVGGLAGYPGPAGPPGPPGPPGTSGHPGSPGSPGYQGPPGEPGQAGPSGPPGPPGAIGPSG
PAGKDGESGRPGRPGERGLPGPPGIKGPAGIPGFPGMKGHRGFDGRNGEKGETGAPGLKGENGLPGENGAPGPMG
PRGAPGERGRPGLPGAAGARGNDGARGSDGQPGPPGPPGTAGFPGSPGAKGEVGPAGSPGSNGAPGQRGEPGPQG
HAGAQGPPGPPGINGSPGGKGEMGPAGIPGAPGLMGARGPPGPAGANGAPGLRGGAGEPGKNGAKGEPGPRGERG
EAGIPGVPGAKGEDGKDGSPGEPGANGLPGAAGERGAPGFRGPAGPNGIPGEKGPAGERGAPGPAGPRGAAGEPG
RDGVPGGPGMRGMPGSPGGPGSDGKPGPPGSQGESGRPGPPGPSGPRGQPGVMGFPGPKGNDGAPGKNGERGGPG
GPGPQGPPGKNGETGPQGPPGPTGPGGDKGDTGPPGPQGLQGLPGTGGPPGENGKPGEPGPKGDAGAPGAPGGKG
DAGAPGERGPPGLAGAPGLRGGAGPPGPEGGKGAAGPPGPPGAAGTPGLQGMPGERGGLGSPGPKGDKGEPGGPG
ADGVPGKDGPRGPTGPIGPPGPAGQPGDKGEGGAPGLPGIAGPRGSPGERGETGPPGPAGFPGAPGQNGEPGGKG
ERGAPGEKGEGGPPGVAGPPGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGARGLPGPPGSNGNPGPPGPSGSPG
KDGPPGPAGNTGAPGSPGVSGPKGDAGQPGEKGSPGAQGPPGAPGPLGIAGITGARGLAGPPGMPGPRGSPGPQG
VKGESGKPGANGLSGERGPPGPQGLPGLAGTAGEPGRDGNPGSDGLPGRDGSPGGKGDRGENGSPGAPGAPGHPG
PPGPVGPAGKSGDRGESGPAGPAGAPGPAGSRGAPGPQGPRGDKGETGERGAAGIKGHRGFPGNPGAPGSPGPAG
QQGAIGSPGPAGPRGPVGPSGPPGKDGTSGHPGPIGPPGPRGNRGERGSEGSPGHPGQPGPPGPPGAPGPCCGGV
GAAAIAGIGGEKAGGFAPYYGDEPMDFKINTDEIMTSLKSVNGQIESLISPDGSRKNPARNCRDLKFCHPELKSG
EYWVDPNQGCKLDAIKVFCNMETGETCISANPLNVPRKHWWTDSSAEKKHVWFGESMDGGFQFSYGNPELPEDVL
DVQLAFLRLLSSRASQNITYHCKNSIAYMDQASGNVKKALKLMGSNEGEFKAEGNSKFTYTVLEDGCTKHTGEWS
KTVFEYRTRKAVRLPIVDIAPYDIGGPDQEFGVDVGPVCFL

FIGURE 923

ACGCGTCCGAGCTGGCTCAGGGCGTCCGCTAGGCTCGGACGACCTGCTGAGCCTCCCAAACCGCTTCCATAAGGC
TTTGCCTTTCCAACTTCAGCTACAGTGTTAGCTAAGTTTGGAAAGAAGGAAAAAAGAAAATCCCTGGGCCCCTTT
TCTTTTGTTCTTTGCCAAAGTCGTCGTTGTAGTCTTTTTGCCCAAGGCTGTTGTGTTTTTAGAGGTGCTATCTCC
AGTTCCTTGCACTCCTGTTAACAAGCACCTCAGCGAGAGCAGCAGCAGCGATAGCAGCCGCAGAAGAGCCAGCGG
GGTCGCCTAGTGTC**ATG**ACCAGGGCGGGAGATCACAACCGCCAGAGAGGATGCTGTGGATCCTTGGCCGACTACC
TGACCTCTGCAAAATTCCTTCTCTACCTTGGTCATTCTCTCTCTACTTGGGGAGATCGGATGTGGCACTTTGCGG
TGTCTGTGTTTCTGGTAGAGCTCTATGGAAACAGCCTCCTTTTGACAGCAGTCTACGGGCTGGTGGTGGCAGGGT
CTGTTCTGGTCCTGGGAGCCATCATCGGTGACTGGGTGGACAAGAATGCTAGACTTAAAGTGGCCCAGACCTCGC
TGGTGGTACAGAATGTTTCAGTCATCCTGTGTGGAATCATCCTGATGATGGTTTTCTTACATAAACATGAGCTTC
TGACCATGTACCATGGATGGGTTCTCACTTCCTGCTATATCCTGATCATCACTATTGCAAATATTGCAAATTTGG
CCAGTACTGCTACTGCAATCACAATCCAAAGGGATTGGATTGTTGTTGTTGCAGGAGAAGACAGAAGCAAACTAG
CAAATATGAATGCCACAATACGAAGGATTGACCAGTTAACCAACATCTTAGCCCCCATGGCTGTTGGCCAGATTA
TGACATTTGGCTCCCCAGTCATCGGCTGTGGCTTTATTTCGGGATGGAACTTGGTATCCATGTGCGTGGAGTACG
TCCTGCTCTGGAAGGTTTACCAGAAAACCCCAGCTCTAGCTGTGAAAGCTGGTCTTAAAGAAGAGGAAACTGAAT
TGAAACAGCTGAATTTACACAAAGATACTGAGCCAAAACCCCTGGAGGGAACTCATCTAATGGGTGTGAAAGACT
CTAACATCCATGAGCTTGAACATGAGCAAGAGCCTACTTGTGCCTCCCAGATGGCTGAGCCCTTCCGTACCTTCC
GAGATGGATGGGTCTCCTACTACAACCAGCCTGTGTTTCTGGCTGGCATGGGTCTTGCTTTCCTTTATATGACTG
TCCTGGGCTTTGACTGCATCACCACAGGGTACGCCTACACTCAGGGACTGAGTGGTTCCATCCTCAGTATTTTGA
TGGGAGCATCAGCTATAACTGGAATAATGGGAACTGTAGCTTTTACTTGGCTACGTCGAAAATGTGGTTTGGTTC
GGACAGGTCTGATCTCAGGATTGGCACAGCTTTCCTGTTTGATCTTGTGTGTGATCTCTGTATTCATGCCTGGAA
GCCCCCTGGACTTGTCCGTTTCTCCTTTTGAAGATATCCGATCAAGGTTCATTCAAGGAGAGTCAATTACACCTA
CCAAGATACCTGAAATTACAACTGAAATATACATGTCTAATGGGTCTAATTCTGCTAATATTGTCCCGGAGACAA
GTCCTGAATCTGTGCCCATAATCTCTGTCAGTCTGCTGTTTGCAGGCGTCATTGCTGCTAGAATCGGTCTTTGGT
CCTTTGATTTAACTGTGACACAGTTGCTGCAAGAAAATGTAATTGAATCTGAAAGAGGCATTATAAATGGTGTAC
AGAACTCCATGAACTATCTTCTTGATCTTCTGCATTTCATCATGGTCATCCTGGCTCCAAATCCTGAAGCTTTTG
GCTTGCTCGTATTGATTTCAGTCTCCTTTGTGGCAATGGGCCACATTATGTATTTCCGATTTGCCCAAAATACTC
TGGGAAACAAGCTCTTTGCTTGCGGTCCTGATGCAAAAGAAGTTAGGAAGGAAAATCAAGCAAATACATCTGTTG
TT**TGA**GACAGTTTAACTGTTGCTATCCTGTTACTAGATTATATAGAGCACATGTGCTTATTTGTACTGCAGAAT
TCCAATAAATGGCTGGGTGTTTTGCTCTGTTTTTACCACAGCTGTGCCTTGAGAACTAAAAGCTGTTTAGGAAAC
CTAAGTCAGCAGAAATTAACTGATTAATTTCCCTTATGTTGAGGCATGGAAAAAAAATTGGAAAAGAAAAACTCA
GTTTAAATACGGAGACTATAATGATAACACTGAATTCCCCTATTTCTCATGAGTAGATACAATCTTACGTAAAAG
AGTGGTTAGTCACGTGAATTCAGTTATCATTTGACAGATTCTTATCTGTACTAGAATTCAGATATGTCAGTTTTC
TGCAAAACTCACTCTTGTTCAAGACTAGCTAATTTATTTTTTTGCATCTTAGTTATTTTTAAAAACAAATTCTTC
AAGTATGAAGACTAAATTTTGATAACTAATATTATCCTTATTGATCCTATTGATCTTAAGGTATTTACATGTATG
TGGAAAAACAAAACACTTAACTAGAATTCTCTAATAAGGTTTATGGTTTAGCTTAAAGAGCACCTTTGTATTTTT
ATTATCAGATGGGGCAACATATTGTATGAAGCATATGTAGCACTTCACAGCATGGTTATCATGTAAGCTGCAGGT
AGAAGCAAAGCTGTAAAGTAGATTTATCACACAATGACTGCATACAGACTTCAAATATGTCAATAGTTTGGTCAT
AGAACCTAGAAGCCAAAAGCCACACAGAAGGGCAAGAATCCCAATTTAACTCATGTTATCATCATTAGTGATCTG
TGTTGTAGAACATGAGGGTGTAAGCCTTCAGCCTGGCAAGTTACATGTAGAAAGCCCACACTTGTGAAGGTTTTG
TTTTACAAATCACTTGATTTAACACACTCAGGTAGAATATTTTTATTTTTACTGTTTTATACCCAGAAGTTATTT
CTACATTGTTCTACAGCAAGAATATTCATAAAAGTATCCCTTTCAAATGCCTTTGAGAAGAATAGAAGAAAAAAA
GTTTGTATATATTTTAAAAAATTGTTTTAAAAGTCAGTTTGCAACATGTCTGTACCAAGATGGTACTTTGCCTTA
ACCGTTTATATGCACTTTCATGGAGACTGCAATACGTTGCTATGAGCACTTTCTTTATCCTTGGAGTTTAATCCT
TTGCTTCATCTTTCTACAGTATGACATAATGATTTGCTATGTTGTAAAATCTTTGTAAAAAATTTCTATATAAAA
ATATTTTGAAAATCTTAAAAAAAAAAAAAAAAA

FIGURE 924

MTRAGDHNRQRGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELYGNSLLLTAVYGLVVAGSVLVL
GAIIGDWVDKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANIANLASTAT
AITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWK
VYQKTPALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTFRDGWV
SYYNQPVFLAGMGLAFLYMTVLGFDCITTGYAYTQGLSGSILSILMGASAITGIMGTVAFTWLRRKCGLVRTGLI
SGLAQLSCLILCVISVFMPGSPLDLSVSPFEDIRSRFIQGESITPTKIPEITTEIYMSNGSNSANIVPETSPESV
PIISVSLLFAGVIAARIGLWSFDLTVTQLLQENVIESERGIINGVQNSMNYLLDLLHFIMVILAPNPEAFGLLVL
ISVSFVAMGHIMYFRFAQNTLGNKLFACGPDAKEVRKENQANTSVV

FIGURE 925

TTTTGTGAAGAGACGAAGACTGAGCGGTTGCGGCCGCGTTGCCGACCTCCAGCAGCAGTCGGCTTCTCTACGCAG
AACCCGGGAGTAGGAGACTCAGAATCGAATCTCTTCTCCCTCCCCTTCTTGTTTTCGGCTTTGTGAGAAACCTTA
CCATCAAACACAATGGCCAGCAACGTTACCAACAAGACAGATCCTCGTTCCATGAACTCCCGTGTATTCATTGGG
AATCTCAACACTCTTGTGGTCAAGAAATCTGATGTGGAGGCAATCTTTTCGAAGTATGGCAAAATTGTGGGCTGC
TCTGTTCATAAGGGCTTTGCCTTCTTTCAGTATGTTAATGAGAGAAATGCCCGGGCTGCTGTAGCAGGAGAGGAT
GGCAGAATGATTGCTGGCCAGGTTTTAGATATTAACCTGGCTGCAGAGCCAAAAGTGAACCGAGGAAAAGCAGGT
GTGAAACGATCTGCAGCGGAGATGTACGGCTCCTCTTTTGACTTGGATTGTGACTTTCAACGGGACTATTATGAT
AGGATGTACAGTTACCCAGCACGTGTACCTCCTCCTCCTCCTATTGCTCGGGCTGTAGTGCCCTCGAAACGTCAG
CGTGTATCAGGAAACACTTCACAAAGGGGCATAAGTGGCTTCAATTCTAAGAGTGGACAGCGGGGATCTTCCAAG
TCTGGAAAGTTGAAAGGAGATGACCTTCAGGCCATTAAGAGGGAGCTGACCCAGATAAAACAAAAAGTGGATTCT
TTCCTGGAAAACCTGGAAAAAATTGAAAAGGAACAGAGCAAACAAGCAGTAGAGATGAACAATGTTAAGTCAGAA
GAGGAGCAGAGCAGCAGCTCCGTGAAGAAAGATGAGACTAATGTGAAGATGGAGTCTGAGGGGGGTGCAGATGAC
TCTGCTGAGGAGGGGGACCTACTGGATGATGATGATAATGAAGATGGGGGGATGACCAGCTGGAGTTGATCAAGG
ATGATGAAAAAGAGGCTGAGGAAGGAGAGGATGACAGAGACAGCGCCAATGGCGAGGATGACTCTTAAGCACATA
GTGGGGTTTAGAAATCTTATCCCATTATTTCTTTACCTAGGCGCTTGTCTAAGATCAAATTTTTCACCAGATCCT
CTCCCCTAGTATCTTCAGCACATGCTCACTGTTTTCCCCATCCTTGTCCTTCCCATGTTCATTAATTAATTCATA
TTGCCCCGCGCCTAGTCCCATTTTCACTTCCTTTGACGCTCCTAGTAGTTTTGTTAAGTCTTACCCTGTAATTTT
TGCTTTTAATTTTGATACCTCTTTATGACTTAACAATAAAAATGATGTATGGTTTTTATCAACTGTCTCCAAAAT
AATCTCTTGTTATGCAGGGAGTACAGTTCTTTTCATTCATACATAAGTTCAGTAGTTGCTTCCCTAACTGCAAAG
GCAATCTCATTTAGTTGAGTAGCTCTTGAAAGCAGCTTTGAGTTAGAAGTATGTGTGTTACACCCCCACATTAGT
GTGCTGTGTGGGGCAGTTCAACACAAATGTAACAATGTATTTTTGTGAATGAGAGTTGGCATGTCAAATGCATCC
TCTAGAAAAATAATTAGTGTTATAGTCTTAAGATTTGTTTTCTAAAGTTGATACTGTGGGTTATTTTTGTGAACA
GCCTGATGTTTGGGACCTTTTTTCCTCAAAATAAACAAGTCCTTATTAAACCAGG

FIGURE 926

GCCGACCTCCAGCAGCAGTCGGCTTCTCTACGCAGAACCCGGGAGTAGGAGACTCAGAATCGAATCTCTTCTCCC
TCCCCTTCTTGTTTTCGGCTTTGTGAGAAACCTTACCATCAAACACAATGGCCAGCAACGTTACCAACAAGACAG
ATCCTCGTTCCATGAACTCCCGTGTATTCATTGGGAATCTCAACACTCTTGTGGTCAAGAAATCTGATGTGGAGG
CAATCTTTTCGAAGTATGGCAAAATTGTGGGCTGCTCTGTTCATAAGGGCTTTGCCTTCTTTCAGTATGTTAATG
AGAGAAATGCCCGGGCTGCTGTAGCAGGAGAGGATGGCAGAATGATTGCTGGCCAGGTTTTAGATATTAACCTGG
CTGCAGAGCCAAAAGTGAACCGAGGAAAAGCAGGTGTGAAACGATCTGCAGCGGAGATGACCTTCAGGCCATTAA
GAGGGAGCTGACCCAGATAAAACAAAAAGTGGATTCTTTCCTGGAAAACCTGGAAAAAATTGAAAAGGAACAGAG
CAAACAAGCAGTAGAGATGAACAATGTTAAGTCAGAAGAGGAGCAGAGCAGCAGCTCCGTGAAGAAAGATGAGAC
TAATGTGAAGATGGAGTCTGAGGGGGGTGCAGATGACTCTGCTGAGGAGGGGGACCTACTGGATGATGATGATAA
TGAAGATGGGGGGATGACCAGCTGGAGTTGATCAAGGATGAGGATGACTCTTAAGCACATAGTGGGGTTTAGAAA
TCTTATCCCATTATTTCTTTACCTAGGCGCTTGTCTAAGATCAAATTTTTCACCAGATCCTCTCCCCTAGTATCT
TCAGCACATGCTCACTGTTTTCCCCATCCTTGTCCTTCCCATGTTCATTAATTAATTCATATTGCCCCGCGCCTA
GTCCCATTTTCACTTCCTTTGACGCTCCTAGTAGTTTTGTTAAGT

FIGURE 927

GAGACGAAGACTGAGCGGTTGCGGCCGCGTTGCCGACCTCCCCTTCTTGTTTTCGGCTTTGTGAGAAACCTTACC
ATCAAACACAATGGCCAGCAACGTTACCAACAAGACAGATCCTCGTTCCATGAACTCCCGTGTATTCATTGGGAA
TCTCAACACTCTTGTGGTCAAGAAATCTGATGTGGAGGCAATCTTTTCGAAGTATGGCAAAATTGTGGGCTGCTC
TGTTCATAAGGGCTTTGCCTTCTTTCAGTATGTTAATGAGAGAAATGCCCGGGCTGCTGTAGCAGGAGAGGATGG
CAGAATGATTGCTGGCCAGGTTTTAGATATTAACCTGGCTGCAGAGCCAAAAGTGAACCGAGGAAAAGCAGGTGT
GAAACGATCTGCAGCGGAGATGTACGGCTCCTCTTTTGACTTGGATTGTGACTTTCAACGGGACTATTATGATAG
GATGTACAGTTACCCAGCACGTGTACCTCCTCCTCCTCCTATTGCTCGGGCTGTAGTGCCCTCGAAACGTCAGCG
TGTATCAGGAAACACTTCACAAAGGGGCATAAGTGGCTTCAATTCTAAGAGTGGACAGCGGGGATCTTCCAAGTC
TGGAAAGTTGAAAGGAGATGACCTTCAGGCCATTAAGAGGGAGCTGACCCAGATAAAACAAAAAGTGGATTCTTT
CCTGGAAAACCTGGAAAAAATTGAAAAGGAACAGAGCAAACAAGCACTGGAGTTGATCAAGGATGATGAAAAAGA
GGCTGAGGAAGGAGAGGATGACAGAGACAGCGCCAATGGCGAGGATGACTCTTAAGCACATAGTGGGGTTTAGAA
ATCTTATCCCATTATTTCTTTACCTAGGCGCTTGTCTAAGATCAAATTTTTCACCAGATCCTCTCCCCTAGTATC
TTCAGCACATGCTCACTGTTTTCCCCATCCTTGTCCTTCCCATGTTCATTAATTAATTCATATTGCCCCGCGCCT
AGTCCCATTTTCACTTCCTTTGACGCTCCTAGTAGTTTT

FIGURE 928

ATCTTTTAGAGAAATCTCGGGTTGTTAAACAGCCAAGAGGTGAAAGAAACTTCCATGTGTTCTATCAGCTGCTCT
CTGGTGCCTCTGAAGAGCTCCTCAATAAACTTAAGCTTGAGAGGGATTTCAGCAGGTATAACTACCTGAGTCTGG
ATTCGGCCAAAGTGAATGGAGTGGATGATGCAGCAAATTTTAGAACCGTGCGGAATGCCATGCAGATTGTGGGCT
TTATGGATCATGAAGCTGAGTCTGTCTTGGCGGTGGTGGCAGCAGTGTTGAAACTGGGGAACATTGAGTTCAAGC
CCGAATCTCGAGTGAATGGTCTAGATGAAAGCAAAATCAAAGATAAAAATGAGTTAAAAGAAATTTGTGAATTGA
CCGGCATTGATCAATCAGTTCTAGAACGAGCATTCAGTTTCCGAACAGTTGAGGCCAAACAGGAGAAAGTTTCAA
CTACACTGAATGTGGCTCAGGCTTATTATGCCCGTGATGCTCTGGCTAAAAACCTCTACAGCAGGTTGTTTTCAT
GGTTGGTAAATCGAATCAATGAAAGCATTAAGGCACAAACAAAAGTGAGAAAGAAGGTCATGGGTGTTCTGGACA
TTTATGGCTTTGAGATTTTCGAGGACAACAGCTTTGAGCAGTTCATTATTAATTATTGTAACGAAAAGCTGCAAC
AAATCTTCATTGAACTTACTCTTAAAGAAGAGCAGGAGGAGTATATACGGGAGGATATAGAATGGACTCACATTG
ACTACTTCAATAATGCTATCATTTGTGACCTAATAGAAAATAACACAAATGGAATCCTGGCCATGCTGGATGAAG
AGTGCCTCAGACCTGGCACAGTCACTGATGAGACCTTCTTAGAAAAGCTGAACCAAGTATGTGCCACCCACCAGC
ATTTTGAGAGCAGGATGAGCAAGTGCTCTCGGTTCCTCAATGACACGTCTCTGCCTCACAGCTGCTTCAGGATCC
AGCATTATGCTGGAAAGGTGCTGTACCAGGTGGAAGGATTCGTTGACAAAAACAATGACCTTCTCTATCGAGACC
TGTCCCAAGCCATGTGGAAGGCCAGCCATGCCCTCATCAAGTCTTTGTTCCCCGAAGGGAATCCCGCCAAGATCA
ACCTGAAAAGGCCTCCTACAGCAGGCTCACAGTTCAAGGCATCCGTGGCCACTCTGATGAAAAACCTACAGACCA
AGAACCCAAACTATATTAGGTGTATCAAACCGAATGATAAAAAAGCAGCACACATCTTCAACGAGGCTCTAGTGT
GTCATCAGATCAGGTACCTGGGGCTTTTGGAGAACGTCCGAGTGCGGAGGGCAGGCTACGCCTTCAGGCAGGCCT
ATGAACCTTGCCTAGAAAGATACAAAATGCTTTGTAAACAAACATGGCCTCATTGGAAAGGACCAGCCAGGTCTG
GTGTGGAGGTCCTATTTAATGAATTAGAAATTCCCGTGGAAGAATACTCCTTTGGTAGATCAAAGATATTCATCC
GAAACCCAAGAACATTATTCAAATTAGAAGACCTGAGGAAGCAACGCCTGGAGGACTTGGCCACTCTCATTCAGA
AGATATATCGGGGGTGGAAATGCCGCACACACTTCCTGCTAATGAAAAAAAGCCAAATTGTGATTGCCGCCTGGT
ACAGGAGATATGCGCAACAAAAGAGGTACCAGCAGACAAAGAGTTCCGCCTTAGTAATTCAGTCTTATATCCGGG
GTTGGAAGGCTCGAAAAATTCTGCGGGAACTGAAGCATCAAAAGCGCTGTAAGGAAGCAGTCACGACCATTGCTG
CATATTGGCATGGGACCCAGGCTCGAAGGGAATTGAAACGCTTGAAGGAGGAGGCTAGGCGTAAGCATGCAGTTG
CTGTCATTTGGGCTTACTGGCTTGGACTGAAGGTACGTAGAGAATACAGGAAATTCTTCAGAGCCAATGCTGGAA
AGAAAATCTATGAGTTTACGCTTCAGAGAATTGTGCAAAAATACTTCTTGGAAATGAAAAATAAGATGCCTTCCT
TATCTCCAATAGACAAGAATTGGCCCTCAAGACCTTACTTATTCTTGGATTCTACTCACAAGGAGCTAAAAAGGA
TTTTCCACTTGTGGAGGTGTAAAAAATACAGGGACCAATTCACAGACCAGCAGAAACTTATTTATGAAGAGAAAC
TAGAAGCCAGTGAACTCTTCAAAGACAAGAAGGCTTTATACCCATCTAGTGTTGGGCAACCATTCCAAGGGGCTT
ACCTGGAAATCAACAAGAACCCCAAGTATAAGAAACTCAAAGATGCCATTGAAGAAAAGATCATCATTGCTGAAG
TCGTGAACAAAATTAACCGTGCTAATGGGAAGAGTACATCTCGGATTTTCCTCTTAACAAACAATAATCTCCTTC
TTGCTGACCAAAAGTCTGGACAAATCAAGTCAGAGGTTCCATTGGTGGATGTGACCAAGGTATCAATGAGCTCAC
AAAATGATGGCTTCTTCGCCGTCCACCTCAAAGAGGGCTCAGAAGCAGCTAGTAAAGGAGACTTTCTCTTCAGCA
GTGATCACCTGATTGAAATGGCCACCAAGCTCTATCGCACAACTCTCAGCCAAACCAAACAGAAGCTCAATATTG
AGATTTCCGATGAGTTCCTGGTACAGTTCAGACAGGACAAAGTATGTGTGAAGTTTATTAGGAACCCTGTAGTAT
GATATTTAACAATATAGGCTTCAAGAAGGGCTGGTCCTAAGAGGGGGCAGAAATGAATGACCAGGTTAAATCCCT
CTACATGTGGTTTCTGTTTG

FIGURE 929

AGGTCAGAAATGTGAATTCCAGGATGCCTATGTTCTGTTGAGTGAAAAGAAAATTTCTAGTATCCAGTCCATTGT
ACCTGCTCTTGAAATTGCCAATGCTCACCGTAAGCCTTTGGTCATAATCGCTGAAGATGTTGATGGAGAAGCTCT
AAGTACACTCGTCTTGAATAGGCTAAAGGTTGGTCTTCAGGTTGTGGCAGTCAAGGCTCCAGGGTTTGGTGACAA
TAGAAAGAACCAGCTTAAAGATATGGCTATTGCTACTGGTGGTGCAGTGTTTGGAGAAGAGGGATTGACCCTGAA
TCTTGAAGACGTTCAGCCTCATGACTTAGGAAAAGTTGGAGAGGTCATTGTGACCAAAGACGATGCCATGCTCTT
AAAAGGAAAAGGTGACAAGGCTCAAATTGAAAAACGTATTCAAGAAATCATTGAGCAGTTAGATGTCACAACTAG
TGAATATGAAAAGGAAAAACTGAATGAACGGCTTGCAAAACTTTCAGATGGAGTGGCTGTGCTGAAGGTTGGTGG
GACAAGTGATGTTGAAGTGAATGAAAAGAAAGACAGAGTTACAGATGCCCTTAATGCTACAAGAGCTGCTGTTGA
AGAAGGCATTGTTTTGGGAGGGGGTTGTGCCCTCCTTCGATGCATTCCAGCCTTGGACTCATTGACTCCAGCTAA
TGAAGATCAAAAAATTGGTATAGAAATTATTAAAAGAACACTCAAAATTCCAGCAATGACCATTGCTAAGAATGC
AGGTGTTGAAGGATCTTTGATAGTTGAGAAAATTATGCAAAGTTCCTCAGAAGTTGGTTATGATGCTATGGCTGG
AGATTTTGTGAATATGGTGGAAAAAGGAATCATTGACCCAACAAAGGTTGTGAGAACTGCTTTATTGGATGCTGC
TGGTGTGGCCTCTCTGTTAACTACAGCAGAAGTTGTAGTCACAGAAATTCCTAAAGAAGAGAAGGACCCTGGAAT
GGGTGCAATGGGTGGAATGGGAGGTGGTATGGGAGGTGGCATGTTCTAACTCCTAGACTAGTGCTTTACCTTTAT
TAATGAACTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCAATAACTTCAGAGAAGTCAGTTGGAGAAAATGAA
GAAAAAGGCTGGCTGAAAATCACTATAACCATCAGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGC
TGTCATTGTCCATGCCTACAGATAATTTATTTTGTATTTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG
TACAAGAGCCATGTACCAGTGTACTGCTTTCAACTTAAATCACTGAGGCATTTTTACTACTATTCTGTTAAAATC
AGGATTTTAGTGCTTGCCACCACCAGATGAGAAGTTAAGCAGCCTTTCTGTGGAGAGTGAGAATAATTGTGTACA
AAGTAGAGAAGTATCCAATTATGTGACAACCTTTGTGTAATAAAAATTTGTTTAA

FIGURE 930

GCTACACTAGAGCAGAGTACGAGTCTGAGGCGGAGGGAGTA**ATG**GCAGGACAAGCGTTTAGAAAGTTTCTTCCAC
TCTTTGACCGAGTATTGGTTGAAAGGAGTGCTGCTGAAACTGTAACCAAAGGAGGCATTATGCTTCCAGAAAAAT
CTCAAGGAAAAGTATTGCAAGCAACAGTAGTCGCTGTTGGATCGGGTTCTAAAGGAAAGGGTGGAGAGATTCAAC
CAGTTAGCGTGAAAGTTGGAGATAAAGTTCTTCTCCCAGAATATGGAGGCACCAAAGTAGTTCTAGATGACAAGG
ATTATTTCCTATTTAGAGATGGTGACATTCTTGGAAAGTACGTAGAC**TGA**AATAAGTCACTATTGAAATGGCATC
AACATGATGCTGCCCATTCCACTGAAGTTCTGAAATCTTTCGTCATGTAAATAATTTCCATATTTCTCTTTTATA
ATAAACTAATGATAACTAATGACATCCAGTGTCTCCAAAATTGTTTCCTTGTACTGATATAAACACTTCCAAATA
AAAATATGTAAAT

FIGURE 931

MAGQAFRKFLPLFDRVLVERSAAETVTKGGIMLPEKSQGKVLQATVVAVGSGSKGKGGEIQPVSVKVGDKVLLPE
YGGTKVVLDDKDYFLFRDGDILGKYVD

FIGURE 932

GATTTGACCCTTGAGCCGTAGGGAGCGCGGCATTTTCTGGAAAGTTCTGGAACCGAGCGAGGCCCGGGAACTAGA
CTAAGCCGGCCGGAGAGGGCTGAGCGCGCTAGCACACCCTGCGCGGAAATGCTTCGGTTACCCACAGTCTTTCGC
CAGATGAGACCGGTGTCCAGGGTACTGGCTCCTCATCTCACTCGGGCTTATGCCAAAGATGTAAAATTTGGTGCA
GATGCCCGAGCCTTAATGCTTCAAGGTGTAGACCTTTTAGCCGATGCTGTGGCCGTTACAATGGGGCCAAAGGGA
AGAACAGTGATTATTGAGCAGAGTTGGGGAAGTCCCAAAGTAACAAAAGATGGTGTGACTGTTGCAAAGTCAATT
GACTTAAAAGATAAATACAAAAACATTGGAGCTAAACTTGTTCAAGATGTTGCCAATAACACAAATGAAGAAGCT
GGGGATGGCACTACCACTGCTACTGTACTGGCACGCTCTATAGCCAAGGAAGGCTTCGAGAAGATTAGCAAAGGT
GCTAATCCAGTGGAAATCAGGAGAGGTAGGAATGTCTGTTGTCACCACAGTGTTCTAAACTTCAGTGTGCTTTAA
GGCATTGATTCCTTGGACCTAAGGAAAGTGTTAACTTGAGGAAATTAATCCTTCTCTCATTCCTCCTCTTGGCCT
GGAGAAATCTTAAACTGGGTTTTCCTTTAGCAAGCTTGGCTGT

FIGURE 933

TGGAAAGAGTGGAACGAGAAAACCTTTCAGACTATTGTGTTCTGGGCCAGCGTCCAATGCATTTACCAAATATGA
ACCAGCTGGCATCCCTGGGGAAAACCAACGAACAGTCTCCTCACAGCCAAATTCACCACAGTACTCCAATCCGAA
ACCAAGTGCCCGCATTACAGCCCATCATGAGCCCTGGTCTTCTTTCTCCCCAGCTTAGTCCACAACTTGTAAGGC
AACAAATAGCCATGGCCCATCTGATAAACCAACAGATTGCCGTTAGCCGGCTCCTGGCTCACCAGCATCCTCAAG
CCATCAACCAGCAGTTCCTGAACCATCCACCCATCCCCAGAGCAGTTAAGCCAGAGCCAACCAACTCTTCCGTGG
AAGTCTCTCCAGATATCTACCAGCAAGTCAGAGATGAGCTGAAGAGGGCCAGTGTGTCCCAAGCTGTCTTTGCAA
GAGTGGCATTCAACCGCACACAGGTACAATTAGCATTAAACACTGTAATTAACAGTAATACTGGGGACAGAATTG
AGATAGGTTATAATTATTTTTATCTCTTTAAAAAGCTTTATGGATCTCAGGACATAGAATTAGATTAATTAATAA
TCCTTAGTTAATGAAACGCTATTACCATTGATCCATGCATGACCATGATTAATTAACTAATTGATTAATTTTGAT
GAGGTAATGGACATCTTTGAACCCAACATGCAACTCAGGACCCCAAATGTTACTAATGACTTGGGTATGTACTCT
CTCATCCTCTCCATTTACTGTTTGCAGATGTAACCCTGATCTTGAATTTTGTGATTATCAGTCTCTTGCCATTTT
TTAAAACAAATTATAAAACTATGCATGCCCAGACAATCTATTTTTTTCCCTTGGTTTGAACGTTATAAAAGAAA
TAAAATTATGTTTTATAATTTTATAAGTAAAGTTTTATTTAAAAATTTATAAAAATCCTTCAAAACATAAAAGTT
AGATTTAAGATATTGATAAAATGATAATGGATAGTTTACTTTTATTTTTAATGTTTGAGAGAATTATATGCCAAT
TATAACACTAAATGTTGAAAATGTAAACAGTTAATTCACACGTCTTATTTTTATTGAGGGTGCTTATATGTAAGA
CATTCTTTTCTGCTAGTAGTTCTTAAACTGGAGTGTGCATCAGAATCACCTGGAGGGCTGTGAAACACAGACTGC
TGGGCCTCATCCCATAGTTTCTGATTGAGTAAGTCTGAGGTTGGACTCAGAAATGGACATTTCTAACAAGATCCC
AGGTGATTATGATGGTACTGATCCGGGGCCGCATGTTGAGAAAAACTTACCTAGCCCTTATATGAGTAAGAACAA
AGCAGATGTGCATAATCTCGGGGAGCTAACGATCTAGTGGTGAAAACCAGGTAACCAGATAATTAGAGTAAAATG
TGAAGTGTTATGAGTAATGTTGGAGAGTGTAAGCAATAGTTGTGGTGGAGGTTCATGGTGAGCTGGAGGTGAGGA
ATACTTCCAGGAGAATGAATATGGTAAGCCTTCAAGAAAACAGTAGATTAAAATTTCAGCACCCTCGTAAATGCA
AGGCAGGAAGCTAAGCTCTATGTGGGTGCAAAGAGGAAAAAGATAATGGGCAAGCACATATGTAAACAACACTCT
AGAGTATTAGGTTGTCAATGGGTTAGACCTTGAAGGATTAATAAAGTACAGCAGGCAAAGATGATGAAGAAGAAG
ATTATTATTTTAAGGTAAAGACATTCATAGGAAAGATGTTGAGTTAAAAAATGCAGGAATAATTTGAAGACATAA
AACAACTGATTTCTGAGAAAAACCCTGTGAACGTACAGAATGTAGGAATGCTTTCATTTATCTGATACCTGTTCA
GAGACACATGATAACACACGCTGTAGATGGACCTTACAAATGAAAGAAAGCATGCTGGATTGAAACCTCAATAAT
TTGGAAAATACAGGAATGTTTCCAAATTTAATGATTACTTCAGAAGTTAAGGGGCTGGGCACAGTGGCTCATGTC
TGTAGTCCTAGCACTTTGGGAGGCCAAGGTGGGCGGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGGCAAG
ATGGTAAAACACCATCTCTACTAAAACAGAACAAAACAAAAAAATTAGCTGGGCGTGGTGATGCGTGCCTGTAGT
CTCAGCTACTCAGGAGGCTGAGGCAGAAGAATCCCTTGAACCCAGGAGGCGGAGGCTGCAGTGAGCCGAGATCAT
GCCACTGCACTCCAGCCTGAGTGAGAGTGAAACTCCATCTCAAAAAAAAAAAAAAAAA

FIGURE 934

GAGAGGAGACACCGCCGCAGTTGCCGGTACATCGGGGATTTCTGGCTCTTTCCTCTTCGCCTTAAATTCGGGTGT
CTTTT**ATG**AATAATCAAAAGCAGCAAAAGCCAACGCTATCAGGCCAGCGTTTTAAAACTAGAAAAAGAGATGAAA
AAGAGAGGTTTGACCCTACTCAGTTTCAAGACTGTATTATTCAAGGCTTAACTGAAACCGGTACTGATTTGGAAG
CAGTAGCTAAGTTTCTTGATGCTTCTGGAGCAAAACTTGATTACCGTCGATATGCAGAAACACTCTTTGACATTC
TGGTGGCTGGTGGAATGCTGGCCCCAGGTGGTACACTGGCAGATGACATGATGCGTACAGATGTCTGCGTGTTTG
CAGCCCAAGAAGATCTAGAGACCATGCAAGCATTTGCTCAGGTTTTTAACAAGTTAATCAGGCGCTACAAATACC
TGGAGAAAGGTTTTGAAGATGAAGTAAAAAAGCTGCTGCTGTTCTTGAAGGGTTTTTCAGAGTCGGAGAGGAACA
AGCTAGCTATGTTGACTGGTGTTCTTCTGGCTAATGGAACACTTAATGCATCCATTCTTAATAGCCTTTATAATG
AAAATTTGGTTAAAGAAGGAGTTTCAGCAGCTTTTGCTGTGAAGCTCTTTAAATCATGGATAAATGAAAAAGATA
TCAATGCAGTAGCTGCAAGTCTTCGGAAAGTCAGCATGGATAACAGACTGATGGAACTCTTTCCTGCCAATAAGC
AAAGTGTTGAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAAGAGCTTTCAGAATATGTTCGGAATCAGC
AAACCATCGGAGCTCGTAAGGAGCTCCAGAAAGAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATA
TAATTTTATATGTCAAGGAGGAGATGAAAAAAAACAACATCCCAGAGCCAGTTGTCATCGGAATAGTCTGGTCAA
GTGTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAGCTTGTAGCAGAGCAAGCCATCAAGCACTTGAAGCAAT
ACAGCCCTCTACTTGCTGCCTTTACTACTCAAGGTCAGTCTGAGCTGACTCTGTTACTGAAGATTCAGGAGTATT
GCTATGACAACATTCATTTCATGAAAGCCTTCCAGAAAATAGTGGTGCTTTTTTATAAAGCTGAAGTCCTGAGCG
AGGAGCCCATTTTGAAGTGGTATAAAGATGCACATGTTGCAAAGGGGAAGAGTGTTTTCCTTGAGCAAATGAAAA
AGTTTGTAGAATGGCTCAAAAATGCTGAAGAAGAATCTGAATCTGAAGCTGAAGAAGGTGAC**TGA**ATTTTGAAAC
TACACCCTCAGTAAAGCAAACAGGAGTTGTAGATAAAATGTCATGTCTCATGTGTCCTGGTTCTTACATCTTCCT
ACCTCCCTGTATCAAGCATGATATAAGGGCTTTCATGGCAAATTTTATTTTAACTGTTTCTATGGTTGCTGGAAA
TGTTGGGTTTAGTTTCTAAAACCATGTTTTAAGTAGCTACAGGAGCTATAGATTTGAATCTAATGTTGCATTAGT
CTTTTCAGTTATCTTCTACCTCCTGTATTTTCTACTGTAATAATGTAATTTAAGGCCTTCCACAATGAACAGTTC
ACTTTATTCCCTGGGTTTTCTATAAACAGTTTTAAGGATATGATTTGGTTAAAAAAATAATTTGTTATAAAAAATTC
TGTTTGCAAATTAAACTGGAAAAGTATCCAGAGTCTCAAAAGGCAATGATTTGTGAGATAATATGGCATGCCCGG
AGCCCTGCTCATCAATGAAAAACCCATATGTAATAATCGAATTCATTTAACATGAATCTTGAGTACGTGGACCAT
TGCTTGCATGTTAACTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGCATTTTTAACTCCAGATATCCTAAAGCTC
AATTGTTTGGTCTCTGGTTTTCATCCTTAGAGAAGCCATGGAGAACAGACTTGAAAAGTTTAGGAAATCATAATG
TGGCAGAGGTGGTGGGAAGAAGAAAGTTGAGCTTTTTCCCCTTGAGAAACTTCTGCATTTAGTTTCTATCTTTCC
AGGCAAAACAAATGGGTATTCTTTTCATACAACCATTTTCAAATGAACCTTAGAAAAGTCTTAACATTTAAGGTA
TTTTATGCACAGAATACACTTAGATTGATAGGAAAGAACTCGTAATGGAGTTTGAGTAAAGAAAATGACTGATGT
ACTAAACCCAGTAAAAATTGTTGAAAATGTTAAAGGTCAGCATGTTCTAATTGGGAATCTAGATATAGCTTAGAT
TTCCTATTGGCTTAGAGTATTTGCTATAACAAATGAAGTGCAATGACAATTATATATTCCTACTCGGTCATACTG
GACTGGCTTCGTTCTCTTAATATACTCAGTAATGACTCAAGCCTCTGGCTATTAACATACCCTAGTTGCCGTTTT
TTAATTGCCATGAGCCAAATACTTCTTGGTATACAATTGATCCATTTATTTTAATGGCTGCCTTTTCATTTTCAT
CTTTTCTTGCTGCTACCCATCTATGTATGTAGTCATTGGGGGGAAAATGTAGCCACATTTTTTATGGGAAGACTT
TGTGTTAAAAGTGAACATTTTGAAGGTTTTTAACTGGTGAAACTAGCCTGGAATAATGCCACCAGAGACTGAGTG
GAAATCGCCCCTTTTGAAGGTGCCATTCTTATGAGCCAAAAGTTTGTCATTTAAAAGTTCATTTTGAGGGAATAA
CATGTAATATAATTTGAAATAAAGGTATAGTAACCTTAAAAAGAACATTATAACTGATTGTTGTGAATGGGGTGA
ATTTGTTAAAATGAGTAACTTTGATAAAGTTTTTCATGCACAGGCAAAATGTATTCACTAGATTTCTACGTAGTG
ATCTGCTTTTACTTTGTAATTTGTAGTTCTCAAAAGACTTTTTTTAAAAAAATAAAGTCCATACTTACACTT

FIGURE 935

MNNQKQQKPTLSGQRFKTRKRDEKERFDPTQFQDCIIQGLTETGTDLEAVAKFLDASGAKLDYRRYAETLFDILV
AGGMLAPGGTLADDMMRTDVCVFAAQEDLETMQAFAQVFNKLIRRYKYLEKGFEDEVKKLLLFLKGFSESERNKL
AMLTGVLLANGTLNASILNSLYNENLVKEGVSAAFAVKLFKSWINEKDINAVAASLRKVSMDNRLMELFPANKQS
VEHFTKYFTEAGLKELSEYVRNQQTIGARKELQKELQEQMSRGDPFKDIILYVKEEMKKNNIPEPVVIGIVWSSV
MSTVEWNKKEELVAEQAIKHLKQYSPLLAAFTTQGQSELTLLLKIQEYCYDNIHFMKAFQKIVVLFYKAEVLSEE
PILKWYKDAHVAKGKSVFLEQMKKFVEWLKNAEEESESEAEEGD

FIGURE 936

ACGCAGAGAAGTTTCCGGGACTGAAACTTGAACTTTACCTGATTTCTGT<u>ATG</u>TTGTCATCTTGCGTACGCCCAGT
CCCCACGACAGTCCGGTTTGTAGATTCCCTGATCTGCAATTCTTCCCGTTCCTTCATGGATTTGAAGGCTCTCCT
TTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAGAGTTGGGACAATGTTGGATTACTGGTGGAACCAAG
CCCACCACATACTGTAAATACACTCTTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAA
GAAGGCAGACCTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACATGGAA
GGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCGCC
CCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCTTGTACCTCCAGGCCCATACATCCTTCCAAAGCTCC
CAACTACCCTACAGAGGGAAACCACCGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTC
TGCAGTGAAAGGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACACGGAT
TAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGGAACAAACAACTTTATCAGAA
GACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACATACTGGAATGGGACGGTTATGCACACTGGATGAATC
TGTCTCCCTGGCAACCATGATTGATCGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGT
GGGGAGAACCTTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAGGGTGT
TGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCTGCTTCCCAAGGAATAAATGT
CATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTTTCTGACCTTCGAGATATGCTGGATTCTCACTTGGA
GAATAAGATAAATATTATCCTATCAGAGACTGACAGGGACCCTCTTCAGGTGGTA<u>TAA</u>TTGCAGAAACATCAGGA
TAACACATTCTACAAATCAGCTGGATGCCAACTTAAATTTGTAACATGAGTCAGTGGGACTGGTGTGCTTCCAGA
GAGTGTCTTCGAGGGTATCATCATTTCCGGTTTGTTAATCTTATTCACCAAATGTTCTATCGCTCGTAAGGTAAA
ACTGTAATATAACTACCATATTAAATAACAAATGTTCATTATAAACTCTAGGAAAGATTGAATAAAATCTGTTTA
CTTAACATTC

FIGURE 937

MLSSCVRPVPTTVRFVDSLICNSSRSFMDLKALLSSLNDFASLSFAESWDNVGLLVEPSPPHTVNTLFLTNDLTE
EVMEEVLQKKADLILSYHPPIFRPMKRITWNTWKERLVIRALENRVGIYSPHTAYDAAPQGVNNWLAKGLGACTS
RPIHPSKAPNYPTEGNHRVEFNVNYTQDLDKVMSAVKGIDGVSVTSFSARTGNEEQTRINLNCTQKALMQVVDFL
SRNKQLYQKTEILSLEKPLLLHTGMGRLCTLDESVSLATMIDRIKRHLKLSHIRLALGVGRTLESQVKVVALCAG
SGSSVLQGVEADLYLTGEMSHHDTLDAASQGINVILCEHSNTERGFLSDLRDMLDSHLENKINIILSETDRDPLQ
VV

FIGURE 938

CTCCTTTCTGCCCGTGGACGCCGCCGAAGAAGCATCGTTAAAGTCTCTCTTCACCCTGCCGTCATGTCTAAGTCA
GAGTCTCCTAAAGAGCCCGAACAGCTGAGGAAGCTCTTCATTGGAGGGTTGAGCTTTGAAACAACCGATGAGAGC
CTGAGGAGCCATTTTGAGCAACGGGGAACGCTCACAGACTGTGTGGTAATGAGAGATCCAAACACCAAGTGCTCC
ACGGGCTTTGGGTTTGTCACATATGCCACTGTGAAGGAGGTGGAGGCAGCTATGAATGCAAGGCCACAGAAGGTG
GATGGAAGAGTCGTGGAACCAAAGAGAGCTGTCTCGAGAGAAGATTCTCAAAGACCAGGTGCCCACTTAACTGTG
AAAAAGATATTTGTTGGTGGCATTAAAGAAGACACTGAAGAACATCACCTAAGAGATTATTTTGAACAGTATGGA
AAAATTGAAGTGATTGAAATCATGACTGACCGAGGCAGTGGGAAGAAAAGGGGCTTTGCCTTTGTAACCTTTGAT
GACCATGACTCCGTGGATAAGATTGTCATTCAGAAATACCACACTGTGAATGGCCACAACTGTGAAGTTAGAAAA
GCCCTGTCAAAGCAAGAGATGACTAGTGCTTCATCTAGCCAAAGAGGTCGAAGTGGTTCTGGAAACTTTGGTGGT
GGTCGTGGAGGTGGTTTCAGTGGGAATGACAACTTTGGTCATGGAAGAAACTTCAGTGGTCATGGTGGCTTTGGT
GGCAGCCGTGGTGGTGGTGGATATGATGGCAGTGGGGATGGCTATAATGGATTTGGTAATGATGGAAGCCATTTT
GGAGGTGGTGGAAGCTACAATGATTTTGGCAATTACAAAAATCAGTCTTCAAATTTTGGACCCGTGAAGGGAGGA
AATTTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTGGAGGCCAATACTTTGCAAAACCACGAAACTAAGGTGGC
TATGGCGGTTCCAGCAGTAGCAGTAGCTATGGCAGTGGCAGAAGATTTTAATTAGGAAACAAAGCTTAGCAGGAG
AGGAGAGCCAGAGAAGTGACAGGGAAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCACAGTGGTGGCA
GGGCCTAGCTGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAAACTCGAGGACTGTAT
TTGTGACTAATTGTATAACAGGTTATTTTAGTTTCTGTTCTGTGGAAAGTGTAAAGCATTCCAACAAAGGGTTTT
AATGTAGATTTTTTTTTTTGCACCCATGCTGTTGATTGCTAAATGTAATAGTCTGATCGTGACGCTGAATAAATG
TCTTTTTTTTTAATGTGCTGTGTAAAGTTAGTCTACTCTGAAGCCATCTTGGTAAATTTCCCCAACAGTGTGAAG
TTAGAATTCCTTCAGGGTGATGCCAGGTTCTATTTGGAATTTATATACAACCTGCTTGGGTGGAGAAGCTATTGT
CTTCGGAAACCTTGGTGTAGTTGAACTGATAGTTACTGTTGTGACCTGAAGTTCACCATTAAAAGGGATTACCCA
AGCAAAATCATGGAATTATTGGTTATAAAAGTGATTGTTGGCACATCCTATGCAATATATCTAAATTGAATAATG
GTACCAGATAAAATTATAGATGGGAATGAAGCTTGTGTATCATCCATTATCATGTGTAATCAATAAACGATTTAA
TTCTCTGGAA

FIGURE 939

MSKSESPKEPEQLRKLFIGGLSFETTDESLRSHFEQRGTLTDCVVMRDPNTKCSTGFGFVTYATVKEVEAAMNAR
PQKVDGRVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAF
VTFDDHDSVDKIVIQKYHTVNGHNCEVRKALSKQEMTSASSSQRGRSGSGNFGGGRGGGFSGNDNFGHGRNFSGH
GGFGGSRGGGGYDGSGDGYNGFGNDGSHFGGGGSYNDFGNYKNQSSNFGPVKGGNFGGRSSGPYGGGGQYFAKPR
NRWLWRFQQVAVAMAVAEDF

FIGURE 940

GAGGCGTAGCGGAAGTTACTGCAGCCGCGGTGTTGTGCTGTGGGGAAGGGAGAAGGATTTGTAAACCCCGGAGCG
AGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGAGACCCCCGGGTGAAGCCACCGTCATCATGTCTGACCAGGAG
GCAAAACCTTCAACTGAGGACTTGGGGGATAAGAAGGAAGGTGAATATATTAAACTCAAAGTCATTGGACAGGAT
AGCAGTGAGATTCACTTCAAAGTGAAAATGACAACACATCTCAAGAAACTCAAAGAATCATACTGTCAAAGACAG
GGTGTTCCAATGAATTCACTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCTGATAATCATACTCCAAAAGAACTG
GGAATGGAGGAAGAAGATGTGATTGAAGTTTATCAGGAACAAACGGGGGGTCATTCAACAGTTTAGATATTCTTT
TTATTTTTTTTCTTTTCCCTCAATCCTTTTTTATTTTTAAAAATAGTTCTTTTGTAATGTGGTGTTCAAAACGGA
ATTGTTATTCATTATTGTTTGTTTTCATTGTGCTGATTTTTGGTGATCAAGCCTCAGTCCCCTTCATATTACC

FIGURE 941

ATGTTGGTGCTGTTTGAAACGTCTGTGGGTTACGCCATCTTTAAGGTTCTAAATGAGAAGAAACTTCAAGAGGTT
GATAGTTTATGGAAAGAATTTGAAACTCCAGAGAAAGCAAACAAAATAGTAAAGCTAAAACATTTTGAGAAATTT
CAGGATACAGCAGAAGCATTAGCAGCATTCACAGCTCTGATGGAGGGCAAAATCAATAAGCAGCTGAAAAAAGTT
CTGAAGAAAATAGTAAAAGAAGCCCATGAACCGCTGGCAGTAGCTGATGCTAAACTAGGAGGGGTCATAAAGGAA
AAGCTGAATCTCAGTTGTATCCATAGTCCTGTTGTTAATGAACTTATGAGAGGAATTCGTTCACAAATGGATGGA
TTAATCCCTGGGGTAGAACCACGTGAAATGGCAGCTATGTGTCTTGGATTGGCTCACAGCCTGTCTCGATATAGA
TTGAAGTTTAGCGCTGATAAAGTAGACACAATGATTGTTCAGGCAATTTCCTTGTTAGATGACTTGGATAAAGAA
CTAAACAACTACATTATGCGATGTAGAGAATGGTATGGCTGGCATTTCCCTGAATTAGGAAAAATTATTTCAGAT
AATTTAACATACTGCAAGTGTTTACAGAAAGTTGGCGATAGGAAGAACTATGCCTCTGCCAAGCTTTCTGAGTTG
CTGCCAGAAGAAGTTGAAGCAGAAGTGAAAGCAGCTGCAGAGATATCAATGGGAACAGAGGTTTCAGAAGAAGAT
ATTTGCAATATTCTGCATCTTTGCACCCAGGTGATTGAAATCTCTGAATATCGAACCCAGCTCTATGAATATCTA
CAAAATCGAATGATGGCCATTGCACCCAATGTTACAGTCATGGTTGGGGAATTAGTTGGAGCACGGCTTATTGCT
CATGCAGGTTCTCTTTTAAATTTGGCCAAGCATGCAGCTTCTACCGTTCAGATTCTTGGAGCTGAAAAGGCACTT
TTCAGAGCCCTCAAATCTAGACGGGATACCCCTAAGTATGGTCTCATTTATCATGCTTCACTCGTGGCCAGACA
AGTCCCAAACACAAAGGAAAGATTTCTCGAATGCTGGCAGCCAAAACCGTTTTGGCTATCCGTTATGATGCTTTT
GGTGAGGATTCAAGTTCTGCAATGGGAGTTGAGAACAGAGCCAAATTAGAGGCCAGGTTGAGAACTTTGGAAGAC
AGAGGGATAAGAAAAATAAGTGGAACAGGAAAAGCATTAGCAAAAACAGAAAAATATGAACACAAAAGTGAAGTG
AAGACTTACGATCCTTCTGGTGACTCCACACTTCCAACCTGCTCTAAAAAACGCAAAATAGAACAGGTAGATAAA
GAGGATGAAATTACTGAAAAGAAAGCCAAAAAAGCCAAGATTAAAGTTAAAGTTGAAGAAGAGGAAGAAGAAAAA
GTGGCAGAAGAAGAAGAAACATCTGTGAAGAAGAAGAAGAAAAGGGGTAAAAAGAAACACATTAAGGAAGAACCA
CTTTCTGAGGAAGAACCATGTACCAGCACAGCAATTGCTAGTCCAGAGAAAAAGAAGAAAAAGAAAAAAAAGAGA
GAGAACGAGGATTAA

FIGURE 942

GGAGGCCAAGGTGCAACTTTCTTCGGTCGTCCCGAATCCGGGTTCATCCAACACCAGCCGCCTCCACC<u>ATG</u>CCGC
CGAAGTTCGACGGTGCCACTTCTGCCCTGGCCCCCAAGATCGGCCCCCTGGGTCTGTCTCCAAAAAAGGTTGGTG
ATGACATTGCCAAGGCAACGGGTGACTGGAAGGGCCTGAGGATTACAGTGAAACTGACCATTCAGAACAGACAGG
CCCAGATTGAGGTGGTGCCTTCTGCCTCTGCCCTGATCATCAAAGCCCTCAAGGAACCACCAAGAGACAGAAAGA
AACAGAAAAACATTAAACACAGTGGGAATATCACTTTTGATGAGATCGTCAACATTGTTCGACAGATGCGGCACC
GATCCTTAGCCAGAGAACTCTCTGGAACCATTAAAGAGATCCTGGGGACTGCCCAGTCTGTGGGCTGTAATGTTG
ATGGCCGCCATCCTCATGACATCATCGATGACATCAACAGTGGTGCTGTGGAATGCCCAGCCAGT<u>TAA</u>GCACAAA
GGAAAATATTTCAATAAAGGATCATTTGACAACTG

FIGURE 943

MPPKFDGATSALAPKIGPLGLSPKKVGDDIAKATGDWKGLRITVKLTIQNRQAQIEVVPSASALIIKALKEPPRD
RKKQKNIKHSGNITFDEIVNIVRQMRHRSLARELSGTIKEILGTAQSVGCNVDGRHPHDIIDDINSGAVECPAS

FIGURE 944

ATGGAAGATTTGATGGACATGGACATGAGCCTCCTGAGGCCCCAGAACTATCTTTTCGGTTGTGAACTAAAGGCC
GACAAAGATGATCACTTTAAGGTGGATAATGATGAAAATGAGACCATCAGTTTAGGGGCTGGTGCAAGGGATGAA
TTGCACATTGTTGAAGCAGAGGCCATGAATGATGAAGGCAGTCCAATTAAAGTCACACTGGCAACTTTGAAAATG
TCTGTACAGCCAACTGCTTCCCTTGGGGGCTTTGAAATCACACCACCAGTGGTCTTACAGTTGAAGTGTGGTTCA
GGGCCAGTGCATATTAGTAGACAGTGCTTAGTAGCTGTGGAGGAAGATGCAGAGTCAGAAGATGAAGAGGAGGAG
GATGTGAACCTCTTAAGCATATCTGGAAAGCGGTCTGCCTCTGGAGGTGGTAGCAAGGCGCCCAGCTACCGCGCC
CACTGGTCAGAAGTGTGGCCAGCGTCTATGCAGGCCCTGGGAGCTCAGGGTGGCTTGGGGTCCAGGAGCATGGCC
GCAGGTATGGCCGGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAAGGAGACCATGCAAAGCCTGAATGAC
CGCCTGGCCTCCTACCTGGACAGAGTGAGGAGCCTGGAGATGGGAAACTGGAAGCTGGAGAGCAAAATCTGGGAG
CACCTGGAGAAGAAGGGACCCCAGGTCAGAGACTGGGGCCACTACTTCAAGACCATCGAGGAGGACCTGACTCAG
ATCTTCACAAGTACTGTGGACAATACCTGCATCATTCTGCAGATCGACAATGCCCATCTTGCTGCTGATGACTTT
AGAGTCAAGTATGAGACAGAGCCGGCCACGTGCCAGTCTGTGGAGAACGACATCCATGGGCTCCACAAGGTCATT
GATGACACCAGTGTCACTCAGCTGCAGCTAGAGACAGAGATCGAGGCTCTCAAGGAGGAGCTGCTCTTCCTGAAG
AAGAACCACGAAGAGGAAGTAAAAGGCCTACAAGCCCAGATTGCCAGCTCTGTTGACCATGGAGGCCTTGGAGAT
CGACCTGGACTGGATGAAAAATCTGGAGGCCAGCTTGGAGAACAGCCTGAAGGGGGGGTGGAGGCCTGCTACACC
CTGCAGATGGAACAACTCAATGGGATCCTGCTGCACCTGGAGTCAGAGCTGGCACAGACCTGGGCAGAGGGACAG
GGCCAGGCCCAGGAGTACCAGGCCCTGCCAAACATCAAGCAGCAACTCCACGCAAACCATCCAAAAGACTCCCAC
CTGCCAACAGTGGATGGCAAAGTGGTGTCTGAGACCAATGACACCAAAGTTCTGAGACAT**TAA**

FIGURE 945

MEDLMDMDMSLLRPQNYLFGCELKADKDDHFKVDNDENETISLGAGARDELHIVEAEAMNDEGSPIKVTLATLKM
SVQPTASLGGFEITPPVVLQLKCGSGPVHISRQCLVAVEEDAESEDEEEEDVNLLSISGKRSASGGGSKAPSYRA
HWSEVWPASMQALGAQGGLGSRSMAAGMAGGLAGMGGIQNEKETMQSLNDRLASYLDRVRSLEMGNWKLESKIWE
HLEKKGPQVRDWGHYFKTIEEDLTQIFTSTVDNTCIILQIDNAHLAADDFRVKYETEPATCQSVENDIHGLHKVI
DDTSVTQLQLETEIEALKEELLFLKKNHEEEVKGLQAQIASSVDHGGLGDRPGLDEKSGGQLGEQPEGGVEACYT
LQMEQLNGILLHLESELAQTWAEGQGQAQEYQALPNIKQQLHANHPKDSHLPTVDGKVVSETNDTKVLRH

FIGURE 946

GACAGTTTAGCAGAACAGCCTCCGCGGCTCCGGGGAGAAGCAATATGTTAAGGATACCTGTAAGAAAGGCCTTAG
TAGGCCTTTCTAAGTCTCCTAAAGGATGTGTTCGAACAACTGCCACAGCAGCAAGCAACTTGATTGAAGTATTTG
TTGATGGTCAGTCTGTCATGGTGGAACCGGGAACGACCGTCCTCCAAGCTTGTGAGAAGGTTGGCATGCAGATCC
CTCGATTCTGTTATCATGAAAGGTTGTCTGTTGCTGGAAACTGCAGGATGTGCCTTGTTGAAATTGAGAAAGCCC
CTAAGGTTGTAGCTGCTTGTGCCATGCCAGTAATGAAGGGTTGGAATATCCTAACAAACTCAGAAAAATCCAAAA
AAGCCAGGGAAGGTGTGATGGAGTTCTTATTAGCAAATCACCCATTGGACTGTCCTATTTGTGACCAGGGAGGTG
AATGTGATCTGCAGGACCAGTCCATGATGTTTGGAAATGATAGGAGCCGATTTTTAGAGGGGAAGCGTGCTGTGG
AAGACAAGAACATTGGGCCATTGGTAAAGACCATCATGACAAGATGTATACAGTGTACTCGCTGCATCAGGTTTG
CAAGTGAGATTGCAGGAGTAGATGATTTGGGAACAACAGGCAGAGGAAATGATATGCAAGTTGGCACATACATTG
AAAAGATGTTCATGTCTGAACTGTCTGGGAATATCATTGATATCTGCCCTGTAGGTGCCCTAACCTCTAAGCCCT
ATGCCTTTACTGCCCGGCCTTGGGAAACAAGAAAGACAGAATCCATTGATGTAATGGATGCGGTTGGAAGTAATA
TTGTGGTTAGCACAAGAACTGGAGAAGTGATGAGGATTTTGCCACGTATGCATGAGGACATCAATGAAGAGTGGA
TCTCTGATAAAACCAGATTTGCCTATGATGGGCTAAAACGTCAAAGACTTACCGAGCCAATGGTCAGAAATGAAA
AAGGGCTTTTAACCTATACTTCTTGGGAGGATGCGCTCTCTCGCGTAGCTGGAATGTTGCAGAGTTTTCAAGGCA
AAGATGTGGCAGCAATTGCAGGTGGCTTGGTGGATGCTGAAGCCCTGGTAGCTCTCAAAGATTTGCTTAATAGAG
TGGACTCTGACACCTTATGCACTGAAGAGGTCTTCCCCACTGCAGGAGCTGGCACAGATTTGCGTTCCAATTATC
TTCTTAATACTACAATTGCTGGTGTGGAAGAGGCAGATGTTGTTCTTCTGGTTGGTACAAACCCACGTTTTGAGG
CACCACTGTTTAATGCTAGAATTCGAAAGAGCTGGCTGCATAATGACTTAAAAGTGGCCCTTATAGGCAGTCCAG
TGGACCTCACTTACACATATGACCACCTGGGAGACTCCCCCAAAATTCTTCAAGACATTGCTTCGGGAAGCCATC
CATTTAGCCAGGTCCTAAAGGAAGCTAAAAAACCAATGGTGGTTTTAGGCAGTTCTGCACTCCAAAGAAATGATG
GAGCAGCAATTCTTGCAGCTGTTTCTAGCATTGCACAAAAGATTCGGATGACTAGTGGTGTTACTGGTGATTGGA
AAGTTATGAATATCCTTCATAGGATTGCAAGTCAAGTAGCTGCTTTGGACCTTGGCTATAAGCCTGGGGTGGAAG
CAATTCGGAAGAACCCTCCCAAGGTGCTGTTTCTCCTGGGAGCAGATGGAGGTTGTATCACACGACAGGATTTGC
CAAAGGATTGTTTCATTATTTATCAAGGACATCATGGTGATGTTGGGGCTCCCATAGCTGATGTTATTCTCCCAG
GAGCTGCTTACACAGAGAAGTCTGCTACATATGTCAACACTGAGGGTAGAGCTCAGCAGACTAAGGTAGCAGTGA
CACCTCCTGGCTTGGCAAGAGAAGACTGGAAAATTATAAGAGCACTCTCTGAGATTGCTGGAATGACTCTTCCAT
ATGATACTCTGGATCAAGTAAGGAACAGATTGGAAGAAGTCTCTCCTAATCTTGTTCGATATGATGATATTGAAG
GGGCTAATTACTTCCAGCAAGCAAATGAGCTCTCAAAGCTAGTGAACCAGCAGCTTCTTGCTGACCCACTTGTTC
CACCTCAGCTAACTATAAAAGACTTCTACATGACAGATTCAATTAGCAGAGCCTCACAGACAATGGCCAAATGTG
TCAAAGCTGTCACAGAGGGTGCCCAGGCAGTAGAGGAACCATCCATATGCTGAAGCTTCTACTAGGATCCCAGTT
TTGCCGCAGATAATTAATGGACAACTGTAGTGCAGTGATCCTTTACAGGTTTATTTCTTTGTAAAAAAAAATAAT
AATAATTTGAATCATGTAATATTTAAGGTTATACTATGCCTATTTGAAAATGATATTAGTTATCAACTTTGCAGT
TTGAAAAACATGTATTGTGTGTAAAGGTTAAATAACAAAACTATGCAGATGCTCTTAAAAGCATTGATAACCTTT
GTGACGAACATAAAGAGATCCTTAAATT

FIGURE 947

MLRIPVRKALVGLSKSPKGCVRTTATAASNLIEVFVDGQSVMVEPGTTVLQACEKVGMQIPRFCYHERLSVAGNC
RMCLVEIEKAPKVVAACAMPVMKGWNILTNSEKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFGNDR
SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDDLGTTGRGNDMQVGTYIEKMFMSELSGNIIDI
CPVGALTSKPYAFTARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDINEEWISDKTRFAYDGLKRQ
RLTEPMVRNEKGLLTYTSWEDALSRVAGMLQSFQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTEEVFPTA
GAGTDLRSNYLLNTTIAGVEEADVVLLVGTNPRFEAPLFNARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPK
ILQDIASGSHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAQKIRMTSGVTGDWKVMNILHRIASQVAA
LDLGYKPGVEAIRKNPPKVLFLLGADGGCITRQDLPKDCFIIYQGHHGDVGAPIADVILPGAAYTEKSATYVNTE
GRAQQTKVAVTPPGLAREDWKIIRALSEIAGMTLPYDTLDQVRNRLEEVSPNLVRYDDIEGANYFQQANELSKLV
NQQLLADPLVPPQLTIKDFYMTDSISRASQTMAKCVKAVTEGAQAVEEPSIC

FIGURE 948

GCCTCGAGGCGGGCGTCTTCGGTCATCTCCGGCGCTTCTAGGGCTGGTTCCCGTCATCTTCGGGAGCCGTGGAGC
TCTCGGATACAGCCGACACC**ATG**GGTTTCGGAGACCTGAAAAGCCCTGCCGGCCTCCAGGTGCTCAACGATTACC
TGGCGGACAAGAGCTACATCGAGGGGTATGTGCCATCACAAGCAGATGTGGCAGTATTTGAAGCCGTGTCCAGCC
CACCGCCTGCCGACTTGTGTCATGCCCTACGTTGGTATAATCACATCAAGTCTTACGAAAAGGAAAAGGCCAGCC
TGCCAGGAGTGAAGAAAGCTTTGGGCAAATATGGTCCTGCCGATGTGGAAGACACTACAGGAAGTGGAGCTACAG
ATAGTAAAGATGATGATGACATTGACCTCTTTGGATCTGATGATGAGGAGGAAAGTGAAGAAGCAAAGAGGCTAA
GGGAAGAACGTCTTGCACAATATGAATCAAAGAAAGCCAAAAAACCTGCACTTGTTGCCAAGTCTTCCATCTTAC
TAGATGTGAAACCTTGGGATGATGAGACAGATATGGCGAAATTAGAGGAGTGCGTCAGAAGCATTCAAGCAGACG
GCTTAGTCTGGGGCTCATCTAAACTAGTTCCAGTGGGATACGGAATTAAGAAACTTCAAATACAGTGTGTAGTTG
AAGATGATAAAGTTGGAACAGATATGCTGGAGGAGCAGATCACTGCTTTTGAGGACTATGTGCAGTCCATGGATG
TGGCTGCTTTCAACAAGATC**TAA**AATCCATCCTGGATCATGGCATTTAAATAAAAGATTGAAAGATTAAAA

FIGURE 949

MGFGDLKSPAGLQVLNDYLADKSYIEGYVPSQADVAVFEAVSSPPPADLCHALRWYNHIKSYEKEKASLPGVKKA
LGKYGPADVEDTTGSGATDSKDDDDIDLFGSDDEEESEEAKRLREERLAQYESKKAKKPALVAKSSILLDVKPWD
DETDMAKLEECVRSIQADGLVWGSSKLVPVGYGIKKLQIQCVVEDDKVGTDMLEEQITAFEDYVQSMDVAAFNKI

FIGURE 950

GGACAATTTGTGGGCCATTTAATTCAGGGCCCCCAATTCGTACGTGGAGAAGTGGGAATGCAAAAGTACTTTGAC
CTTTAACCTTCGGTCCGGCGCGGTGGAGGGAAACGCCTCCGTCTCTATATAAGGAATTTTCCGGTCTCTTCGGGT
CCTTTTTCCTCTCTTCAGCGTGGGGCGCCCACAATTTGCGCGCTCTCTTTCTGCTGCTCCCCAGCTCTCGGATAC
AGCCGACACC**ATG**GGTTTCGGAGACCTGAAAAGCCCTGCCGGCCTCCAGGTGCTCAACGATTACCTGGCGGACAA
GAGCTACATCGAGGGGTATGTGCCATCACAAGCAGATGTGGCAGTATTTGAAGCCGTGTCCAGCCCACCGCCTGC
CGACTTGTGTCATGCCCTACGTTGGTATAATCACATCAAGTCTTACGAAAAGGAAAAGGCCAGCCTGCCAGGAGT
GAAGAAAGCTTTGGGCAAATATGGTCCTGCCGATGTGGAAGACACTACAGGAAGTGGAGCTACAGATAGTAAAGA
TGATGATGACATTGACCTCTTTGGATCTGATGATGAGGAGGAAAGTGAAGAAGCAAAGAGGCTAAGGGAAGAACG
TCTTGCACAATATGAATCAAAGAAAGCCAAAAAACCTGCACTTGTTGCCAAGTCTTCCATCTTACTAGATGTGAA
ACCTTGGGATGATGAGACAGATATGGCGAAATTAGAGGAGTGCGTCAGAAGCATTCAAGCAGACGGCTTAGTCTG
GGGCTCATCTAAACTAGTTCCAGTGGGATACGGAATTAAGAAACTTCAAATACAGTGTGTAGTTGAAGATGATAA
AGTTGGAACAGATATGCTGGAGGAGCAGATCACTGCTTTTGAGGACTATGTGCAGTCCATGGATGTGGCTGCTTT
CAACAAGATC**TAA**AATCCATCCTGGATCATGGCATTTAAATAAAAGATTGAAAGATTAAAA

FIGURE 951

MGFGDLKSPAGLQVLNDYLADKSYIEGYVPSQADVAVFEAVSSPPPADLCHALRWYNHIKSYEKEKASLPGVKKA
LGKYGPADVEDTTGSGATDSKDDDDIDLFGSDDEEESEEAKRLREERLAQYESKKAKKPALVAKSSILLDVKPWD
DETDMAKLEECVRSIQADGLVWGSSKLVPVGYGIKKLQIQCVVEDDKVGTDMLEEQITAFEDYVQSMDVAAFNKI

FIGURE 952

GAAGGGGCGGGGCCAAAACTGCGCGCCCAATCGGGGTGACGCTCTAGCCTTGCCGGGGACTCGTGGGTAACTTGC
TTTTGGGAGCCAGCGGTATGGCGTCGGGCTGCAAGATTGGCCCGTCCATCCTCAACAGCGACCTGGCCAATTTAG
GGGCCGAGTGCTCCGG**ATG**CTAGACTCTGGGGCCGATTATCTGCACCTGGACGTAATGGACGGGCATTTTGTTCC
CAACATCACCTTTGGTCACCCTGTGGTAGAAAGCCTTCGAAAGCAGCTAGGCCAGGACCCTTTCTTTGACATGCA
CATGATGGTGTCCAAGCCAGAACAGTGGGTAAAGCCAATGGCTGTAGCAGGAGCCAATCAGTACACCTTTCATCT
CGAGGCTACTGAGAACCCAGGGGCTTTGATTAAAGACATTCGGGAGAATGGGATGAAGGTTGGCCTTGCCATCAA
ACCAGGAACCTCAGTTGAGTATTTGGCACCATGGGCTAATCAGATAGATATGGCCTTGGTTATGACAGTGGAACC
GGGGTTTGGAGGGCAGAAATTCATGGAAGATATGATGCCAAAGGTTCACTGGTTGAGGACCCAGTTCCCATCTTT
GGATATAGAGGTCGATGGTGGAGTAGGTCCTGACACTGTCCATAAATGTGCAGAGGCAGGAGCTAACATGATTGT
GTCTGGCAGTGCTATTATGAGGAGTGAAGACCCCAGATCTGTGATCAATCTATTAAGAAATGTTTGCTCAGAAGC
TGCTCAGAAACGTTCTCTTGATCGG**TGA**AACCATAAGGAGCCCAGTGTTCCTGTTCATGAAATCTCCCTTTTACT
GGAAAACAGGAATATTGACTACCAAATCACAATGCAATTGAAGCCGTACTGCTTTTTTGAGCAGTTATTCATTCC
AGTGATTAAAACTGATTGTGCAGAATATTCTAAGAGGTCAGAAATTGGTGTGTATAACTACATTTTTAGTGATGC
AATTTATTGATTAGTGAGTAAGATACTGTTTTTATTGAGAGATTTGATTTTTATAAAGTAAAAATACGGCTGCAT
TAGGGTTACAAACAGAAAAGTGTCTTAATGTCTAAGGAGGGCATATTAGCTACACTACAAAAACAAATTTTGTCT
GTACTTCTGAAAAGAATTTTGTTGTTTCTCAGCTGTTTTCCAAAAGCAAAGGAAGTCTTTATGGTTTTTTTCTAT
TTCATGTTATTGTGATTTGTTTATAAGTTTGGGTGGGGTGCATACCATATTCTTGGTTCTTAAAATCTATCACTT
TTCACCTTACACTTGATGTGTGAAAACTATAAAAACAATGTGTGAAACCCAGGGGTTCTAAAATACAAGCATAGA
TTTTATCAGGGTGTTTTGTCAAAGCAGGTTATTCAGTGATTCCTCCCCACCATTCTTAAGAACGTTAAATAATGC
TGTTGTGTTAGCTCTGAGTAGAAAGGAAAAAGTAAAACCTCTGTTTGGAGGTAATATTGGGTTGAATTCTGACTG
CCCCTTTCTAGCTGGACCTTTAACAAATCACCCAATCTTTTTTGTGTTTCTCTAAAGTCATTTATACATTAAATG
TAATTATAGCAACTGTGGGGTTCTGTTGAGAATTAAGAGCTAACACTATATATGTAAAGTTTCCAGTACTAGTCC
CAGAATTTAGAATATGCTCAACACAAAGTAAACAGCATTATATAAGTTTATATTTTTGTGAGTTATAAAGTACTT
TGATATATTCTCATTAAATCTGTAAATCACCTCTATAAGTAAGTGGTAATAATAAAGCAGATATTTTTGTCCCCA
TTTAAAAAATGAAGAAATTAATGCTTAATAGGGTGGTACCCTGGAAAGGATCTGGGAAGTGGTAGAATTTCTGGT
CTGTACTTTTACAAATGGAGCCCTTGGGAGGTGGGTTAGGTAAAAGAAGCTTTTTACTTAACGTTGTCTTATTTC
CAGTCTAATTTTACGCTGTAGCAGAACCAGATGGCTGAGAAAATTCTGGAACTATGGATCTTGACCCCAAGGATA
TATTATTTTATTCCAAGAAAGATCAGGTAGGCGAAAAGATGACAGGATACAGAGTCAATCCATAAACTAAATATT
TATAACTGTTCTGAATTATACAGAGTCTAAAAATATGTGTCAGCTACTTCATTCCTGTAAATACTCTTGCTGTGT
TATAAATATGGCAAGAAATAAACATGACCAATATCAATAGACTTCTTGAGGCTACTATAAGTTTTGAGAAATAAG
GTTCAAAAAAATAAGAATGCTAACACTTAAGCACAGACTAGAGCTTGCTTGGGTTTCTTCCTGCATTACAAGGTAA
AAATTTGTTAATGTTTGTTTTTATTCAGCTTGGGAAAGCTTTGTGCCATGAATACGTCGCATTTAATAACAAGCA
ACACACGGCATATAGAAATAACTTTAATTAAAAAACTTACATAGAAGATTATAATATCAGACGTGACAAAGATTT
GAGTTTATTTGCCTGGACAACTTGGGTTTGTCTGGCTTTTGTTTTCTTTTTCTTTAAAAATAAATGTACAGTAAA
ACTAC

FIGURE 953

MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDMHMMVSKPEQWVKPMAVAGANQYTFHLEATEN
PGALIKDIRENGMKVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMMPKVHWLRTQFPSLDIEVD
GGVGPDTVHKCAEAGANMIVSGSAIMRSEDPRSVINLLRNVCSEAAQKRSLDR

FIGURE 954A

GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAAAGCAAGCCCGGTTG
TTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGCAATGCGTTGGTTTGTAC
TTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACAC
TGGGAACACTTACCGAGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG
GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGA
CACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGTCTTGGTAATGGAAAAGGAGAATG
GACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGA
GAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC
TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATAATCG
AGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCA
GACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCC
TCCTCCCTATGGCCACTGTGTCACAGACAGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG
AAATAAGCAAATGCTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGG
TGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACTCCTGCACCACAGA
AGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCAC
AGACCACACTGTTTTGGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA
CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTA
TGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGAAGGGGTCAT
GTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGG
TCGTGGGGAATGGACATGCATTGCCTACTCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGT
GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAG
GTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGATTCATGGGA
GAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTT
ACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC
CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGG
CCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGGTGTGGTATA
CGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCAC
CAGCACACCTGTGACCAGCAACACCGTGACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC
TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGT
GGAATATGAGCTGAGTGAGGAGGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTCTGTGAACAT
CCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGAT
CCTGTCTACTTCACAAACAACAGCGCCTGATGCCCCTCCTGACACGACTGTGGACCAAGTTGATGACACCTCAAT
TGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGGTAG
CAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGTTCAGTATAA
CATCACTATCTATGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCC
ACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG
GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCCTGGCGAGCACGGGCA
GAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTACTTCAAAGT
CTTTGCAGTGAGCCATGGGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAA
CCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA
CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTCTGTCTCCAAGTACCC
ACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAA
AGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCAC
CATTGTGATCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGAGGC
ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTCTACAC
CATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTGACACCATTGTCTCCACC
AACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGA
CATTACTGGTTATAGAATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGC

FIGURE 954B

TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAGGA
TGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCCACTGACCTGCGATTCACCAA
CATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTA
CTCACCTGTGAAAAATGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA
TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGAGG
AAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCCAACTCTTTTACTGTGCA
CTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCG
AGAAGATCGGGTGCCCCACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG
CATCGTTGCTCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCGAG
GGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTCCTGCTGTCACAGTGAGATA
TTACAGGATCACTTACGGAGAGACAGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTAC
AGCTACCATCAGCGGCCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG
CCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGA
TGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGTAACCACCAC
TCCCAAAAATGGACCAGGACCAACAAAAACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTT
GCAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGAC
TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTCCATCAAAATTGCTTG
GGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACCTACTCGAGCCCTGAGGATGGAATCCATGAGCTATT
CCCTGCACCTGATGGTGAAGAAGACACTGCAGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGTGT
GGTTGCCTTGCACGATGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA
CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGGATA
TCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGT
GGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAG
ACCAGCTCAGGGAGTTGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA
GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAA
TGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCACAGGTTTACAACCAGGCAC
TGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGC
CATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG
TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCG
CCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAA
GAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACA
CCCCAATCTTCATGGACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGG
GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGATCTT
TGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACCCCCATAAGGCATAGGCCAAGACCATACCC
GCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACAT
CATTTCATGTCATCCTGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC
TCTGACAGGCCTCACCAGAGGTGCCACCTACAACGTCATAGTGGAGGCACTGAAAGACCAGCAGAGGCATAAGGT
TCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTCGTGCTTTGA
CCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTG
CCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA
CAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGAAA
AGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTATGATGATGGGAAGACATACCACGTAGGAGAACAGTG
GCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTG
CCGCAGACCTGGGGGTGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA
TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAAGA
TTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGTCTCTCTGCCAAGATCCATCTAAACTGGAGT
GATGTTAGCAGACCCAGCTTAGAGTTCTTCTTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCA
GCTCAACTCACAGCTTCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT

FIGURE 954C

GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGATCA
ATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAAATTTTAAGTAGGAAAGTC
ACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGA
TATTTTAAATATCCACAGTACTCACTTTTTCCAAATGATCCTAGTAATTGCCTAGAAATATCTTTCTCTTACCTG
TTATTTATCAATTTTTCCCAGTATTTTTATACGGAAAAAATTGTATTGAAAACACTTAGTATGCAGTTGATAAGA
GGAATTTGGTATAATTATGGTGGGTGATTATTTTTTATACTGTATGTGCCAAAGCTTTACTACTGTGGAAAGACA
ACTGTTTTAATAAAAGATTTACATTCC

FIGURE 955

CGGCAGCCCTCCTACCTGCGCACGTGGTGCCGCTGCTGCTGCCTCCCGCTCGCCCTGAACCCAGTGCCTGCAGCC
ATGGCTCCCGGCCAGCTCGCCTTATTTAGTGTCTCTGACAAAACCGGCCTTGTGGAATTTGCAAGAAACCTGACC
GCTCTTGGTTTGAATCTGGTCGCTTCCGGAGGGACTGCAAAAGCTCTCAGGGATGCTGGTCTGGCAGTCAGAGAT
GTCTCTGAGTTGACGGGATTTCCTGAAATGTTGGGGGGACGTGTGAAAACTTTGCATCCTGCAGTCCATGCTGGA
ATCCTAGCTCGTAATATTCCAGAAGATAATGCTGACATGGCCAGACTTGATTTCAATCTTATAAGAGTTGTTGCC
TGCAATCTCTATCCCTTTGTAAAGACAGTGGCTTCTCCAGGTGTAACTGTTGAGGAGGCTGTGGAGCAAATTGAC
ATTGGTGGAGTAACCTTACTGAGAGCTGCAGCCAAAAACCACGCTCGAGTGACAGTGGTGTGTGAACCAGAGGAC
TATGTGGTGGTGTCCACGGAGATGCAGAGCTCCGAGAGTAAGGACACCTCCTTGGAGACTAGACGCCAGTTAGCC
TTGAAGGCATTCACTCATACGGCACAATATGATGAAGCAATTTCAGATTATTTCAGGAAACAGTACAGCAAAGGC
GTATCTCAGATGCCCTTGAGATATGGAATGAACCCACATCAGACCCCTGCCCAGCTGTACACACTGCAGCCCAAG
CTTCCCATCACAGTTCTAAATGGAGCCCCTGGATTTATAAACTTGTGCGATGCTTTGAACGCCTGGCAGCTGGTG
AAGGAACTCAAGGAGGCTTTAGGTATTCCAGCCGCTGCCTCTTTCAAACATGTCAGCCCAGCAGGTGCTGCTGTT
GGAATTCCACTCAGTGAAGATGAGGCCAAAGTCTGCATGGTTTATGATCTCTATAAAACCCTCACACCCATCTCA
GCGGCATATGCAAGAGCAAGAGGGGCTGATAGGATGTCTTCATTTGGTGATTTTGTTGCATTGTCCGATGTTTGT
GATGTACCAACTGCAAAAATTATTTCCAGAGAAGTATCTGATGGTATAATTGCCCCAGGATATGAAGAAGAAGCC
TTGACAATACTTTCCAAAAAGAAAAATGGAAACTATTGTGTCCTTCAGATGGACCAATCTTACAAACCAGATGAA
AATGAAGTTCGAACTCTCTTTGGTCTTCATTTAAGCCAGAAGAGAAATAATGGTGTCGTCGACAAGTCATTATTT
AGCAATGTTGTTACCAAAAATAAAGATTTGCCAGAGTCTGCCCTCCGAGACCTCATCGTAGCCACCATTGCTGTC
AAGTACACTCAGTCTAACTCTGTGTGCTACGCCAAGAACGGGCAGGTTATCGGCATTGGAGCAGGACAGCAGTCT
CGTATACACTGCACTCGCCTTGCAGGAGATAAGGCAAACTATTGGTGGCTTAGACACCATCCACAAGTGCTTTCG
ATGAAGTTTAAAACAGGAGTGAAGAGAGCAGAAATCTCCAATGCCATCGATCAATATGTGACTGGAACCATTGGC
GAGGATGAAGATTTGATAAAGTGGAAGGCACTGTTTGAGGAAGTCCCTGAGTTACTCACTGAGGCAGAGAAGAAG
GAATGGGTTGAGAAACTGACTGAAGTTTCTATCAGCTCTGATGCCTTCTTCCCTTTCCGAGATAACGTAGACAGA
GCTAAAAGGAGTGGTGTGGCGTACATTGCGGCTCCCTCCGGTTCTGCTGCTGACAAAGTTGTGATTGAGGCCTGC
GACGAACTGGGAATCATCCTCGCTCATACGAACCTTCGGCTCTTCCACCACTGATTTTACCACACACTGTTTTTT
GGCTTGCTTATGTGTAGGTGAACAGTCACGCCTGAAACTTTGAGGATAACTTTTTAAAAAAATAAAACAGTATCT
CTTAAAACAATGTTTTGATCTACATAAACATTGTAAAAATTTTCAATCACGCTTTTTAACTTTCTTACCACAAAA
AAATGATAAGTGGGTGAAGTGATGGTTATGTTAATTAGCGTGC

FIGURE 956

MAPGQLALFSVSDKTGLVEFARNLTALGLNLVASGGTAKALRDAGLAVRDVSELTGFPEMLGGRVKTLHPAVHAG
ILARNIPEDNADMARLDFNLIRVVACNLYPFVKTVASPGVTVEEAVEQIDIGGVTLLRAAAKNHARVTVVCEPED
YVVVSTEMQSSESKDTSLETRRQLALKAFTHTAQYDEAISDYFRKQYSKGVSQMPLRYGMNPHQTPAQLYTLQPK
LPITVLNGAPGFINLCDALNAWQLVKELKEALGIPAAASFKHVSPAGAAVGIPLSEDEAKVCMVYDLYKTLTPIS
AAYARARGADRMSSFGDFVALSDVCDVPTAKIISREVSDGIIAPGYEEEALTILSKKKNGNYCVLQMDQSYKPDE
NEVRTLFGLHLSQKRNNGVVDKSLFSNVVTKNKDLPESALRDLIVATIAVKYTQSNSVCYAKNGQVIGIGAGQQS
RIHCTRLAGDKANYWWLRHHPQVLSMKFKTGVKRAEISNAIDQYVTGTIGEDEDLIKWKALFEEVPELLTEAEKK
EWVEKLTEVSISSDAFFPFRDNVDRAKRSGVAYIAAPSGSAADKVVIEACDELGIILAHTNLRLFHH

FIGURE 957

GCAGCCAATTAAGCCAACTGAGTTCCTTTCCTTGTGGGGGCCCAGTGTGCAATGGCTGCACACAGCAGCTTCCTT
GGTAGTGTACACAGCCTGTTGGTTGTATGGGTTGCTCTGAGGGACCTTGGAGACAGGCCTTTCCAATGGATGTTC
ATGTTTCTGACCTTGCGCTACCCCAATGTAGGCTCCAAACAGGCATGCGAGGTGCCTTTGGAATGCCCCAGGGCA
CTGTGGCCAGGGTTCACATTGGCCAAGTTATCATGTCCATCCGCACCAAGCTGCAGAACAAGGAGCATGTGATTG
AGGCCCTGCGCAGGGCCAAGTTCAAGCTTCCTGGCCACCAGAAGATCCACATCTCAAAGAAGTGGGGCTTCACCA
AGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAGAAGTGGCTCATCCCAGATGGCTGTGGGGTCAAGTACA
TCCCCAATCGTGGCCCTCTGGACAAGTGGCGGGCCCTGCACTCATGAGGGCTTCCAATGTGCTGCCCCCCTCTTA
ATACTCACCAATAAATTCTACTTCCTGTCAAAAAAATGTCACTAATGTACCCTAAATTTTCTTTTTTATTTTTAT
TTTTTATTTATTTATTTATTTTTTTGAGATGGTGTCTTGCTCTTTTGCCCAGACTGGAGTGAAGTAGCATGATCT
TGGCTTACTGCAACCTCCACCCCCCAG

FIGURE 958

GGCGGGCGACCAAAGCGCCTGAGGACCGGCAACATGGTGCGGTCGGGGAATAAGGCAGCTGTTGTGCTGTGTATG
GACGTGGGCTTTACCATGAGTAACTCCATTCCTGGTATAGAATCCCCATTTGAACAAGCAAAGAAGGTGATAACC
ATGTTTGTACAGCGACAGGTGTTTGCTGAGAACAAGGATGAGATTGCTTTAGTCCTGTTTGGTACAGATGGCACT
GACAATCCCCTTTCTGGTGGGGATCAGTATCAGAACATCACAGTGCACAGACATCTGATGCTACCAGATTTTGAT
TTGCTGGAGGACATTGAAAGCAAAATCCAACCAGGTTCTCAACAGGCTGACTTCCTGGATGCACTAATCGTGAGC
ATGGATGTGATTCAACATGAAACAATAGGAAAGAAGTTTGAGAAGAGGCATATTGAAATATTCACTGACCTCAGC
AGCCGATTCAGCAAAAGTCAGCTGGATATTATAATTCATAGCTTGAAGAAATGTGACATCTCCCTGCAATTCTTC
TTGCCTTTCTCACTTGGCAAGGAAGATGGAAGTGGGGACAGAGGAGATGGCCCCTTTCGCTTAGGTGGCCATGGG
CCTTCCTTTCCACTAAAAGGAATTACCGAACAGCAAAAAGAAGGTCTTGAGATAGTGAAAATGGTGATGATATCT
TTAGAAGGTGAAGATGGGTTGGATGAAATTTATTCATTCAGTGAGAGTCTGAGAAAACTGTGCGTCTTCAAGAAA
ATTGAGAGGCATTCCATTCACTGGCCCTGCCGACTGACCATTGGCTCCAATTTGTCTATAAGGATTGCAGCCTAT
AAATCGATTCTACAGGAGAGAGTTAAAAAGACTTGGACAGTTGTGGATGCAAAAACCCTAAAAAAAGAAGATATA
CAAAAAGAAACAGTTTATTGCTTAAATGATGATGATGAAACTGAAGTTTTAAAAGAGGATATTATTCAAGGGTTC
CGCTATGGAAGTGATATAGTTCCTTTCTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGC
TTCTCTGTTTTGGGATTTTGTAAATCTTCTCAGGTTCAGAGAAGATTCTTCATGGGAAATCAAGTTCTAAAGGTC
TTTGCAGCAAGAGATGATGAGGCAGCTGCAGTTGCACTTTCCTCCCTGATTCATGCTTTGGATGACTTAGACATG
GTGGCCATAGTTCGATATGCTTATGACAAAAGAGCTAATCCTCAAGTCGGCGTGGCTTTTCCTCATATCAAGCAT
AACTATGAGTGTTTAGTGTATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCATCCTTGAAA
AACAGTAAGAAATATGCTCCCACCGAGGCACAGTTGAATGCTGTTGATGCTTTGATTGACTCCATGAGCTTGGCA
AAGAAAGATGAGAAGACAGACACCCTTGAAGACTTGTTTCCAACCACCAAAATCCCAAATCCTCGATTTCAGAGA
TTATTTCAGTGTCTGCTGCACAGAGCTTTACATCCCCGGGAGCCTCTACCCCCAATTCAGCAGCATATTTGGAAT
ATGCTGAATCCTCCCGCTGAGGTGACAACAAAAAGTCAGATTCCTCTCTCTAAAATAAAGACCCTTTTTCCTCTG
ATTGAAGCCAAGAAAAAGGATCAAGTGACTGCTCAGGAAATTTTCCAAGACAACCATGAAGATGGACCTACAGCT
AAAAAATTAAAGACTGAGCAAGGGGGAGCCCACTTCAGCGTCTCCAGTCTGGCTGAAGGCAGTGTCACCTCTGTT
GGAAGTGTGAATCCTGCTGAAAACTTCCGTGTTCTAGTGAAACAGAAGAAGGCCAGCTTTGAGGAAGCGAGTAAC
CAGCTCATAAATCACATCGAACAGTTTTTGGATACTAATGAAACACCGTATTTTATGAAGAGCATAGACTGCATC
CGAGCCTTCCGGGAAGAAGCCATTAAGTTTTCAGAAGAGCAGCGCTTTAACAACTTCCTGAAAGCCCTTCAAGAG
AAAGTGGAAATTAAACAATTAAATCATTTCTGGGAAATTGTTGTCCAGGATGGAATTACTCTGATCACCAAAGAG
GAAGCCTCTGGAAGTTCTGTCACAGCTGAGGAAGCCAAAAAGTTTCTGGCCCCCAAAGACAAACCAAGTGGAGAC
ACAGCAGCTGTATTTGAAGAAGGTGGTGATGTGGACGATTTATTGGACATGATATAGGTCGTGGATGTATGGGGA
ATCTAAGAGAGCTGCCATCGCTGTGATGCTGGGAGTTCTAACAAAACAAGTTGGATGCGGCCATTCAAGGGGAGC
CAAAATCTCAAGAAATTCCCAGCAGGTTACCTGGAGGCGGATCATCTAATTCTCTGTGGAATGAATACACACATA
TATATTACAAGGGATAATTTAGACCCCATACAAGTTTATAAAGAGTCATTGTTATTTTCTGGTTGGTGTATTATT
TTTTCTGTGGTCTTACTGATCTTTGTATATTACATACATGCTTTGAAGTTTCTGGAAAGTAGATCTTTTCTTGAC
CTAGTATATCAGTGACAGTTGCAGCCCTTGTGATGTGATTAGTGTCTCATGTGGAACCATGGCATGGTTATTGAT
GAGTTTCTTAACCCTTTCCAGAGTCCTCCTTTGCCTGATCCTCCAACAGCTGTCACAACTTGTGTTGAGCAAGCA
GTAGCATTTGCTTCCTCCCAACAAGCAGCTGGGTTAGGAAAACCATGGGTAAGGACGGACTCACTTCTCTTTTTA
GTTGAGGCCTTCTAGTTACCACATTACTCTGCCTCTGTATATAGGTGGTTTTCTTTAAGTGGGGTGGAAGGGGA
GCACAATTTCCCTTCATACTCCTTTTAAGCAGTGAGTTATGGTGGTGGTCTCATGAAGAAAAGACCTTTTGGCCC
AATCTCTGCCATATCAGTGAACCTTTAGAAACTCAAAAACTGAGAAATTTACTTCAGTAGTTAGAATTATATCAC
TTCACTGTTCTCTACTTGCAAGCCTCAAAGAGAGAAAGTTTCGTTATATTAAAACACTTAGGTAACTTTTCGGTC
TTTCCCATTTCTACCTAAGTCAGCTTTCATCTTTGTGGATGGTGTCTCCTTTACTAAATAAGAAAATAACAAAGC
CCTTATTCTCTTTTTTTCTTGTCCTCATTCTTGCCTTGAGTTCCAGTTCCTCTTTGGTGTACAGACTTCTTGGTA
CCCAGTCACCTCTGTCTTCAGCACCCTCATAAGTCGTCACTAATACACAGTTTTGTACATGTAACATTAAAGGCA
TAAATGACTC

FIGURE 959

MVRSGNKAAVVLCMDVGFTMSNSIPGIESPFEQAKKVITMFVQRQVFAENKDEIALVLFGTDGTDNPLSGGDQYQ
NITVHRHLMLPDFDLLEDIESKIQPGSQQADFLDALIVSMDVIQHETIGKKFEKRHIEIFTDLSSRFSKSQLDII
IHSLKKCDISLQFFLPFSLGKEDGSGDRGDGPFRLGGHGPSFPLKGITEQQKEGLEIVKMVMISLEGEDGLDEIY
SFSESLRKLCVFKKIERHSIHWPCRLTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD
DETEVLKEDIIQGFRYGSDIVPFSKVDEEQMKYKSEGKCFSVLGFCKSSQVQRRFFMGNQVLKVFAARDDEAAAV
ALSSLIHALDDLDMVAIVRYAYDKRANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQ
LNAVDALIDSMSLAKKDEKTDTLEDLFPTTKIPNPRFQRLFQCLLHRALHPREPLPPIQQHIWNMLNPPAEVTTK
SQIPLSKIKTLFPLIEAKKKDQVTAQEIFQDNHEDGPTAKKLKTEQGGAHFSVSSLAEGSVTSVGSVNPAENFRV
LVKQKKASFEEASNQLINHIEQFLDTNETPYFMKSIDCIRAFREEAIKFSEEQRFNNFLKALQEKVEIKQLNHFW
EIVVQDGITLITKEEASGSSVTAEEAKKFLAPKDKPSGDTAAVFEEGGDVDDLLDMI

FIGURE 960A

CTTTTTGAGGCAAGTTGGATGAACAGAGAAGGGAAGAGAGGAAGAACGAGAGGAAGAGAAGGGAAGGAAGTGTTT
GTGTAGAAGAGAGAGAAAGACGAATAGAGTTAGGAAAAGGAAGACAAGCAGGTGGGCAGGAAGGACATGCACCGA
GACCAGGCAGGGGCCCAACTTTCACGTCCAGCCCTGGCCTGGGGTCGGGAGAGGTGGGCGCTAGAAGATGCAGCC
CAGGATGTGGCAATCAATGACACTATTGGGGTTTCCCAGGATGGATTGGTCAGGGGGAGAAAGGAAAAGGCAAAA
CACTCCAGGACCTCTCCCGGATCTGTCTCCTCCTCTAGCCAGCAGTATGGACAGCTGGACCCCTGAACTTCCTCT
CCTCTTACCTGGGCAGAGTGTTGTCTCTCCCCAAATTTATAAAACTAAAATGCATTCCATTCCTCTGAAAGCAA
AACAAATTCATAATTGAGTGATATTAAATAGAGAGGTTTTCGGAAGCAGATCTGTGAATATGAAATACATGTGCA
TATTTCATTCCCCAGGCAGACATTTTTTAGAAATCAATACATGCCCCAATATTGGAAAGACTTGTTCTTCCACGG
TGACTACAGTACATGCTGAAGCGTGCCGTTTCAGCCCTCATTTAATTCAATTTGTAAGTAGCGCAGCAGCCTCTG
TGGGGGAGGATAGGCTGAAAAAAAAAAGTGGGCTCGTATTTATCTACAGGACTCCATATAGTCATATATAGGCAT
ATAAATCTATTCTTTTTCTTTGTTTTTTTCTTTCTTCCTTTCTTTCAAAGGTTTGCATTAACTTTTCAAAGTAGT
TCCTATAGGGGCATTGAGGAGCTTCCTCATTCTGGGAAAACTGAGAAAACCCATATTCTCCTAATACAACCCGTA
ATAGCATTTTTGCCTGCCTCGAGGCAGAGTTTCCCGTGAGCAATAAACTCAGCTTTTTTGTGGGGCACAGTACTG
GATTTGACAGTGATTCCCCACGTGTGTTCATCTGCACCCACCGAGCCAGGCAGAGGCCAGCCCTCCGTGGTGCAC
ACAGCACGCGCCTCAGTCCATCCCATTTTAGTCTTTAAACCCTCAGGAAGTCACAGTCTCCGGACACCACACCAC
ATGAGCCCAACAGGTCCACGATGGATCCACCAGTCCCACCCCAGCCTTTTCCTTTCATCTGAACAGAATGTGCAT
TTTTGGAAGCCTCCCTCACTCTCCATGCTGGCAGAGCAGGAGGGAGACTGAAGTAAGAGATGGCAGAGGGAGATG
GTGGCAAAAAGGTTTAGATGCAGGAGAACAGTAAGATGGATGGTTCCGGCCAGAGTCGATGTGGGGAGGAACAGA
GGGCTGAAGGGAGAGGGGGCTGACTGTTCCATTCTAGCTTTGGCACAAAGCAGCAGAAAGGGGGAAAAGCCAATA
GAAATTTCCTTAGCTTCCCCACCATATGTATTTTCTAGGATTTGAGAGGAAAGAGAGGAAAATGGGGGAATGGGT
TGCAAAATAGAAATGAGCTTAATCCAGGCCGCAGAGCCAGGGAAGGTGAGTAACTTTAGGAGGGTGCTAGACTTT
AGAAGCCAGATAGGAAGAATCAGTCTAAACTGGCCATGCTTTGGAAGGGACAAGACTATGTGCTCCGCTGCCCAC
CTTCAGCCTGCAATGAGGGACTGAGGCCCACGAGTCTTTCCAGCTCTTCCTCCATTCTGGCCAGTCCCTGCATCC
TCCCTGGGGTGGAGGATGGAAGGAAAGCTGGGACAAGCAGGGAACGCATGATTCAGGGATGCTGTCACTCGGCAG
CCAGATTCCGAAACTCCCATTCTCCAATGACTTCCTCAACCAATGGGTGGCCTTGTGACTGTTCTTTAAGGCTGA
AGATATCCAGGAAAGGGGGCTTGGACACTGGCCAAGGAGACCCCTTCGTGCTGTGGACACAGCTCTCTTCACTCT
TTGCTCATGGCATGACACAGCGGAGACCGCCTCCAACAACGAATTTGGGGCTACGAAGAGGAATAGCGAAAAAGC
AAATCTGTTTCAACTGATGGGAACCCTATAGCTATAGAACTTGGGGGCTATCTCCTATGCCCCTGGACAGGACAG
TTGGCTGGGGACAGGAGAAGTGCTCAATCTTCATGAGACAAAGGGGCCCGATAGGGCCAGCAGCCACAAGGCCTT
GACCTGCCGAGTCAGCATGCCCCATCTCTCTGCACAGCTGTCCCCTAAACCCAACTCACGTTTCTGTATGTCTTA
GGCCAGTATCCCAAACCTCTTCCACGTCACTGTTCTTTCCACCCATTCTCCCTTTGCATCTTGAGCAGTTATCCA
ACTAGGATCTGCCAAGTGGATACTGGGGTGCCACTCCCCTGAGAAAAGACTGAGCCAGGAACTACAAGCTCCCCC
CACATTCCTCCCAGCCTGGACCTAATTCTTGAGAGGGGCTCTCTCTTCACGGACTGTGTCTGGACTTTGAGCAGG
CTTCTGCCCCTTGCGTTGGCTCTTTGCTGCCAGCCATCAGGTGGGGATTAGAGCCTGGTGTAAGTGCGCCAGAC
TCTTCCGGTTTCCAAAGTTCGTGCCTGCGAACCCAAACCTGTGAGTCTCTTCTGCATGCAGGAGTTTCTCCTGGG
CAGCTGGTCACTCCCCAGAGAAGCTGGGCCTTCATGGACACATGGAACTAAGCCTCCCAAATGGGAGTTCTGGCT
GAGCCCAGGGTGGGGAGATCCTGGGAAGGGAGGCACTGGAGGAAGACGGCACCTCTTCCCCCATGGCAGGGTGTG
AGGGAGGCAGGTTTGGAATGGTGCGAGTATGGCAATCTAAGCAGGGGTCTGGTCTCTTTGACTCCAGGCTGGCCT
TTGGCCGACTGTCTGCTCACCCAGAGACCTTGGACTCCGGACTATCCATGGCTCCGAATCTAAGTGCTGCCCACT
CCCATGCTCACACCCACAGAAGGTCTTCCCATCCCCTTTAGATTCGTGCCTCACTCCACCAGTGAGGAAGATGCC
TCTGTCTTTCCCACGACTGCCAGGAGATAGGGAAGCCCAGCCAGGACTGACCCTCCTTCCTCCAGCCTGCCCTGA
CCCACCTGGCAAAGCAGGGCACATGGGGAGGAAGAGACTGGAACCTTTCTTTGACAGCCAGGCCTAGACAGACAG
GCCTGGGGACACTGGCCCCATGAGGGGAGGAAGGCAGGCGCACGAGGTCCAGGGAGGCCCTTTTCTGATCATGCC
CCTTCTCTCCCACCCCATCTCCCCACCACCACCTCTGTGGCCTCCATGGTACCCCCACAGGGCTGGCCTCCCCTA
GAGGGTGGGCCTCAACCACCTGCTCCCGCCACGCACCGGTTAGTGAGACAGGGCTGCCACGGCAACCGCCAAGCC
CCCCTCAAGGTGGGACAGTACCCCGGACCCATCCACTCACTCCTGAGAGGGCTCCGGCCCAGAATGGGAACCTCA
GAGAAGAGCTCTAAGGAGAAGAAACCCCATAGCGTCAGAGAGGATATGTCTGGCTTCCAAGAGAAAGGAGGCTCC
GTTTTGCAAAGTGGAGGAGGGACGAGGGACAGGGGTTTCACCAGCCAGCAACCTGGGCCTTGTACTGTCTGTGTT

FIGURE 960B

TTTAAAACCACTAAAGTGCAAGAATTACATTGCACTGTTTCTCCACTTTTTATTTTCTCTTAGGCTTTTGTTTCT
ATTTCAAACATACTTTCTTGGTTTTCTAATGGAGTATATAGTTTAGTCATTTCACAGACTCTGGCCTCCTCTCCT
GAAATCCTTTTGGATGGGGAAAGGGAAGGTGGGGAGGGTCCGAGGGGAAGGGGACCCCAGCTTCCCTGTGCCCGC
TCACCCCACTCCACCAGTCCCCGGTCGCCAGCCGGAGTCTCCTCTCTACCGCCACTGTCACACCGTAGCCCACAT
GGATAGCACAGTTGTCAGACAAGATTCCTTCAGATTCCGAGTTGCCTACCGGTTGTTTTCGTTGTTGTTGTTGTT
GTTTTTCTTTTTCTTTTTTTTTTTGAAGACAGCAATAACCACAGTACATATTACTGTAGTTCTCTATAGTTTTAC
ATACATTCATACCATAACTCTGTTCTCTCCTCTTTTTTGTTTTCAACTTTAAAAACAAAAATAAACGATGATAAT
CTTTACTGGTGAAAAGGATGGAAAAATAAATCAACAAATGCAACCAGTTTGTGAG

FIGURE 961

MLWKGQDYVLRCPPSACNEGLRPTSLSSSSSILASPCILPGVEDGRKAGTSRERMIQGCCHSAARFRNSHSPMTS
STNGWPCDCSLRLKISRKGGLDTGQGDPFVLWTQLSSLFAHGMTQRRPPPTTNLGLRRGIAKKQICFN

FIGURE 962

CCTCTGTGGCCTCC<u>ATG</u>GTACCCCCACAGGGCTGGCCTCCCCTAGAGGGTGGGCCTCAACCACCTGCTCCCGCCA
CGCACCGGTTAGTGAGACAGGGCTGCCACGGCAACCGCCAAGCCCCCCTCAAGGTGGGACAGTACCCCGGACCCA
TCCACTCACTCCTGAGAGGGCTCCGGCCCAGAATGGGAACCTCAGAGAAGAGCTCTAAGGAGAAGAAACCCCATA
GCGTCAGAGAGGATATGTCTGGCTTCCAAGAGAAAGGAGGCTCCGTTTTGCAAAGTGGAGGAGGGACGAGGGACA
GGGGTTTCACCAGCCAGCAACCTGGGCCTTGTACTGTCTGTGTTTTTAAAACCACTAAAGTGCAAGAATTACATT
GCACTGTTTCTCCACTTTTTATTTTCTCT<u>TAG</u>GCTTTTGTTTCTATTTCAAACATACTTTCTTGGTTTTCTAATG
GAGTATATAGTTTAGTCATTTCACAGACTCTGGCCTCCTCTCCTGAAATCCTTTTGGATGGGGAAAGGGAAGGTG
GGGAGGGTCCGAGGGGAAGGGGACCCCAGCTTCCCTGTGCCCGCTCACCCCACTCCACCAGTCCCCGGTCGCCAG
CCGGAGTCTCCTCTCTACCGCCACTGTCACACCGTAGCCCACATGGATAGCACAGTTGTCAGACAAGATTCCTTC
AGATTCCGAGTTGCCTACCGGTTGTTTTCGTTGTTGTTGTTGTTGTTTTTCTTTTTCTTTTTTTTTTTGAAGACA
GCAATAACCACAGTACATATTACTGTAGTTCTCTATAGTTTTACATACATTCATACCATAACTCTGTTCTCTCCT
CTTTTTTGTTTTCAACTTTAAAAACAAAAATAAACGATGATAATCTTTACTGGTGAAAAGGATGGAAAAATAAAT
CAACAAATGCAACCAGTTTGTGAGAAAAAAAAAAAAAAAGCCGAAAAAAAAAAAAAA

FIGURE 963

MVPPQGWPPLEGGPQPPAPATHRLVRQGCHGNRQAPLKVGQYPGPIHSLLRGLRPRMGTSEKSSKEKKPHSVRED
MSGFQEKGGSVLQSGGGTRDRGFTSQQPGPCTVCVFKTTKVQELHCTVSPLFIFS

FIGURE 964

GGCGAGGGAGGAGGAAGAAGCGGAGGAGGCGGCTCCCGCGCTCGCAGGGCCGTGCCACCTGCCCGCCCGCCCGCT
CGCTCGCTCGCCCGCCGCGCCGCGCTGCCGACCGCCAGCATGCTGCCGAGAGTGGGCTGCCCCGCGCTGCCGCTG
CCGCCGCCGCCGCTGCTGCCGCTGCTGCTGCTGCTACTGGGCGCGAGTGGCGGCGGCGGCGGGGCGCGCGCGGAG
GTGCTGTTCCGCTGCCCGCCCTGCACACCCGAGCGCCTGGCCGCCTGCGGGCCCCCGCCGGTTGCGCCGCCCGCC
GCGGTGGCCGCAGTGGCCGGAGGCGCCCGCATGCCATGCGCGGAGCTCGTCCGGGAGCCGGGCTGCGGCTGCTGC
TCGGTGTGCGCCCGGCTGGAGGGCGAGGCGTGCGGCGTCTACACCCCGCGCTGCGGCCAGGGGCTGCGCTGCTAT
CCCCACCCGGGCTCCGAGCTGCCCCTGCAGGCGCTGGTCATGGGCGAGGGCACTTGTGAGAAGCGCCGGGACGCC
GAGTATGGCGCCAGCCCGGAGCAGGTTGCAGACAATGGCGATGACCACTCAGAAGGAGGCCTGGTGGAGAACCAC
GTGGACAGCACCATGAACATGTTGGGCGGGGGAGGCAGTGCTGGCCGGAAGCCCCTCAAGTCGGGTATGAAGGAG
CTGGCCGTGTTCCGGGAGAAGGTCACTGAGCAGCACCGGCAGATGGGCAAGGGTGGCAAGCATCACCTTGGCCTG
GAGGAGCCCAAGAAGCTGCGACCACCCCCTGCCAGGACTCCCTGCCAACAGGAACTGGACCAGGTCCTGGAGCGG
ATCTCCACCATGCGCCTTCCGGATGAGCGGGGCCCTCTGGAGCACCTCTACTCCCTGCACATCCCCAACTGTGAC
AAGCATGGCCTGTACAACCTCAAACAGTGCAAGATGTCTCTGAACGGGCAGCGTGGGGAGTGCTGGTGTGTGAAC
CCCAACACCGGGAAGCTGATCCAGGGAGCCCCCACCATCCGGGGGGACCCCGAGTGTCATCTCTTCTACAATGAG
CAGCAGGAGGCTCGCGGGGTGCACACCCAGCGGATGCAGTAGACCGCAGCCAGCCGGTGCCTGGCGCCCCTGCCC
CCCGCCCCTCTCCAAACACCGGCAGAAAACGGAGAGTGCTTGGGTGGTGGGTGCTGGAGGATTTTCCAGTTCTGA
CACACGTATTTATATTTGGAAAGAGACCAGCACCGAGCTCGGCACCTCCCCGGCCTCTCTCTTCCCAGCTGCAGA
TGCCACACCTGCTCCTTCTTGCTTTCCCCGGGGGAGGAAGGGGGTTGTGGTCGGGGAGCTGGGGTACAGGTTTGG
GGAGGGGGAAGAGAAATTTTTATTTTTGAACCCCTGTGTCCCTTTTGCATAAGATTAAAGGAAGGAAAAGT

FIGURE 965

AGCGGATCTCCACCATGCGCCTTCCGGATGAGCGGGGCCCTCTGGAGCACCTCTACTCCCTGCACATCCCCAACT
GTGACAAGCATGGCCTGTACAACCTCAAACAGTGCTGGTGTGTGAACCCCAACACCGGGAAGCTGATCCAGGGAG
CCCCCACCATCCGGGGGGACCCCGAGTGTCATCTCTTCTACAATGAGCAGCAGGAGGCTCGCGGGGTGCACACCC
AGCGGATGCAGTAGACCGCAGCCAGCCGGTGCCTGGCGCCCCTGCCCCCCGCCCCTCTCCAAACACCGGCAGAAA
ACGGAGAGTGCTTGGGTGGTGGGTGCTGGAGGATTTTCCAGTTCTGACACACGTATTTATATTTGGAAAGAGACC
AGCACCGAGCTCGGCACCTCCCCGGCCTCTCTCTTCCCAGCTGCAGATGCCACACCTGCTCCTTCTTGCTTTCCC
CGGGGGAGGAAGGGGGTTGTGGTCGGGGAGCTGGGGTACAGGTTTGGGGAGGGGGAAGAGAAATTTTTATTTTTG
AACCCCTGTGTCCCTTTTGCATAAGATTAAAGGAAGG

FIGURE 966

CTTCCTTTCTGGGCTCGGACCTAGGTCGCGGCGAC**ATG**GCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAAT
ACGGGACCCGCTATGGGGCCTCCCTCCGGAAAATGGTGAAGAAAATTGAAATCAGCCAGCACGCCAAGTACACTT
GCTCTTTCTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGGATCTGGCACTGTGGTTCCTGCATGAAGACAG
TGGCTGGCGGTGCCTGGACGTACAATACCACTTCCGCTGTCACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGT
TGAAAGACCAG**TAG**ACGCTCCTCTACTCTTTGAGACATCACTGGCCTATAATAAATGGGTTAATTTATGTAACAA
AAAAAAAAAAAAAAAAA

FIGURE 967

MAKRTKKVGIVGKYGTRYGASLRKMVKKIEISQHAKYTCSFCGKTKMKRRAVGIWHCGSCMKTVAGGAWTYNTTS
AVTVKSAIRRLKELKDQ

FIGURE 968

CCCCCCGCCACCTCACACACCCCCATCCGGGAGACCCACGTGCAGCTGGGCCCGGGCTGGCGCCGCACCTCGGGG
TCTGCGCGTCTCCCCGGCGCGTTCCGGGCGCAGCCCCACGACACGGACCCCTGGCGGGGCGGCATCCGAGAAGTC
GCAGGCGGAGAGGGGGCGTCCTGGAGGCCGGGCGCGGGGACGCTGCGGCCCGCGGCCACACAAAGGAGGCGGCGG
GAAGGCGGGGCAAGGCGGGCCGGGGGCGGGGGCGGCAGGAAGGGGCGGGGGCCCGCGCGGCGCCGCCGATAAAGC
CCCCGCCGCCGCGGCAGCCAGCTTGCGCTGTGGGGCTGCCCGGGCTGCGCGGCGTCTGCAGGCGCCACCGCTGCC
TCTTTCCGGCTGTGACCCTCCTCGCCGCCGCCGCTTGGCTGCGTCCTCCGACTCCCCGCGCCGCCGAGACCAGGC
TCCCGCTCCGGTTGCGGCCGCACCGCCCTCCGCGGCCGCCCCCTGGGGATCCAGCGAGCGCGGTCGTCCTTGGTG
GAAGGAACCATGAACTGGCATCTCCCCCTCTTCCTCTTGGCCTCTGTGACGCTGCCTTCCATCTGCTCCCACTTC
AATCCTCTGTCTCTCGAGGAACTAGGCTCCAACACGGGGATCCAGGTTTTCAATCAGATTGTGAAGTCGAGGCCT
CATGACAACATCGTGATCTCTCCCCATGGGATTGCGTCGGTCCTGGGGATGCTTCAGCTGGGGGCGGACGGCAGG
ACCAAGAAGCAGCTCGCCATGGTGATGAGATACGGCGTAAATGGAGTTGGTAAAATATTAAAGAAGATCAACAAG
GCCATCGTCTCCAAGAAGAATAAAGACATTGTGACAGTGGCTAACGCCGTGTTTGTTAAGAATGCCTCTGAAATT
GAAGTGCCTTTTGTTACAAGGAACAAAGATGTGTTCCAGTGTGAGGTCCGGAATGTGAACTTTGAGGATCCAGCC
TCTGCCTGTGATTCCATCAATGCATGGGTTAAAAATGAAACCAGGGATATGATTGACAATCTGCTGTCCCCAGAT
CTTATTGATGGTGTGCTCACCAGACTGGTCCTCGTCAACGCAGTGTATTTCAAGGGTCTGTGGAAATCACGGTTC
CAACCCGAGAACACAAAGAAACGCACTTTCGTGGCAGCCGACGGGAAATCCTATCAAGTGCCAATGCTGGCCCAG
CTCTCCGTGTTCCGGTGTGGGTCGACAAGTGCCCCCAATGATTTATGGTACAACTTCATTGAACTGCCCTACCAC
GGGGAAAGCATCAGCATGCTGATTGCACTGCCGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCCACACATC
AGCACCAAGACCATAGACAGCTGGATGAGCATCATGGTGCCCAAGAGGGTGCAGGTGATCCTGCCCAAGTTCACA
GCTGTAGCACAAACAGATTTGAAGGAGCCGCTGAAAGTTCTTGGCATTACTGACATGTTTGATTCATCAAAGGCA
AATTTTGCAAAAATAACAAGGTCAGAAAACCTCCATGTTTCTCATATCTTGCAAAAAGCAAAAATTGAAGTCAGT
GAAGATGGAACCAAAGCTTCAGCAGCAACAACTGCAATTCTCATTGCAAGATCATCGCCTCCCTGGTTTATAGTA
GACAGACCTTTTCTGTTTTTCATCCGACATAATCCTACAGGTGCTGTGTTATTCATGGGGCAGATAAACAAACCC
TGAAGAGTATACAAAAGAAACCATGCAAAGCAACGACTACTTTGCTACGAAGAAAGACTCCTTTCCTGCATCTTT
CATAGTTCTGTTAAATATTTTTGTACATCGCTTCTTTTTCAAAACTAGTTCTTAGGAACAGACTCGATGCAAGTG
TTTCTGTTCTGGGAGGTATTGGAGGGAAAAAACAAGCAGGATGGCTGGAACACTGTACTGAGGAATGAATAGAAA
GGCTTCCAGATGTCTAAAAGATTCTTTAAACTACTGAACTGTTACCTAGGTTAACAACCCTGTTGAGTATTTGCT
GTTTGTCCAGTTCAGGAATTTTTGTTTTGTTTTGTCTATATGTGCGGCTTTTCAGAAGAAATTTAATCAGTGTGA
CAGAAAAAAAAATGTTTTATGGTAGCTTTTACTTTTTATGAAAAAAAAATTATTTGCCTTTTAAATTCTTTTCCC
CCATCCCCCTCCAAAGTCTTGATAGCAAGCGTTATTTGGTGGTAGAAACGGTGAAATCTCTAGCCTCTTTGTGT
TTTTGTTGTTGTTGTTGTTGTTGTTTTATATAATGCATGTATTCACTAAAATAAAATTTAAAAAACTCCTGTCTT
GCTAGACAAGGTTGCTGTTGTGCAGTGTGCCTGTCACTACTGGTCTGTACTCCTTGGATTTGCATTTTTGTATTT
TGTACAAAGTAAAAATAAACTGTTATGAGTAGT

FIGURE 969

MNWHLPLFLLASVTLPSICSHFNPLSLEELGSNTGIQVFNQIVKSRPHDNIVISPHGIASVLGMLQLGADGRTKK
QLAMVMRYGVNGVGKILKKINKAIVSKKNKDIVTVANAVFVKNASEIEVPFVTRNKDVFQCEVRNVNFEDPASAC
DSINAWVKNETRDMIDNLLSPDLIDGVLTRLVLVNAVYFKGLWKSRFQPENTKKRTFVAADGKSYQVPMLAQLSV
FRCGSTSAPNDLWYNFIELPYHGESISMLIALPTESSTPLSAIIPHISTKTIDSWMSIMVPKRVQVILPKFTAVA
QTDLKEPLKVLGITDMFDSSKANFAKITRSENLHVSHILQKAKIEVSEDGTKASAATTAILIARSSPPWFIVDRP
FLFFIRHNPTGAVLFMGQINKP

FIGURE 970

ATGCGTGCTGAAAAGAGAAAAAAGAATGCCCCAGAGGAGGTCAGCAGGCTTAAAAGTATTCTCAAACTAGACGAT
GACGTTTTAATGAAAGATGTTCAAGAGATAGCAACTGTGGTGGTACCCAAACCCAAACATTGCCAAGAGAAAATG
CAATGTGAGGTAAAAGATGAAAAAGATGACATGAAAATGGAGACTGATATTAAGAGAAACAAAAAGACTCTTCTA
GACCAGCATGGACAGTACCCAATATGGATGAACCAAAGGCAAAGAAAAAGGCTAAAGGCAAAGCGAGAGAAAAGA
AAGGAGAAAAACAAAGCAAAAGCAGTGAAAGTGGCAAAGGGTTTGGCCTGTAGTATTGTTTCCATAATAGTCCAT
TTCGCAGAAATAAGAAGGAGAATAAAACTTAGAGAAAAAGAGGAGGCCAAAAGGGGCAAGGTAGTGGCTACTTGC
AGAAACCTGAAAAATATGTGTGACAAAGCCGCCATAATAAGTGCCAGCCGAGCTGCAGCAGCCCGTCTCAGGGGC
ACCGCAGCCTCCCCGGGCCCTACGGCCGCCCGCCAGCAGGATGGCTGGAATGGCCTTAGTCATGAGGCTTTTAGA
ATTGTTTCAAGGCAGGATTATGCGTCAGAAGCAATCAATGGAGCAGCTGGTGGTGTTTATTTGGGTACTACCAAC
TCCTGTGTGGCAGTTATGGAAGGTAAACAAGCAAAGGTGCTGGAGAATGCCGAAGGTGCCAGAACTACCCCTTCA
GTTGTGGCCTTTACAGCAGATGTACAGAAAGACATTAAAAATATTCCCTTTAAAATTGTCTGTGCCTCCAATGGT
GATGCCTGGGTTGAGGCTCATGGGAAACTGTATTCTCCAAGTCAGATCGGAGCATTTGTGTCGATGAAGATGAAA
GAGACTGCAGAAAATTACTTGGGGCACACAGCAAAAAATGCTGTGATCGCAGTCCCAGCTTATTTCAATGACTTG
CAGAGGCAGGCCACTAAAGATGCTGGCCAGATATCTGGACTGAATGTGCTTCGGGTGATTAATGAACCCACAGCT
GCTGCTCTTGCCTATGGTCTAGACAAATCAAAAGACAAAGTCATTGCTGTATATGATTTAGGTGGTGGAACTTTT
GATATTTCTATCCTGGAATTTCAGAAAGGAGTATTCGAGGTGAAATCCACAAATGGGGACACTTTCTTAGGTGGG
GAAGACTTTGACCAGGCCTTGCTACAGCACATTGTGAAGGAGTTCAAGAGAGAGACGGGGGTTGATTTGACCAAA
GACAACGTGGCATTTCAGAGGGTGTGGGAAGCTGCTGAAAAGGCTAAATGTGAACTCTCCTCATCTGTGCAGACT
GACATCAATTTGCCCTATCTTACAATGGATTCTTCTGGACCCAAGCATTTGAATACAAAGTTGACCCATGCTCAA
TTTGAAGGGATTGTCACTGATCTAATCAGGAGGACTATCGCTCCATGCCAAAAAGCTATGCAAGATGCAGAAGTC
AGCAAGAGTGATATAGGAGAAGTGATTCTTGTGGAGCCCCCAAGTAAAGCTGTCAATCCTGATGAGGCTGTGGCC
ATTGGAGCTGCCATTCAGGGAGATGTGTTGGCCGGCGATGTCACAGATGTGCTGCTCCTTGATGTCATTCCCCTG
TCTCTGGGTATTGAAACTCTGCGAGGTGTCTTTACCAAACTTATTAATAGGAATACCACTATTCCAACCAAGAAG
AGCCAGGTATTCTCAACTGCTGCTGATGGGCAGACACAAGTGGAAATTAAAGTGTGTCAGGGTGAGAGAGAGATG
GCTGGAGACAACAAACTCCTTGGACAGTTTACTTTGATTGGAATTCCACCAGCCCCTCGTGGAGTTCCTCAGATC
AAAGTTACATTTGACATTGATGCCAATGGGATCATACATGTTTCAGCTAAAGATAAAGGCACAGGACATGAGCAG
CAGATTGTAATCCAGTCTTCTGGTGGGTTAAGCAAAGATGATGTTGAAAATATGGTTAAAAATGCAGAGAAATAT
GCTAAGGAAGACCAGCGAAGGAAGGAATGA

FIGURE 971

CGGAGCTGTCCATCAGCACCAAAGGCCGCGGGCGGGCTCAGGGCATGGGGCCGCGGTTCTGGGGCGGCCCGAGCC
CCGGCTCCTGCGCCTTCCCCTTCCTCAGGCCCAGCCCGAGTTCCCGGACGCCGCGGGACTGGAGTGCCAGCCGGT
GTTGGACGTGGAGCGGCGCCGCCACCGCGCCGACACCATTCTCTCCGGCCCAGCAGCCCCCTTCCTCGCACGACG
GACTTTCCCTGGACCCCAGTCAGTTGGAGCCTCTGGCGCCCCGCAACCCCGGCCCCTCGGGCCTCTGCACAGCCT
CTTTCACTCAGAAGCTCAGGTCGCCTCCAGCCCAGCACTATGCCGGGGACTGTGGCAACACTGCGGTTCCAGCTG
CTGCCCCCTGAGCCAGATGATGCCTTCTGGGGTGCACCTTGTGAACAGCCCCTGGAGCGCAGGTACCAGGCACTG
CCGGCCCTCGTCTGCATCATGTGCTGTTTGTTTGGAGTCGTCTACTGCTTCTTCGGTTACCGCTGCTTCAAGGCA
GTGCTCTTTCTCACTGGGTTGCTGTTTGGCTCGGTGGTCATCTTCCTCCTCTGCTACCGAGAGCGGGTGCTAGAG
ACACAGCTGAGTGCTGGGGCGAGCGCGGGCATCGCTCTGGGCATCGGGCTGCTCTGCGGGCTGGTGGCCATGCTA
GTGCGCAGCGTGGGCCTCTTCCTGGTGGGGCTGCTGCTCGGCCTGCTGCTCGCAGCTGCTGCCCTGCTGGGCTCC
GCACCCTACTACCAGCCAGGCTCCGTGTGGGGTCCACTGGGGCTGTTGCTGGGGGGCGGCCTGCTCTGTGCCCTG
CTCACTCTGCGCTGGCCCCGCCCACTCACCACCCTGGCCACCGCCGTGACTGGTGCTGCGCTGATCGCCACTGCC
GCTGACTACTTCGCCGAGCTGCTACTGCTGGGGCGCTACGTGGTGGAGCGACTCCGGGCTGCTCCTGTGCCCCCA
CTCTGCTGGCGAAGCTGGGCCCTGCTGGCACTCTGGCCCCTGCTCAGCCTGATGGGCGTTCTGGTGCAGTGGAGG
GTGACAGCTGAGGGGGACTCCCACACGGAAGTGGTCATCAGCCGGCAGCGCCGACGCGTGCAACTGATGCGGATT
CGGCAGCAGGAAGATCGCAAGGAGAAAAGGCGGAAAAAGAGACCTCCTCGGGCTCCCCTCAGAGGTCCCCGGGCT
CCTCCCAGGCCTGGGCCACCAGACCCTGCTTATCGGCGCAGGCCAGTGCCCATCAAACGCTTCAATGGAGACGTC
CTCTCCCCGAGCTATATCCAGAGCTTCCGAGACCGGCAGACCGGGAGCTCCCTGAGCTCCTTCATGGCCTCACCC
ACAGATGCGGACTATGAGTATGGGTCCCGGGGACCTCTGACAGCCTGCTCAGGCCCCCCAGTGCGGGTATAGCCA
TATCTGTCTGTCTAGACTCTGCAGTCACCAGCTCTGCCAGCTCGAGGAGGCCTGCTAGGCTGCCACTCAGCCTCC
TGGCTTTGGCTGTCCCTCTCCCCAGCCTGGAGAGGGCTGGCCTGGTCACTAGAAGGGAGGATTGTCTCAGGCGAG
TCTTGGCCTGAGAGGAAAGCCCCCTCCCAAGCTCCCAAGAGGCTCCTGAGGAACTCGGGGTGTGAACCCCATTGG
GGTGTGCTCAGGGTTGTGAGTGTGTTGCCCGTGTGTCTGTGTGTATGTGTGGGGGTGGGCAGGCTTGGAGGGG
ACGCTGGGACCCTTGCCTTAGATTTCTGACTGGTAGGGTTTCTCCAGGCTCAGCCCCACCTCTTCACTCCCTGCC
AAGGTCCCATGGGCCACCTCCTGCATGTCTCCGCGGAGGGGCTACCTTCCTTCCCATCGCCCTGCCTCGCAGCCA
GACTCATCTAAGGGTTCTTGTCCTTGTCTATGGGGCAAACTGTAGCATCCCTCACCCTGGTCCCCTGGCCTCTGT
AAAGCCACCAGCCTGAGGGCAGTGGCAGGAGATGGGGGTGGGGGGGTGCTGCTCTGGGCTGGGTTGGGAAGGGAG
TTGGGGAGGGGTTTAAATGCACGGTGCATGTCTGGTGTCTGTCATGCCAACCTAGACACCTCATGCTTCTGTCTC
CCCCACCCCACTCTGTTTTACATCTTTTATAAATGTGCCAAACTGTGTGGCCTCTGCCA

FIGURE 972

MPGTVATLRFQLLPPEPDDAFWGAPCEQPLERRYQALPALVCIMCCLFGVVYCFFGYRCFKAVLFLTGLLFGSVV
IFLLCYRERVLETQLSAGASAGIALGIGLLCGLVAMLVRSVGLFLVGLLLGLLLAAAALLGSAPYYQPGSVWGPL
GLLLGGGLLCALLTLRWPRPLTTLATAVTGAALIATAADYFAELLLLGRYVVERLRAAPVPPLCWRSWALLALWP
LLSLMGVLVQWRVTAEGDSHTEVVISRQRRRVQLMRIRQQEDRKEKRRKKRPPRAPLRGPRAPPRPGPPDPAYRR
RPVPIKRFNGDVLSPSYIQSFRDRQTGSSLSSFMASPTDADYEYGSRGPLTACSGPPVRV

FIGURE 973

CGGAGCACATGCTGAGCGGAGCGGCTGGGGCTGCGCGGCGTGGCGGAGCAGCGCTCGCTCCCTCGCTCACTCGCT
CGCTCGCAGGGACACACGCAGGGGCTGACAGCTGTGCTGGTGCTGATAAGGGAAGCCACAAGGAGACGATCGAGG
AGAGAGACAAGCGGCAGCAGAGGCAGCAGCGGCAGAGGCAGCACCAGGGCTGCGGAGCTGCTGGGAGTGGGAGTG
ACTCCCCCACCTCGGGCCCCCACCCTGTCCCTGTCCTCTTCCCGCTTGCCCTGAGTTTAGAAGAGCAGCCGCTGC
CACCACTGCCACTCGGGAGGGCACCAGGGCTGCTGGCTAGGGAGGGACAGGGCAGGGAGGCTCTGGCCAGTCCCA
GCAGCCGGGGACAG**ATG**CCGATCGAGATTGTGTGCAAAATCAAATTTGCTGAGGAGGATGCGAAACCCAAGGAGA
AGGAGGCAGGGGATGAGCAGAGCCTCCTCGGGGCTGTTGCCCCTGGAGCAGCCCCCCGAGACCTGGCCACCTTTG
CCAGCACCAGCACCCTGCATGGACTGGGCCGGGCCTGTGGCCCAGGCCCCCACGGACTGCGCAGAACCCTGTGGG
CACTGGCCCTACTCACCTCGCTGGCTGCCTTCCTGTACCAGGCGGCTGGCCTGGCCCGGGGCTACCTGACCCGGC
CTCACCTGGTGGCAATGGACCCCGCTGCCCCAGCCCCAGTGGCGGGCTTCCCGGCTGTCACCCTCTGCAATATCA
ACCGCTTCCGGCATTCGGCACTCAGCGATGCCGACATCTTCCACCTGGCCAATCTGACAGGGCTGCCCCCCAAAG
ACCGGGATGGGCACCGTGCGGCTGGCCTGCGCTACCCAGAGCCTGACATGGTAGACATCCTCAACCGCACTGGCC
ACCAGCTCGCCGACATGCTTAAGAGCTGCAACTTCAGTGGGCATCACTGCTCCGCCAGCAACTTCTCTGTGGTCT
ATACTCGCTATGGGAAGTGTTACACCTTCAACGCGGACCCGCGGAGCTCGCTGCCCAGCCGGGCAGGGGGCATGG
GCAGTGGCCTGGAGATCATGCTGGACATCCAGCAGGAGGAGTACCTGCCCATCTGGAGGGAGACAAATGAGACGT
CGTTTGAGGCAGGTATTCGGGTGCAGATCCACAGCCAGGAGGAGCCGCCCTACATCCACCAGCTGGGGTTCGGGG
TGTCCCCAGGCTTCCAGACCTTTGTGTCCTGCCAGGAACAGCGGCTGACCTACCTGCCCCAGCCCTGGGGCAACT
GCCGCGCAGAGAGTGAGCTCAGGGAGCCTGAGCTTCAGGGCTACTCGGCCTACAGTGTGTCTGCCTGCCGGCTGC
GCTGTGAAAAGGAGGCCGTGCTTCAGCGCTGCCACTGCCGGATGGTGCACATGCCAGGCAATGAGACCATCTGCC
CACCAAATATCTACATCGAGTGTGCAGACCACACACTGGACTCCCTGGGTGGGGGCCCTGAGGGCCCGTGCTTCT
GCCCCACCCCCTGCAACCTGACACGCTATGGGAAAGAGATCTCCATGGTCAGGATCCCCAACAGGGGCTCAGCCC
GGTACCTGGCGAGGAAGTACAACCGCAACGAGACCTACATACGGGAGAACTTCCTGGTCCTAGATGTCTTCTTTG
AGGCCCTGACCTCTGAAGCCATGGAGCAGCGAGCAGCCTATGGCCTGTCAGCCCTGCTGGGAGACCTCGGGGGAC
AGATGGGCCTGTTCATTGGGGCCAGCATCCTCACGTTGCTGGAGATCCTCGACTACATCTATGAGGTGTCCTGGG
ATCGACTGAAGCGGGTATGGAGGCGTCCCAAGACCCCCCTGCGGACCTCCACTGGGGGCATCTCCACTTTGGGGC
TTCAGGAGCTGAAGGAACAGAGTCCCTGCCCGAGCCTGGGCCGAGCGGAGGGTGGGGGGGTCAGCAGTCTGCTCC
CCAATCACCACCACCCCCACGGTCCCCCAGGAGGTCTCTTTGAAGATTTTGCTTGC**TAG**GACGGTGCTGTGACTG
AAAGGACCCAGGAGTCTGGGACCCCTCCTGGGATCCCCAGCACATTCTCCTGCTCCTGGGAGAGGCCTGGGGGCG
GTGCTCACTGGGAGGGCCAGGACTCAGTTCCTGCTCTCATCCTCCCCTGCCCTGATGTCAGCTGCTTTGCACAAA
GGTCCTTCTTGTCCACACCCCTTATCCCCAGGCTGGTGCCCCGGGAGGGCTGGAGACCAGGCCATGGGCCCTCAC
GGAGAGGAAGGGAAGGAAGGAGAGGGAGGGGGAGGATAGAGCCCATCCCAGCCGGGGAGGGGGAGCCCTCTGTAC
ATTTGTAAATATTTAGGGAAAGCCGGGTGGGGGGAGGGGATACAGATGTAGAAGGTGGGTAGGGCTACAGGGGTG
GGTGATTTAGGGACAGCCAGGGTCCCAGCCCCAATGTCAGCAGGATAGGGAGAGCCCCAGGACTCAGGAGTGCTG
GGCTGGTCCTACTTCCTGCCCCTCTCCAGGCCCAGCTCCCCTCTTGGCAGGGGGAGAGGATGGCCCAGCAGGCCT
GGCCCAGCTCCCAGTTCCCCCTGCACCAGCCCCACCCCTAGAGTCCCTTCTATAGGGAGGGGGCAGGAGACCTTC
CAGACTTCGGCTGAGCTTGGAGGGTGGGAAGGGAGCCTTCTCAGTCCTCTCTCCCTCCAGTCTGATTTTATAAAG
TGCTGACGAG

FIGURE 974

MPIEIVCKIKFAEEDAKPKEKEAGDEQSLLGAVAPGAAPRDLATFASTSTLHGLGRACGPGPHGLRRTLWALALL
TSLAAFLYQAAGLARGYLTRPHLVAMDPAAPAPVAGFPAVTLCNINRFRHSALSDADIFHLANLTGLPPKDRDGH
RAAGLRYPEPDMVDILNRTGHQLADMLKSCNFSGHHCSASNFSVVYTRYGKCYTFNADPRSSLPSRAGGMGSGLE
IMLDIQQEEYLPIWRETNETSFEAGIRVQIHSQEEPPYIHQLGFGVSPGFQTFVSCQEQRLTYLPQPWGNCRAES
ELREPELQGYSAYSVSACRLRCEKEAVLQRCHCRMVHMPGNETICPPNIYIECADHTLDSLGGGPEGPCFCPTPC
NLTRYGKEISMVRIPNRGSARYLARKYNRNETYIRENFLVLDVFFEALTSEAMEQRAAYGLSALLGDLGGQMGLF
IGASILTLLEILDYIYEVSWDRLKRVWRRPKTPLRTSTGGISTLGLQELKEQSPCPSLGRAEGGGVSSLLPNHHH
PHGPPGGLFEDFAC

FIGURE 975

CCTCGCCGCATCCACTCTCCGGCCGGCCGCCTGCCCGCCGCCTCCTCCGTGCGCCCGCCAGCCTCGCCCGCGCCG
TCACC**ATG**AGCCAGGCCTACTCGTCCAGCCAGCGCGTGTCCTCCTACCGCCGCACCTTCGGCGGGGCCCCGGGCT
TCCCACTCGGCTCCCCGCTGAGTTCGCCCGTGTTCCCGCGGGCGGGTTTCGGCTCTAAGGGCTCCTCCAGCTCGG
TGACGTCCCGCGTGTACCAGGTGTCGCGCACGTCGGGCGGGGCCGGGGGCCTGGGGTCGCTGCGGGCCAGCCGGC
TGGGGACCACCCGCACGCCCTCCTCCTACGGCGCAGGCGAGCTGCTGGACTTCTCACTGGCCGACGCGGTGAACC
AGGAGTTTCTGACCACGCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTCAATGACCGCTTCGCCAACTACATCG
AGAAGGTGCGCTTCCTGGAGCAGCAGAACGCGGCGCTCGCCGCCGAAGTGAACCGGCTCAAGGGCCGCGAGCCGA
CGCGAGTGGCCGAGCTCTACGAGGAGGAGCTGCGGGAGCTGCGGCGCCAGGTGGAGGTGCTCACTAACCAGCGCG
CGCGCGTCGACGTCGAGCGCGACAACCTGCTCGACGACCTGCAGCGGCTCAAGGCCAAGCTGCAGGAGGAGATTC
AGTTGAAGGAAGAAGCAGAGAACAATTTGGCTGCCTTCCGAGCGGACGTGGATGCAGCTACTCTAGCTCGCATTG
ACCTGGAGCGCAGAATTGAATCTCTCAACGAGGAGATCGCGTTCCTTAAGAAAGTGCATGAAGAGGAGATCCGTG
AGTTGCAGGCTCAGCTTCAGGAACAGCAGGTCCAGGTGGAGATGGACATGTCTAAGCCAGACCTCACTGCCGCCC
TCAGGGACATCCGGGCTCAGTATGAGACCATCGCGGCTAAGAACATTTCTGAAGCTGAGGAGTGGTACAAGTCGA
AGGTGTCAGACCTGACCCAGGCAGCCAACAAGAACAACGACGCCCTGCGCCAGGCCAAGCAGGAGATGATGGAAT
ACCGACACCAGATCCAGTCCTACACCTGCGAGATTGACGCCCTGAAGGGCACTAACGATTCCCTGATGAGGCAGA
TGCGGGAATTGGAGGACCGATTTGCCAGTGAGGCCAGTGGCTACCAGGACAACATTGCGCGCCTGGAGGAGGAAA
TCCGGCACCTCAAGGATGAGATGGCCCGCCATCTGCGCGAGTACCAGGACCTGCTCAACGTGAAGATGGCCCTGG
ATGTGGAGATTGCCACCTACCGGAAGCTGCTGGAGGGAGAGGAGAGCCGGATCAATCTCCCCATCCAGACCTACT
CTGCCCTCAACTTCCGAGAAACCAGCCCTGAGCAAAGGGGTTCTGAGGTCCATACCAAGAAGACGGTGATGATCA
AGACCATCGAGACACGGGATGGGGAGGTCGTCAGTGAGGCCACACAGCAGCAGCATGAAGTGCTC**TAA**AGACAGA
GACCCTCTGCCACCAGAGACCGTCCTCACCCCTGTCCTCACTGCTCCCTGAAGCCAGCCTTCTTCCATCCCAGGA
CACCACACCCAGCCTCAGTCCTCCCCTCACAGCCTCTGACCCCTCCTCACTGGCCATCCCTCGTGGTCCCCAACA
GCGACATAGCCCATCCCTGCCTGGTCACAGGGCATGCCCCGGCCACCTCTGCGGACCCCAGCTGTGAGCCTTGGC
TGTTGGCAGTGAGTGAGCCTGGCTCTTGTGCTGGATGGAGCCCAGGCGGGAGCGGTGGCCCTGTCCCTCCCACCT
CTGTGACCTCAGGCACTAGCCTTTGGCTCTGGAGACAGCCCCAGAGCAGGGTGTTGGGATACTGCAGGGCCAGGA
CTGAGCCCCGCAGACCTCCCCAGCCCCTAGCCCAGGAGAGAGAAAGCCAGGCAGGTAGCCAGGGGGACTAGCCCC
TGTGGAGACTGGGGGGCTTGAAATTGTCCCCGTGGTCTCTTACTTTCCTTTCCCCAGCCCAGGGTGGACTTAGAA
AGCAGGGGCTACAAGAGGGAATCCCCGAAGGTGCTGGAGGTGGGAGCAGGAGATTGAGAAGGAGAGAAAGTGGGT
GAGATGCTGGAGAAGAGAGGAGAGGAGAGAGGCAGAGAGCGGTCTCAGGCTGGTGGGAGGGGCGCCCACCTCCCC
ACGCCCTCCCCTCCCCTGCTGCAGGGGCTCTGGAGAGAAACAATAAAGAGATTCACACACAAGCC

FIGURE 976

MSQAYSSSQRVSSYRRTFGGAPGFPLGSPLSSPVFPRAGFGSKGSSSSVTSRVYQVSRTSGGAGGLGSLRASRLG
TTRTPSSYGAGELLDFSLADAVNQEFLTTRTNEKVELQELNDRFANYIEKVRFLEQQNAALAAEVNRLKGREPTR
VAELYEEELRELRRQVEVLTNQRARVDVERDNLLDDLQRLKAKLQEEIQLKEEAENNLAAFRADVDAATLARIDL
ERRIESLNEEIAFLKKVHEEEIRELQAQLQEQQVQVEMDMSKPDLTAALRDIRAQYETIAAKNISEAEEWYKSKV
SDLTQAANKNNDALRQAKQEMMEYRHQIQSYTCEIDALKGTNDSLMRQMRELEDRFASEASGYQDNIARLEEEIR
HLKDEMARHLREYQDLLNVKMALDVEIATYRKLLEGEESRINLPIQTYSALNFRETSPEQRGSEVHTKKTVMIKT
IETRDGEVVSEATQQQHEVL

FIGURE 977

GCACGAGGGTGATGAAGGCCTACGAGTGCGGCGCGGCCTGAAGGGGCACGCGGGGGACCTGCAAAGCTAGTGAGG
GGCGGGGCAGGCGGCGCGGTGGGGGCGGGCCGAGCCCGGAGGCCAGATGAGCGGACACAGCCCCACGCGCGGGGC
CATGCAGGTGGCCATGAACGGTAAGGCCCGCAAAGAGGCGGTGCAGACTGCGGCTAAGGAACTCCTCAAGTTCGT
GAACCGGAGTCCCTCTCCTTTCCATGCTGTGGCTGAATGCCGCAACCGCCTTCTCCAGGCTGGCTTCAGTGAACT
CAAGGAGACTGAGAAATGGAATATTAAGCCCGAGAGCAAGTACTTCATGACCAGGAACTCCTCCACCATCATAGC
TTTTGCTGTAGGGGGCCAGTACGTTCCTGGCAATGGCTTCAGCCTCATCGGGGCCCACACGGACAGCCCCTGCCT
CCGGGTGAAACGTCGGTCTCGCCGCAGCCAGGTGGGCTTCCAGCAAGTCGGTGTGGAGACCTATGGTGGTGGGAT
CTGGAGCACCTGGTTTGACCGTGACCTGACTCTGGCTGGACGCGTCATTGTCAAGTGCCCTACCTCAGGTCGGCT
GGAGCAGCAGCTGGTGCACGTGGAGCGGCCCATTCTTCGCATCCCACACCTGGCCATCCATCTGCAGCGAAATAT
CAACGAGAACTTTGGGCCCAACACAGAGATGCATCTAGTCCCCATTCTTGCCACAGCCATCCAGGAGGAGCTGGA
GAAGGGGACTCCTGAGCCAGGGCCTCTCAATGCTGTGGATGAGCGGCACCATTCGGTCCTCATGTCCCTGCTCTG
TGCCCATCTGGGGCTGAGCCCCAAGGACATAGTGGAGATGGAGCTCTGCCTTGCAGACACCCAGCCTGCGGTCTT
GGGTGGTGCCTATGATGAGTTCATCTTTGCTCCTCGGCTGGACAATCTGCACAGCTGCTTCTGTGCCCTGCAGGC
CTTGATAGATTCCTGTGCAGGCCCTGGCTCCCTGGCCACAGAGCCTCACGTGCGCATGGTCACACTCTATGACAA
CGAAGAGGTGGGGTCTGAGAGTGCACAGGGAGCACAGTCACTGCTGACAGAGCTGGTGCTGCGGCGGATCTCAGC
CTCGTGCCAGCACCCGACAGCCTTCGAGGAAGCCATACCCAAGTCCTTCATGATCAGCGCAGACATGGCCCATGC
TGTGCATCCCAACTACCTGGACAAGCATGAGGAGAACCACCGGCCTTTATTCCACAAGGGCCCCGTGATCAAGGT
GAACAGCAAGCAACGCTATGCTTCAAACGCGGTGTCAGAGGCCCTGATCCGAGAGGTGGCCAACAAAGTCAAGGT
CCCCCTGCAGGATCTCATGGTCCGGAATGACACCCCCTGTGGAACCACCATTGGACCTATCTTGGCTTCTCGGCT
GGGGCTGCGGGTGCTGGATTTAGGCAGCCCCCAACTGGCCATGCACTCTATCCGGGAGATGGCCTGCACCACAGG
AGTCCTCCAGACCCTCACCCTCTTCAAGGGCTTCTTTGAGCTGTTCCCTTCTCTAAGCCATAATCTCTTAGTGGA
TTGAGCCCTCTTGGAAAGACTTCTCTGCCATCCCTTTGCACCTGAGAGGGGAAGTTCTCAGCTGAGCTGAAGCTG
GATTATTAAAGTGGATTGTCACTCAGAAAAAAAAAAAAAAAAAAA

FIGURE 978

MQVAMNGKARKEAVQTAAKELLKFVNRSPSPFHAVAECRNRLLQAGFSELKETEKWNIKPESKYFMTRNSSTIIA
FAVGGQYVPGNGFSLIGAHTDSPCLRVKRRSRRSQVGFQQVGVETYGGGIWSTWFDRDLTLAGRVIVKCPTSGRL
EQQLVHVERPILRIPHLAIHLQRNINENFGPNTEMHLVPILATAIQEELEKGTPEPGPLNAVDERHHSVLMSLLC
AHLGLSPKDIVEMELCLADTQPAVLGGAYDEFIFAPRLDNLHSCFCALQALIDSCAGPGSLATEPHVRMVTLYDN
EEVGSESAQGAQSLLTELVLRRISASCQHPTAFEEAIPKSFMISADMAHAVHPNYLDKHEENHRPLFHKGPVIKV
NSKQRYASNAVSEALIREVANKVKVPLQDLMVRNDTPCGTTIGPILASRLGLRVLDLGSPQLAMHSIREMACTTG
VLQTLTLFKGFFELFPSLSHNLLVD

FIGURE 979

CTTTGCATTGTTCCTCATCCGCCTCCTTGCTCGCCGCAGCCGCCTCCGCCGCGCGCCTCCTCCGCCGCCGCGGAC
TCCGGCAGCTTTATCGCCAGAGTCCCTGAACTCTCGCTTTCTTTTTAATCCCCTGCATCGGATCACCGGCGTGCC
CCACCATGTCAGACGCAGCCGTAGACACCAGCTCCGAAATCACCACCAAGGACTTAAAGGAGAAGAAGGAAGTTG
TGGAAGAGGCAGAAAATGGAAGAGACGCCCCTGCTAACGGGAATGCTAATGAGGAAAATGGGGAGCAGGAGGCTG
ACAATGAGGTAGACGAAGAAGAGGAAGAAGGTGGGGAGGAAGAGGAGGAGGAAGAAGAAGGTGATGGTGAGGAAG
AGGATGGAGATGAAGATGAGGAAGCTGAGTCAGCTACGGGCAAGCGGGCAGCTGAAGATGATGAGGATGACGATG
TCGATACCAAGAAGCAGAAGACCGACGAGGATGACTAGACAGCAAAAAAGGAAAAGTTAAACTAAAAAAAAAAAG
GCCGCCGTGACCTATTCACCCTCCACTTCCCGTCTCAGAATCTAAACGTGGTCACCTTCGAGTAGAGAGGCCCGC
CCGCCCACCGTGGGCAGTGCCACCCGCAGATGACACGCGCTCTCCACCACCCAACCCAAACCATGAGAATTTGCA
ACAGGGGAGGAAAAAAGAACCAAAACTTCCAAGGCCCTGCTTTTTTTCTTAAAAGTACTTTAAAAAGGAAATTTG
TTTGTATTTTTTATTTACATTTTATATTTTTGTACATATTGTTAGGGTCAGCCATTTTTAATGATCTCGGATGAC
CAAACCAGCCTTCGGAGCGTTCTCTGTCCTACTTCTGACTTTACTTGTGGTGTGACCATGTTCATTATAATCTCA
AAGGAGAAAAAAAACCTTGTAAAAAAAGCAAAAATGACAACAGAAAAACAATCTTATTCCGAGCATTCCAGTAAC
TTTTTTGTGTATGTACTTAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCAAAGATAAAAG
GTTTCTTTTTTTTTCCTTTTTTGTCTATGAAGTTGCTGTTTATTTTTTTTGGCCTGTTTGATGTATGTGTGAAAC
AATGTTGTCCAACAATAAACAGG

FIGURE 980A

GCGGCAAGCCCCGCCTCAGCCCCTCTGGCAGGCTCCCGCCAGCGTCGCTGCGGCTCCGGCCCGGGAGCGAGCGCC
CGGAGCTCGGAAAGATGCGGCGCCCGCGGCGGCCTGGGGTCTCGGGGGATCCGGGGGTCTCCGGCTGCTCCTCT
GCCTCCTGCTGCTGAGCAGCCGCCCGGGGGGCTGCAGCGCCGTTAGTGCCCACGGCTGTCTATTTGACCGCAGGC
TCTGCTCTCACCTGGAAGTCTGTATTCAGGATGGCTTGTTTGGGCAGTGCCAGGTGGGAGTGGGGCAGGCCCGGC
CCCTTTTGCAAGTCACCTCCCCAGTTCTCCAACGCTTACAAGGTGTGCTCCGACAACTCATGTCCCAAGGATTGT
CCTGGCACGATGACCTCACCCAGTATGTGATCTCTCAGGAGATGGAGCGCATCCCCAGGCTTCGCCCCCCAGAGC
CCCGTCCAAGGGACAGGTCTGGCTTGGCACCCAAGAGACCTGGTCCTGCTGGAGAGCTGCTTTTACAGGACATCC
CCACTGGCTCCGCCCCTGCTGCCCAGCATCGGCTTCCACAACCACCAGTGGGCAAAGGTGGAGCTGGGGCCAGCT
CCTCTCTGTCCCCTCTGCAGGCTGAGCTGCTCCCGCCTCTCTTGGAGCACCTGCTGCTGCCCCCACAGCCTCCCC
ACCCTTCACTGAGTTACGAACCTGCCTTGCTGCAGCCCTACCTGTTCCACCAGTTTGGCTCCCGTGATGGCTCCA
GGGTCTCAGAGGGCTCCCCAGGGATGGTCAGTGTCGGCCCCCTGCCCAAGGCTGAAGCCCCTGCCCTCTTCAGCA
GAACTGCCTCCAAGGGCATATTTGGGGACCACCCTGGCCACTCCTACGGGGACCTTCCAGGGCCTTCACCTGCCC
AGCTTTTTCAAGACTCTGGGCTGCTCTATCTGGCCCAGGAGTTGCCAGCACCCAGCAGGGCCAGGGTGCCAAGGC
TGCCAGAGCAAGGGAGCAGCAGCCGGGCAGAGGACTCCCCAGAGGGCTATGAGAAGGAAGGACTAGGGGATCGTG
GAGAGAAGCCTGCTTCCCCAGCTGTGCAGCCAGATGCGGCTCTGCAGAGGCTGGCCGCTGTGCTGGCGGGCTATG
GGGTAGAGCTGCGTCAGCTGACCCCTGAGCAGCTCTCCACACTCCTGACCCTGCTGCAGCTACTGCCCAAGGGTG
CAGGAAGAAATCCGGGAGGGGTTGTAAATGTTGGAGCTGATATCAAGAAAACAATGGAGGGGCCGGTGGAGGGCA
GAGACACAGCAGAGCTTCCAGCCCGCACATCCCCCATGCCTGGACACCCCACTGCCAGCCCTACCTCCAGTGAAG
TCCAGCAGGTGCCAAGCCCTGTCTCCTCTGAGCCTCCCAAAGCTGCCAGACCCCCTGTGACACCTGTCCTGCTAG
AGAAGAAAAGCCCACTGGGCCAGAGCCAGCCCACGGTGGCAGGACAGCCCTCAGCCCGCCCAGCAGCAGAGGAAT
ATGGCTACATCGTCACTGATCAGAAGCCCCTGAGCCTGGCTGCAGGAGTGAAGCTGCTGGAGATCCTGGCTGAGC
ATGTGCACATGTCCTCAGGCAGCTTCATCAACATCAGTGTGGTGGGACCAGCCCTCACCTTCCGCATCCGGCACA
ATGAGCAGAACCTGTCTTTGGCTGATGTGACCCAACAAGCAGGGCTGGTGAAGTCTGAACTGGAAGCACAGACAG
GGCTCCAAATCTTGCAGACAGGAGTGGGACAGAGGGAGGAGGCAGCTGCAGTCCTTCCCCAAACTGCGCACAGCA
CCTCACCCATGCGCTCAGTGCTGCTCACTCTGGTGGCCCTGGCAGGTGTGGCTGGGCTGCTGGTGGCTCTGGCTG
TGGCTCTGTGTGTGCGGCAGCATGCGCGGCAGCAAGACAAGGAGCGCCTGGCAGCCCTGGGGCCTGAGGGGGCCC
ATGGTGACACTACCTTTGAGTACCAGGACCTGTGCCGCCAGCACATGGCCACGAAGTCCTTGTTCAACCGGGCAG
AGGGTCCACCGGAGCCTTCACGGGTGAGCAGTGTGTCCTCCCAGTTCAGCGACGCAGCCCAGGCCAGCCCCAGCT
CCCACAGCAGCACCCCGTCCTGGTGCGAGGAGCCGGCCCAAGCCAACATGGACATCTCCACGGGACACATGATTC
TGGCATACATGGAGGATCACCTGCGGAACCGGGACCGCCTTGCCAAGGAGTGGCAGGCCCTCTGTGCCTACCAAG
CAGAGCCAAACACCTGTGCCACCGCGCAGGGGGAGGGCAACATCAAAAAGAACCGGCATCCTGACTTCCTGCCCT
ATGACCATGCCCGCATAAAACTGAAGGTGGAGAGCAGCCCTTCTCGGAGCGATTACATCAACGCCAGCCCCATTA
TTGAGCATGACCCTCGGATGCCAGCCTACATAGCCACGCAGGGCCCGCTGTCCCATACCATCGCAGACTTCTGGC
AGATGGTGTGGGAGAGCGGCTGCACCGTCATCGTCATGCTGACCCCGCTGGTGGAGGATGGTGTCAAGCAGTGTG
ACCGCTACTGGCCAGATGAGGGTGCCTCCCTCTACCACGTATATGAGGTGAACCTGGTGTCGGAGCACATCTGGT
GCGAGGACTTTCTGGTGCGGAGCTTCTACCTGAAGAACGTGCAGACCCAGGAGACGCGCACGCTCACGCAGTTCC
ACTTCCTCAGCTGGCCGGCAGAGGGCACACCGGCCTCCACGCGGCCCCTGCTGGACTTCCGCAGGAAGGTGAACA
AGTGCTACCGGGGCCGCTCCTGCCCCATCATCGTGCACTGCAGTGATGGTGCGGGGAGGACCGGCACCTACATCC
TCATCGACATGGTCCTGAACCGCATGGCAAAAGGAGTGAAGGAGATTGACATCGCTGCCACCCTGGAGCATGTCC
GTGACCAGCGGCCTGGCCTTGTCCGCTCTAAGGACCAGTTTGAATTTGCCCTGACAGCCGTGGCGGAGGAAGTGA
ATGCCATCCTCAAGGCCCTGCCCCAGTGAGACCCTGGGGCCCCTTGGCGGGCAGCCCAGCCTCTGTCCCTCTTTG
CCTGTGTGAGCATCTCTGTGTACCCACTCCTCACTGCCCCACCAGCCACCTCTTGGGCATGCTCAGCCCTTCCTA
GAAGAGTCAGGAAGGGAAAGCCAGAAGGGGCACGCCTGCCCAGCCTCGCATGCCAGAGCCTGGGGCATCCCAGAG
CCCAGGGCATCCCATGGGGGTGCTGCAGCCAGGAGGAGAGGAAAGGACATGGGTAGCAATTCTACCCAGAGCCTT
CTCCTGCCTACATTCCCTGGCCTGGCTCTCCTGTAGCTCTCCTGGGGTTCTGGGAGTTCCCTGAACATCTGTGTG
TGTCCCCCTATGCTCCAGTATGGAAGAATGGGGTGGAGGGTCGCCACACCCGGCTCCCCCTGCTTCTCAGCCCCG
GGCCTGCCTCTGACTCACACTTGGGCGCTCTGCCCTCCCTGGCCTCACGCCCAGCCTCCTCCCACCACCCTCCCA
CCATGCGCTGCTCAACCTCTCTCCTTCTGGCGCAAGAGAACATTTCTAGAAAAAACTACTTTTGTACCAGTGTGA

FIGURE 980B

ATAAAGTTAGTGTGTTGTCTGTGCAGCTGCAAAAAAAAAAAAAAAAAAA

FIGURE 981

MRRPRRPGGLGGSGGLRLLLCLLLLSSRPGGCSAVSAHGCLFDRRLCSHLEVCIQDGLFGQCQVGVGQARPLLQV
TSPVLQRLQGVLRQLMSQGLSWHDDLTQYVISQEMERIPRLRPPEPRPRDRSGLAPKRPGPAGELLLQDIPTGSA
PAAQHRLPQPPVGKGGAGASSSLSPLQAELLPPLLEHLLLPPQPPHPSLSYEPALLQPYLFHQFGSRDGSRVSEG
SPGMVSVGPLPKAEAPALFSRTASKGIFGDHPGHSYGDLPGPSPAQLFQDSGLLYLAQELPAPSRARVPRLPEQG
SSSRAEDSPEGYEKEGLGDRGEKPASPAVQPDAALQRLAAVLAGYGVELRQLTPEQLSTLLTLLQLLPKGAGRNP
GGVVNVGADIKKTMEGPVEGRDTAELPARTSPMPGHPTASPTSSEVQQVPSPVSSEPPKAARPPVTPVLLEKKSP
LGQSQPTVAGQPSARPAAEEYGYIVTDQKPLSLAAGVKLLEILAEHVHMSSGSFINISVVGPALTFRIRHNEQNL
SLADVTQQAGLVKSELEAQTGLQILQTGVGQREEAAAVLPQTAHSTSPMRSVLLTLVALAGVAGLLVALAVALCV
RQHARQQDKERLAALGPEGAHGDTTFEYQDLCRQHMATKSLFNRAEGPPEPSRVSSVSSQFSDAAQASPSSHSST
PSWCEEPAQANMDISTGHMILAYMEDHLRNRDRLAKEWQALCAYQAEPNTCATAQGEGNIKKNRHPDFLPYDHAR
IKLKVESSPSRSDYINASPIIEHDPRMPAYIATQGPLSHTIADFWQMVWESGCTVIVMLTPLVEDGVKQCDRYWP
DEGASLYHVYEVNLVSEHIWCEDFLVRSFYLKNVQTQETRTLTQFHFLSWPAEGTPASTRPLLDFRRKVNKCYRG
RSCPIIVHCSDGAGRTGTYILIDMVLNRMAKGVKEIDIAATLEHVRDQRPGLVRSKDQFEFALTAVAEEVNAILK
ALPQ

FIGURE 982

AGTTCTCACTGAGACCTGTCACCCCGACTCAACGTGAGACGCACCGCCCGGACTCACC**ATG**CGTGAATGCATCTC
AGTCCACGTGGGGCAGGCAGGTGTCCAGATGGGCAATGCCTGCTGGGAGCTCTATTGCTTGGAACATGGGATTCA
GCCTGATGGGCAGATGCCCAGTGACAAGACCATTGGTGGAGGGGACGACTCCTTCACCACCTTCTTCTGTGAAAC
TGGTGCTGGAAAACACGTACCCCGGGCAGTTTTTGTGGATCTGGAGCCTACGGTCATTGATGAGATCCGAAATGG
CCCATACCGACAGCTCTTCCACCCAGAGCAGCTCATCACTGGGAAAGAGGATGCTGCCAACAACTATGCCCGTGG
TCACTATACCATTGGCAAGGAGATCATTGACCCAGTGCTGGATCGGATCCGCAAGCTGTCTGACCAGTGCACAGG
ACTTCAGGGCTTCCTGGTGTTCCACAGCTTTGGTGGGGGCACTGGCTCTGGCTTCACCTCACTCCTGATGGAGCG
GCTCTCTGTTGACTATGGCAAGAAATCCAAGCTGGAATTCTCCATCTACCCAGCCCCCCAGGTGTCTACAGCCGT
GGTCGAGCCCTACAACTCTATCCTGACCACCCACACCACCCTGGAGCACTCAGACTGTGCCTTCATGGTGGACAA
CGAAGCAATCTATGACATCTGCCGCCGCAACCTAGACATCGAGCGCCCAACCTACACCAACCTCAATCGCCTCAT
TAGCCAAATTGTCTCCTCCATCACAGCTTCTCTGCGCTTTGACGGGGCCCTCAATGTGGACCTGACAGAGTTCCA
GACCAACCTGGTGCCCTACCCTCGCATCCACTTCCCCCTGGCCACCTATGCACCAGTCATCTCTGCAGAAAAGGC
ATACCACGAGCAGCTGTCGGTGGCAGAGATCACCAATGCCTGCTTTGAGCCTGCCAACCAGATGGTAAAGTGTGA
TCCCCGGCACGGCAAGTACATGGCCTGCTGCCTGCTGTACCGTGGAGATGTGGTGCCCAAGGATGTCAACGCTGC
CATTGCCGCCATCAAGACCAAGCGCAGCATTCAGTTTGTGGACTGGTGCCCCACAGGCTTCAAGGTTGGTATCAA
CTACCAGCCTCCCACTGTGGTGCCTGGGGGTGACCTGGCCAAGGTGCAGCGTGCCGTGTGCATGCTGAGCAACAC
GACCGCCATCGCCGAGGCCTGGGCCCGCCTGGACCACAAGTTCGACCTGATGTATGCCAAGAGGGCGTTTGTGCA
CTGGTATGTGGGTGAGGGCATGGAGGAGGGTGAGTTCTCCGAGGCCCGTGAGGATATGGCTGCCCTGGAGAAGGA
TTATGAGGAGGTGGGCATCGACTCCTATGAGGACGAGGATGAGGGAGAAGAA**TAA**AGCAGCTGCCTGGAGCCTAT
TCACTATGTTTATTGCAAAATCCTTTCGAAATAAACAGTTTCCTTGCACGGTTAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 983

MRECISVHVGQAGVQMGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFTTFFCETGAGKHVPRAVFVDLEPTVI
DEIRNGPYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDPVLDRIRKLSDQCTGLQGFLVFHSFGGGTGSGFT
SLLMERLSVDYGKKSKLEFSIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYT
NLNRLISQIVSSITASLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPAN
QMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIAAIKTKRSIQFVDWCPTGFKVGINYQPPTVVPGGDLAKVQRAV
CMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSEAREDMAALEKDYEEVGIDSYEDEDEGEE

FIGURE 984

GGGCCTGCAGTTGGCAGGAGGGTCCCGGGCCCAGAGCCAGCGGGGCCGTGCTGAGACGGCGTACGTGCCCTGCGT
GAGTGCGTGGCGGCGGCGCGTGCGCTAGGGGAGTGGGCGGTGAGGCCTGGTCCACGTGCGTCCCTTCCCGGGACC
CCCGCAGCTTGGCGCCCAGCGGCTACGTGAGCCAAGGCACCCGGATGTCCGCGCCCCTCTCCGAGTGACCAGTCC
CGGCCTCCGGTCCCGCAGTGCCCGCAGCCTCGGCCGGCGTCCACGCATTGCCATGGTGACTGTGGGCAACTACTG
CGAGGCCGAAGGGCCCGTGGGTCCGGCCTGGATGCAGGATGGCCTGAGTCCCTGCTTCTTCTTCACGCTCGTGCC
CTCGACGCGGATGGCTCTGGGGACTCTGGCCTTGGTGCTGGCTCTTCCCTGCAGACGCCGGGAGCGGCCCGCTGG
TGCTGATTCGCTGTCTTGGGGGGCCGGCCCTCGCATCTCTCCCTACGTGCTGCAGCTGCTTCTGGCCACACTTCA
GGCGGCGCTGCCCCTGGCCGGCCTGGCTGGCCGGGTGGGCACTGCCCGGGGGGCCCCACTGCCAAGCTATCTACT
TCTGGCCTCCGTGCTGGAGAGTCTGGCCGGCGCCTGTGGCCTGTGGCTGCTTGTCGTGGAGCGGAGCCAGGCACG
GCAGCGTCTGGCAATGGGCATCTGGATCAAGTTCAGGCACAGCCCTGGTCTCCTGCTCCTCTGGACTGTGGCGTT
TGCAGCTGAGAACTTGGCCCTGGTGTCTTGGAACAGCCCACAGTGGTGGTGGGCAAGGGCAGACTTGGGCCAGCA
GGTTCAGTTTAGCCTGTGGGTGCTGCGGTATGTGGTCTCTGGAGGGCTGTTTGTCCTGGGTCTCTGGGCCCCTGG
ACTTCGTCCCCAGTCCTATACATTGCAGGTTCATGAAGAGGACCAAGATGTGGAAAGGAGCCAGGTTCGGTCAGC
AGCCCAACAGTCTACCTGGCGAGATTTTGGCAGGAAGCTCCGCCTCCTGAGTGGCTACCTGTGGCCTCGAGGGAG
TCCAGCTCTGCAGCTGGTGGTGCTCATCTGCCTGGGGCTCATGGGTTTGGAACGGGCACTCAATGTGTTGGTGCC
TATATTCTATAGGAACATTGTGAACTTGCTGACTGAGAAGGCACCTTGGAACTCTCTGGCCTGGACTGTTACCAG
TTACGTCTTCCTCAAGTTCCTCCAGGGGGGTGGCACTGGCAGTACAGGCTTCGTGAGCAACCTGCGCACCTTCCT
GTGGATCCGGGTGCAGCAGTTCACGTCTCGGCGGGTGGAGCTGCTCATCTTCTCCCACCTGCACGAGCTCTCACT
GCGCTGGCACCTGGGGCGCCGCACAGGGGAGGTGCTGCGGATCGCGGATCGGGGCACATCCAGTGTCACAGGGCT
GCTCAGCTACCTGGTGTTCAATGTCATCCCCACGCTGGCCGACATCATCATTGGCATCATCTACTTCAGCATGTT
CTTCAACGCCTGGTTTGGCCTCATTGTGTTCCTGTGCATGAGTCTTTACCTCACCCTGACCATTGTGGTCACTGA
GTGGAGAACCAAGTTTCGTCGTGCTATGAACACACAGGAGAACGCTACCCGGGCACGAGCAGTGGACTCTCTGCT
AAACTTCGAGACGGTGAAGTATTACAACGCCGAGAGTTACGAAGTGGAACGCTATCGAGAGGCCATCATCAAATA
TCAGGGTTTGGAGTGGAAGTCGAGCGCTTCACTGGTTTTACTAAATCAGACCCAGAACCTGGTGATTGGGCTCGG
GCTCCTCGCCGGCTCCCTGCTTTGCGCATACTTTGTCACTGAGCAGAAGCTACAGGTTGGGGACTATGTGCTCTT
TGGCACCTACATTATCCAGCTGTACATGCCCCTCAATTGGTTTGGCACCTACTACAGGATGATCCAGACCAACTT
CATTGACATGGAGAACATGTTTGACTTGCTGAAAGAGGAGACAGAAGTGAAGGACCTTCCTGGAGCAGGGCCCCT
TCGCTTTCAGAAGGGCCGTATTGAGTTTGAGAACGTGCACTTCAGCTATGCCGATGGGCGGGAGACTCTGCAGGA
CGTGTCTTTCACTGTGATGCCTGGACAGACACTTGCCCTGGTGGGCCCATCTGGGGCAGGGAAGAGCACAATTTT
GCGCCTGCTGTTTCGCTTCTACGACATCAGCTCTGGCTGCATCCGAATAGATGGGCAGGACATTTCACAGGTGAC
CCAGGCCTCTCTCCGGTCTCACATTGGAGTTGTGCCCCAAGACACTGTCCTCTTTAATGACACCATCGCCGACAA
TATCCGTTACGGCCGTGTCACAGCTGGGAATGATGAGGTGGAGGCTGCTGCTCAGGCTGCAGGCATCCATGATGC
CATTATGGCTTTCCCTGAAGGGTACAGGACACAGGTGGGCGAGCGGGGACTGAAGCTGAGCGGCGGGGAGAAGCA
GCGCGTCGCCATTGCCCGCACCATCCTCAAGGCTCCGGGCATCATTCTGCTGGATGAGGCAACGTCAGCGCTGGA
TACATCTAATGAGAGGGCCATCCAGGCTTCTCTGGCCAAAGTCTGTGCCAACCGCACCACCATCGTAGTGGCACA
CAGGCTCTCAACTGTGGTCAATGCTGACCAGATCCTCGTCATCAAGGATGGCTGCATCGTGGAGAGGGGACGACA
CGAGGCTCTGTTGTCCCGAGGTGGGGTGTATGCTGACATGTGGCAGCTGCAGCAGGGACAGGAAGAAACCTCTGA
AGACACTAAGCCTCAGACCATGGAACGGTGACAAAAGTTTGGCCACTTCCCTCTCAAAGACTAACCCAGAAGGGA
ATAAGATGTGTCTCCTTTCCCTGGCTTATTTCATCCTGGTCTTGGGGTATGGTGCTAGCTATGGTAAGGGAAAGG
GACCTTTCCGAAAAACATCTTTTGGGGAAATAAAAATGTGGACTGTG

FIGURE 985

GTGCACTTCAGCTATGCCGATGGGTGAGGCCTTCCTTTTGCTTCCTTTGCTTTTCCGTTCATTTGCACACTGCCT
TCCTGCTTCTCAGTGCTCTGAATCCCTGCTTTTGGAAAAGAGCCTGGGCAGGGGAGGGGCAGGGCCTACTAGCAG
CTCTGGTGATGGAAGGTGCCTGCTGAGCAACCCCACCTTTCCTTGCAGGCGGGAGACTCTGCAGGACGTGTCTTT
CACTGTGATGCCTGGACAGACACTTGCCCTGGTGAGAGGAGACCCAGCCACTTGGCCCAGATGCCTCAAGCTTCC
CTCATTCAGTGCCCATGGTAGCTTGTGACCCAGGCTGTGGAGTCAGAGAGCCCAGTCACGATAGGCAACCGGATT
GAATGGTGCAGCCTCCATGGACACTGGTGACCTCTTGGAGAGGGAACCTCAAAAGCCAGTGGGCCTCGGCCGGCT
GCGGTGGCACATGCCTGTAATCCCAGCACTTTGGGAGGCTTAGGTGGCCAGATCACCTAAGGTGGGCCCATCTGG
GGCAGGGAAGAGCACAATTTTGCGCCTGCTGTTTCGCTTCTACGACATCAGCTCTGGCTGCATCCGAATAGATGG
G

FIGURE 986

GCTGCCCCGGTATCCCCGTGTGGGGCAGGAAGTGGGCTTCCAGATTCCCAGTATCCCCGGTAGGGTCTGCTTCTG
CTCGCTCGGGAAGGGCGGTGGCCGTCCCATTACTCAACCAACCCTCAACGCACTGGTCCTCCCAGTTCCCTCCCC
TCAGTGGGTAAACAAACACACACCAGCGCTTGACTCGACAGACTCGAAAACAACATCTACTCAGAAAAGTTGTTT
CTTTCCTATCTCCTTAAACTTTCCCACTTCCACATATCGGAGCTTCTTCCCACCTCGGCCTACTCAAGCATGAGA
TCGGAGGCGGGAGGGCGGCGACTGGCGGCGCGATGGACCTGACCGGGCTCCTGCTGGACGAAGAAGGCACCTTCT
CCCTCGCCGGCTTCCAGGACTTCACGTTCCTCCCAGGACACCAGAAGCTGAGTGCCCGGATCCGAAGGAGGCTCT
ACTATGGCTGGGACTGGGAAGCCGACTGTAGCCTGGAGGAGCTCTCCAGCCCGGTGGCAGACATTGCTGTCGAAC
TGCTCCAGAAGGCAGCCCCCAGCCCTATTCGCCGACTCCAGAAGAAATATGTAGCTCATGTGTCCCGGGAGGCAT
GCATCTCCCCATGTGCTATGATGCTGGCTCTGGTGTACATTGAACGGCTCCGGCACCGAAACCCAGACTACTTGC
AGCATGTGTCATCCTCTGACTTGTTCCTGATCTCCATGATGGTGGCCAGTAAGTACCTCTATGATGAAGGGGAGG
AGGAGGAGGTCTTCAACGACGAATGGGGAGCTGCTGGGGGTGTGGCCGTGCCCACTCTCAATGCCTTGGAGAGGG
GCTTCCTGAGTGCCATGGATTGGCATCTCTACACTGACCCTCGGGAGATCTTTGAGGTGCTGAGCTGGTTGGAGA
GCTGTGTGGCTGAGCAGCAGGGACGGTGGCGAGGCTGGTACACCTACACAGACCTGTGTGTGCTGCTGGAGCAGC
CGACCTGGCAGTTGGCCCTGGGCTCCCTCTGCCAGCGGCTGGTAAAGCTGTCTTGCCTGTTAGCTGTGGCATATG
TGAGCAGTGTGGCCCTGGCTGTGGCATCGGTGGCCGTAATACATCAGTCTTTGGGGCTGTCCTGCATCCCTACAC
CTGGGCCGCCTGACCTTGGACTGACCTCCCGTTGCCTCCTGGAGCCCTGCATACCTTCTGTGCCACAATGCCTGC
CGTCTCTCGCTAATGTCTCCAGCTGCCTGGAAGGCAGCATGGGGCTGCGGTCACTCTGGGGCAGTCTTCTGGCCT
CACTGACTCCTCCACCATTGCCTCCCCCAGACCCCCCTGCCCCTCCCACTCTTCTTCATAACTGCCACCTTTGCC
AGAAGCTCCAGAGAGACTCCCCAACCTGCCATGCCTGCCTCCACCCCAACCGTACAGTCCCCACTGCGCTGTCCA
GCCCCTGGTACCATACCTATGGCCTGGCTCCCCCCTGGCCTTGGAGCCCGGTGCTCCTTTCACTTCCTCAGCCTC
AGCAATGTTCCCTTTTCAGTGTCATGGAGCTGGCTCGCCTCAAGTCTTTCGTTTTCCCAGGCTAGGTAGGGCTGT
GAGGAATGCATTAAGAGGGTTTGGGAGTTTCTGAGAACCTGGAGGAGCAAAGCTTGATTCAGATCCTGTCTGCCT
CGCTGGGTCCTTGGCAGGTCCCCTGTCCTCCTGGGTGGGAGCTTATGGGGTGGTGGGGCAGAAGGACTGAAGGTA
ATTCACTCCTAGATCGCAGTGGCTGGCTGCTTGGCCAGGACAGTGATGCCGCCAGGGAGAGCTTCCGCTTGGTGA
CCAGGGACATGTCCCAGATGGACATAGAAGCCCCTCTCTGCCTCCCTGGGATTTTTTAGACTTTTACTTTTGATT
TCCCTAGGATGGAAGAGTATAGGTGGGAGATAAGGGAAGTGGGGTGAGAGGAGAAAGGAAATGTTGGCATGGGCC
TGTGTGATGTCCCTGAGGCAGAAGAGC

FIGURE 987

MDLTGLLLDEEGTFSLAGFQDFTFLPGHQKLSARIRRRLYYGWDWEADCSLEELSSPVADIAVELLQKAAPSPIR
RLQKKYVAHVSREACISPCAMMLALVYIERLRHRNPDYLQHVSSSDLFLISMMVASKYLYDEGEEEEVFNDEWGA
AGGVAVPTLNALERGFLSAMDWHLYTDPREIFEVLSWLESCVAEQQGRWRGWYTYTDLCVLLEQPTWQLALGSLC
QRLVKLSCLLAVAYVSSVALAVASVAVIHQSLGLSCIPTPGPPDLGLTSRCLLEPCIPSVPQCLPSLANVSSCLE
GSMGLRSLWGSLLASLTPPPLPPPDPPAPPTLLHNCHLCQKLQRDSPTCHACLHPNRTVPTALSSPWYHTYGLAP
PWPWSPVLLSLPQPQQCSLFSVMELARLKSFVFPG

FIGURE 988

GAAGAT<u>**ATG**</u>GCGGCGTCTGCGTCTGCAGCTGCAGGGGAGGAGGACTGGGTCCTTCCCTCTGAAGTTGAAGTATTG
GAGTCCATCTATCTAGATGAACTACAGGTGATTAAAGGAAATGGCAGAACTTCACCATGGGAGATCTACATCACT
TTGCATCCTGCCACTGCAGAGGACCAGGATTCACAGTATGTCTGCTTCACTCTGGTGCTTCAGGTCCCAGCAGAG
TATCCCCATGAGGTGCCACAGATCTCTATCCGAAATCCCCGAGGACTTTCAGATGAACAGATCCACACGATCTTA
CAGGTGCTGGGCCACGTGGCCAAGGCTGGGCTGGGCACTGCCATGCTGTATGAACTCATTGAGAAAGGGAAGGAA
ATTCTCACAGATAACAACATCCCTCATGGCCAGTGTGTCATCTGCCTCTATGGTTTCCAGGAGAAGGAGGCCTTT
ACCAAAACACCCTGTTACCACTACTTCCACTGCCACTGCCTTGCTCGGTACATCCAGCACATGGAGCAAGAGCTG
AAGGCACAAGGACAGGAGCAGGAACAGGAACGGCAGCATGCTACAACCAAACAGAAGGCAGTCGGTGTGCAGTGT
CCAGTGTGCAGAGAGCCCCTCGTGTATGATCTTGCCTCACTGAAAGCAGCCCCTGAACCCCAACAGCCCATGGAG
CTGTACCAGCCCAGTGCAGAGAGCTTGCGCCAGCAAGAAGAACGCAAGCGGCTCTACCAGAGGCAGCAGGAGCGG
GGGGGAATCATTGACCTTGAGGCTGAGCGAAACCGATACTTCATCAGCCTTCAGCAGCCTCCTGCCCCTGCGGAA
CCTGAGTCAGCTGTAGATGTCTCCAAAGGATCCCAACCACCCAGCACCCTTGCAGCAGAACTATCCACCTCACCA
GCCGTCCAATCCACTTTGCCACCTCCTCTGCCTGTGGCGACCCAGCACATATGTGAGAAGATTCCAGGGACCAGG
TCAAATCAGCAAAGGTTGGGCGAAACCCAGAAAGCTATGCTAGATCCCCCCAAGCCCAGTCGAGGTCCCTGGCGA
CAGCCCGAACGGAGGCACCCAAAGGGAGGGGAGTGCCACGCCCCTAAAGGTACCCGTGACACCCAGGAACTGCCA
CCTCCTGAGGGGCCCCTCAAGGAGCCCATGGACCTAAAGCCAGAACCCCATAGCCAAGGAGTTGAAGGTCCTCCA
CAAGAGAAGGGGCCTGGCAGCTGGCAGGGGCCCCCACCCCGCAGGACTCGGGACTGTGTTCGCTGGGAGCGCTCT
AAAGGCCGGACACCCGGTTCTTCCTACCCTCGCCTGCCTCGGGGCCAG<u>**TAG**</u>CATACCGGCCTGGTACTCGGAGGG
AGTCCCTGGGCCTGGAATCTAAGGATGGTTCCTAGCAGGACTTGGTGGGGGAACAGGGAATTGGGGATGGGAGG
GAGGCAATAAAGATATTTGGCCTTC

FIGURE 989

MAASASAAAGEEDWVLPSEVEVLESIYLDELQVIKGNGRTSPWEIYITLHPATAEDQDSQYVCFTLVLQVPAEYP
HEVPQISIRNPRGLSDEQIHTILQVLGHVAKAGLGTAMLYELIEKGKEILTDNNIPHGQCVICLYGFQEKEAFTK
TPCYHYFHCHCLARYIQHMEQELKAQGQEQEQERQHATTKQKAVGVQCPVCREPLVYDLASLKAAPEPQQPMELY
QPSAESLRQQEERKRLYQRQQERGGIIDLEAERNRYFISLQQPPAPAEPESAVDVSKGSQPPSTLAAELSTSPAV
QSTLPPPLPVATQHICEKIPGTRSNQQRLGETQKAMLDPPKPSRGPWRQPERRHPKGGECHAPKGTRDTQELPPP
EGPLKEPMDLKPEPHSQGVEGPPQEKGPGSWQGPPPRRTRDCVRWERSKGRTPGSSYPRLPRGQ

FIGURE 990

GGCACGAGGGCCAGCTGCTGTAGAAGAGGGGAGGAAACAAGCCAGTGCAAGGGGAGCAAAAGAGAAAAGGAGCCA
GGCTGGGCTTCCTGATCCCACAGCATCGCAGAGCTCGGGAGGCACAGCTCACAGACACAGGAAACACAGGACTGC
TATTCTGCTCTCCTGCCCACGGTGATCTGGTGCCAGCTGGTGGAACAGTGGGTG**ATG**GCGTCCCTGCTGCAAGAC
CAGCTGACCACTGATCAGGACTTGCTGCTGATGCAGGAAGGCATGCCGATGCGCAAGGTGAGGTCCAAAAGCTGG
AAGAAGCTAAGATACTTCAGACTTCAGAATGACGGCATGACAGTCTGGCATGCACGGCAGGCCAGGGGCAGTGCC
AAGCCCAGCTTCTCAATCTCTGATGTGGAGACAATACGTAATGGCCATGATTCCGAGTTGCTGCGTAGCCTGGCA
GAGGAGCTCCCCCTGGAGCAGGGCTTCACCATTGTCTTCCATGGCCGCCGCTCCAACCTGGACCTGATGGCCAAC
AGTGTTGAGGAGGCCCAGATATGGATGCGAGGGCTCCAGCTGTTGGTGGATCTTGTCACCAGCATGGACCATCAG
GAGCGCCTGGACCAATGGCTGAGCGATTGGTTTCAACGTGGAGACAAAAATCAGGATGGTAAGATGAGTTTCCAA
GAAGTTCAGCGGTTATTGCACCTAATGAATGTGGAAATGGACCAAGAATATGCCTTCAGTCTTTTTCAGGCAGCA
GACACGTCCCAGTCTGGAACCCTGGAAGGAGAAGAATTCGTACAGTTCTATAAGGCATTGACTAAACGTGCTGAG
GTGCAGGAACTGTTTGAAAGTTTTTCAGCTGATGGGCAGAAGCTGACTCTGCTGGAATTTTTGGATTTCCTCCAA
GAGGAGCAGAAGGAGAGAGACTGCACCTCTGAGCTTGCTCTGGAACTCATTGACCGCTATGAACCTTCAGACAGT
GGCAAACTGCGGCATGTGCTGAGTATGGATGGCTTCCTCAGCTACCTCTGCTCTAAGGATGGAGACATCTTCAAC
CCAGCCTGCCTCCCCATCTATCAGGATATGACTCAACCCCTGAACCACTACTTCATCTGCTCTTCTCATAACACC
TACCTAGTGGGGGACCAGCTTTGCGGCCAGAGCAGCGTCGAGGGATATATACGGGCCCTGAAGCGGGGGTGCCGC
TGCGTGGAGGTGGATGTATGGGATGGACCTAGCGGGGAACCTGTCGTTTACCACGGACACACCCTGACCTCCCGC
ATCCTGTTCAAAGATGTCGTGGCCACAGTAGCACAGTATGCCTTCCAGACATCAGACTACCCAGTCATCTTGTCC
CTGGAGACCCACTGCAGCTGGGAGCAGCAGCAGACCATGGCCCGTCATCTGACTGAGATCCTGGGGGAGCAGCTG
CTGAGCACCACCTTGGATGGGGTGCTGCCCACTCAGCTGCCCTCGCCTGAGGAGCTTCGGAGGAAGATCCTGGTG
AAGGGGAAGAAGTTAACACTTGAGGAAGACCTGGAATATGAGGAAGAGGAAGCAGAACCTGAGTTGGAAGAGTCA
GAATTGGCGCTGGAGTCCCAGTTTGAGACTGAGCCTGAGCCCCAGGAGCAGAACCTTCAGAATAAGGACAAAAAG
AAGAAATCCAAGCCCATCTTGTGTCCAGCCCTCTCTTCCCTGGTTATCTACTTGAAGTCTGTCTCATTCCGCAGC
TTCACACATTCAAAGGAGCACTACCACTTCTACGAGATATCATCTTTCTCTGAAACCAAGGCCAAGCGCCTCATC
AAGGAGGCTGGCAATGAGTTTGTGCAGCACAATACTTGGCAGTTAAGCCGTGTGTATCCCAGCGGCCTGAGGACA
GACTCTTCCAACTACAACCCCCAGGAACTCTGGAATGCAGGCTGCCAGATGGTGGCCATGAATATGCAGACTGCA
GGGCTTGAAATGGACATCTGTGATGGGCATTTCCGCCAGAATGGCGGCTGTGGCTATGTGCTGAAGCCAGACTTC
CTGCGTGATATCCAGAGTTCTTTCCACCCTGAGAAGCCCATCAGCCCTTTCAAAGCCCAGACTCTCTTAATCCAG
GTGATCAGCGGTCAGCAACTCCCCAAAGTGGACAAGACCAAAGAGGGGTCCATTGTGGATCCACTGGTGAAAGTG
CAGATCTTTGGCGTTCGTCTAGACACAGCACGGCAGGAGACCAACTATGTGGAGAACAATGGTTTTAATCCATAC
TGGGGGCAGACACTATGTTTCCGGGTGCTGGTGCCTGAACTTGCCATGCTGCGTTTTGTGGTAATGGATTATGAC
TGGAAATCCCGAAATGACTTTATTGGTCAGTACACCCTGCCTTGGACCTGCATGCAACAAGGTTACCGCCACATT
CACCTGCTGTCCAAAGATGGCATCAGCCTCCGCCCAGCTTCCATCTTTGTGTATATCTGCATCCAGGAAGGCCTG
GAGGGGGATGAGTCC**TGA**GGTGGGCATTTCACGGGAAGGGTTGGTATGCTGGCTTTAGACGGGGAGAAACATCTG
GAAGGATGCTCGAGAGAACAAATGGAGGTGGTGAAAATCAAGCTTTGGATTGTGCATTCCTAGGCACAAAATTAC
CTCATTCTTCCTAACAAGCAATCTGGGACCTGATTTTCCACCTTTTTCTCTTTTCTTCCCTTCCTTTGTTTTCA
TAAGCCTTTGGTATCTTTCCTGCCCTTTTCCTTTGTGTACTCTATACTGGAGTTCCCTTCTTCCTCTTGCTGTAG
GCTCAATCCCATACCGACATCTACAACTAATCTTTCCCATCAACTCTGTGTGAAGGCAGGTTGCAACTAGAAATT
CAGAGGGGCTTGGAATAGAGAAACCTAAAGAAGCATCATCCCCTCCATCCCCAACTTCCTCAAAGCCCAAAGCCA
AGGGAAGGATAAATCAAGGCTCAAGGCTTCCCCAGCAAAGATTAGGGAAAGAGACTTGACCCCAGGACTGTACTA
CGACTCTTAAGAGAACACTGCACAGCACTCAAAGTCCCCCACTGGACTGCTTCCTCCTTAGCCCCACTGGTATAA
ATACATCTCTCTCCAATTTGGCAAAAAAAAAAAAAAAAAA

FIGURE 991

MASLLQDQLTTDQDLLLMQEGMPMRKVRSKSWKKLRYFRLQNDGMTVWHARQARGSAKPSFSISDVETIRNGHDS
ELLRSLAEELPLEQGFTIVFHGRRSNLDLMANSVEEAQIWMRGLQLLVDLVTSMDHQERLDQWLSDWFQRGDKNQ
DGKMSFQEVQRLLHLMNVEMDQEYAFSLFQAADTSQSGTLEGEEFVQFYKALTKRAEVQELFESFSADGQKLTLL
EFLDFLQEEQKERDCTSELALELIDRYEPSDSGKLRHVLSMDGFLSYLCSKDGDIFNPACLPIYQDMTQPLNHYF
ICSSHNTYLVGDQLCGQSSVEGYIRALKRGCRCVEVDVWDGPSGEPVVYHGHTLTSRILFKDVVATVAQYAFQTS
DYPVILSLETHCSWEQQQTMARHLTEILGEQLLSTTLDGVLPTQLPSPEELRRKILVKGKKLTLEEDLEYEEEEA
EPELEESELALESQFETEPEPQEQNLQNKDKKKKSKPILCPALSSLVIYLKSVSFRSFTHSKEHYHFYEISSFSE
TKAKRLIKEAGNEFVQHNTWQLSRVYPSGLRTDSSNYNPQELWNAGCQMVAMNMQTAGLEMDICDGHFRQNGGCG
YVLKPDFLRDIQSSFHPEKPISPFKAQTLLIQVISGQQLPKVDKTKEGSIVDPLVKVQIFGVRLDTARQETNYVE
NNGFNPYWGQTLCFRVLVPELAMLRFVVMDYDWKSRNDFIGQYTLPWTCMQQGYRHIHLLSKDGISLRPASIFVY
ICIQEGLEGDES

FIGURE 992

TTCTCCCCCAGGCTCACTCACCATGACCAAGCTGAGCGCCCAAGTCAAAGGCTCTCTCAACATCACCACCCCGGG
GCTGCAGATATGGAGGATCGAGGCCATGCAGATGGTGCCTGTTCCTTCCAGCACCTTTGGAAGCTTCTTCGATGG
TGACTGCTACATCATCCTGGCTATCCACAAGACAGCCAGCAGCCTGTCCTATGACATCCACTACTGGATTGGCCA
GGACTCATCCCTGGATGAGCAGGGGGCAGCTGCCATCTACACCACACAGATGGATGACTTCCTGAAGGGCCGGGC
TGTGCAGCACCGCGAGGTCCAGGGCAACGAGAGCGAGGCCTTCCGAGGCTACTTCAAGCAAGGCCTTGTGATCCG
GAAAGGGGGCGTGGCTTCTGGCATGAAGCACGTGGAGACCAACTCCTATGACGTCCAGAGGCTGCTGCATGTCAA
GGGCAAGAGGAACGTGGTAGCTGGAGAGGTAGAGATGTCCTGGAAGAGTTTCAACCGAGGGGATGTTTTCCTCCT
GGACCTTGGGAAGCTTATCATCCAGTGGAATGGACCGGAAAGCACCCGTATGGAGAGACTCAGGGGCATGACTCT
GGCCAAGGAGATCCGAGACCAGGAGCGGGGAGGGCGCACCTATGTAGGCGTGGTGGACGGAGAGAATGAATTGGC
ATCCCCGAAGCTGATGGAGGTGATGAACCACGTGCTGGGCAAGCGCAGGGAGCTGAAGGCGGCCGTGCCCGACAC
GGTGGTGGAGCCGGCACTCAAGGCTGCACTCAAACTGTACCATGTGTCTGACTCCGAGGGGAATCTGGTGGTGAG
GGAAGTCGCCACACGGCCACTGACACAGGACCTGCTCAGTCACGAGGACTGTTACATCCTGGACCAGGGGGGCCT
GAAGATCTACGTGTGGAAAGGGAAGAAAGCCAATGAGCAGGAGAAGAAGGGAGCCATGAGCCATGCGCTGAACTT
CATCAAAGCCAAGCAGTACCCACCAAGCACACAGGTGGAGGTGCAGAATGATGGGGCTGAGTCGGCCGTCTTTCA
GCAGCTCTTCCAGAAGTGGACAGCGTCCAACCGGACCTCAGGCCTAGGCAAAACCCACACTGTGGGCTCCGTGGC
CAAAGTGGAACAGGTGAAGTTCGATGCCACATCCATGCATGTCAAGCCTCAGGTGGCTGCCCAGCAGAAGATGGT
AGATGATGGGAGTGGGGAAGTGCAGGTGTGGCGCATTGAGAACCTAGAGCTGGTACCTGTGGATTCCAAGTGGCT
AGGCCACTTCTATGGGGGCGACTGCTACCTGCTGCTCTACACCTACCTCATCGGCGAGAAGCAGCATTACCTGCT
CTACGTTTGGCAGGGCAGCCAGGCCAGCCAAGATGAAATTACAGCATCAGCTTATCAAGCCGTCATCCTGGACCA
GAAGTACAATGGTGAACCAGTCCAGATCCGGGTCCCAATGGGCAAGGAGCCACCTCATCTTATGTCCATCTTCAA
GGGACGCATGGTGGTCTACCAGGGAGGCACCTCCCGAACTAACAACTTGGAGACCGGGCCCTCCACACGGCTGTT
CCAGGTCCAGGGAACTGGCGCCAACAACACCAAGGCCTTTGAGGTCCCAGCGCGGGCCAATTTCCTCAATTCCAA
TGATGTCTTTGTCCTCAAGACCCAGTCTTGCTGCTATCTATGGTGTGGGAAGGGTTGTAGCGGGGACGAGCGGGA
GATGGCCAAGATGGTTGCTGACACCATCTCCCGGACGGAGAAGCAAGTGGTGGTGGAAGGGCAGGAGCCAGCCAA
CTTCTGGATGGCCCTGGGTGGGAAGGCCCCCTATGCCAACACCAAGAGACTACAGGAAGAAAACCTGGTCATCAC
CCCCCGGCTCTTTGAGTGTTCCAACAAGACTGGGCGCTTCCTGGCCACAGAGATCCCTGACTTCAATCAGGATGA
CTTGGAAGAGGATGATGTGTTCCTACTAGATGTCTGGGACCAGGTCTTCTTCTGGATTGGGAAACATGCCAACGA
GGAGGAGAAGAAGGCCGCAGCAACCACTGCACAGGAATACCTCAAGACCCATCCCAGCGGGCGTGACCCTGAGAC
CCCCATCATTGTGGTGAAGCAGGGACACGAGCCCCCCACCTTCACAGGCTGGTTCCTGGCTTGGGATCCCTTCAA
GTGGAGTAACACCAAATCCTATGAGGACCTGAAGGCGGAGCTTGGCAACTCTAGGGACTGGAGCCAGATCACTGC
TGAGGTCACAAGCCCCAAAGTGGACGTGTTCAATGCTAACAGCAACCTCAGTTCTGGGCCTCTGCCCATCTTCCC
CCTGGAGCAGCTAGTGAACAAGCCTGTAGAGGAGCTCCCCGAGGGTGTGGACCCCAGCAGGAAGGAGGAACACCT
GTCCATTGAAGATTTCACTCAGGCCTTTGGGATGACTCCAGCTGCCTTCTCTGCTCTGCCTCGATGGAAGCAACA
AAACCTCAAGAAAGAAAAAGGACTATTTTGAGAAGAGTAGCTGTGGTTGTAAAGCAGTACCCTACCCTGATTGTA
GGGTCTCATTTTCTCACCGATATTAGTCCTACACCAATTGAAGTGAAATTTTGCAGATGTGCCTATGAGCACAAA
CTTCTGTGGCAAATGCCAGTTTTGTTTAATAATGTACCTATTCCTTCAGAAAGATGATACCCC

FIGURE 993

TGCTCCCTTTTTCTGTCTCTGTCCATGCTGCCATGTTTCTCTGCTGCCAAATTGGGCCCCTTGGCCCCTTCCGGT
TCTGCTTCCTGGGGGCAGGGTTCCTGCCTTGGACCCCCAGTCTGGGAACGGTGGACATCAAGTGCCTTGCATAGA
GCCCCCTCTTCCCCGCCCAGCTTTCCCAGGGGCACAGCTCTAGGCTGGGAGGGGAGAACCAGCCCCTCCCCCTGC
CCCACCTCCTCTCCCCAGGGTCTAACGGTTAAGGGGACCCACATACCAGTGCCAAGGGGGATGTCAAGTGGTGAT
GTCGTTGTGCTCCCCTCCCCCAGAGCGGGTGGGCGGGGGGTGAATATGGTTGGCCTGCATCAGGTGGCCTTCCCA
TTTAAGTGCCTTCTCTGTGACTGAGAGCCCTAGTGTGATGAGAACTAAAGAGAAAGCCAGACCCCT

FIGURE 994

ATGGACTCTGGGAGGCGTTTGGGCCCAGAGAAGTGGATCCGCCGCTTGCGCCGCATGGAGTCCGAATCGGAAAGC
GGGGCTGCTGCTGACACCCCCCACTGGAGACCCTAAGCTTCCATGGTGATGAAGAGATTATCGAGGTGGTAGAA
CTTGATCCCGGTCCGCCGGACCCAGATGACCTGGCCCAGGAGATGGAAGATGTGGACTTTGAGGAAGAAGAGGAG
GAAGAGGGCAACGAAGAGGGCTGGGTTCTAGAACCCCAGGAAGGGGTGGTCGGCAGCATGGAGGGCCCCGACGAT
AGCGAGGTCACCTTTGCATTGCACTCAGCATCTGTGTTTTGTGTGAGCCTGGACCCCAAGACCAATACCTTGGCA
GTGACCGGGGGTGAAGATGACAAAGCCTTCGTATGGCGGCTCAGCGATGGGGAGCTGCTCTTTGAGTGTGCAGGC
CATAAAGACTCTGTGACTTGTGCTGGTTTCAGCCATGACTCCACTCTAGTGGCCACAGGGGACATGAGTGGCCTC
TTGAAAGTGTGGCAGGTGGACACTAAGGAGGAGGTCTGGTCCTTTGAAGCGGGAGACCTGGAGTGGATGGAGTGG
CATCCTCGGGCACCTGTCCTGTTGGCGGGCACAGCTGACGGCAACACCTGGATGTGGAAAGTCCCGAATGGTGAC
TGCAAGACCTTCCAGGGTCCCAACTGCCCAGCCACCTGTGGCCGAGTCCTCCCTGATGGGAAGAGAGCTGTGGTA
GGCTATGAAGATGGGACCATCAGGATTTGGGACCTGAAGCAGGGAAGCCCTATCCATGTACTGAAAGGGACTGAG
GGTCACCAGGGCCCACTCACCTGTGTTGCTGCCAACCAGGATGGCAGCTTGATCCTAACTGGCTCTGTGGACTGC
CAGGCCAAGCTGGTCAGTGCCACCACCGGCAAGGTGGTGGGTGTTTTTAGACCTGAGACTGTGGCCTCCCAGCCC
AGCCTGGGAGAAGGGGAGGAGAGTGAGTCCAACTCGGTGGAGTCCTTGGGCTTCTGCAGTGTGATGCCCCTGGCA
GCTGTTGGCTACCTGGATGGGACCTTGGCCATCTATGACCTGGCTACGCAGACTCTTAGGCATCAGTGTCAGCAC
CAGTCGGGCATCGTGCAGCTGCTGTGGGAGGCAGGCACTGCCGTGGTATATACCTGCAGCCTGGATGGCATCGTG
CGCCTCTGGGACGCCCGGACCGGCCGCCTGCTTACTGACTACCGGGGCCACACGGCTGAGATCCTGGACTTTGCC
CTCAGCAAAGATGCCTCCCTGGTGGTGACCACGTCAGGAGACCACAAAGCGAAAGTATTTTGTGTCCAAAGGCCT
GACCGT**TAA**TGGCTGCAGCCCCTGCCTGTGTGTCTGGTGTTGAGGGGACGAAGGGACCCCTGCCCCTGTCTGCCA
GCAGAGGCAGTAGGGCACAGAGGGAAGAGGAGGGTGGGGCCCTGGATGACTTTCCAGCCTCTTCAACTGACTTGC
TCCCCTCTCCTTTTCTTCTCTTTAGAGACCCAGCCCAGGGCCCTCCCACCCTTGCCCAGACCTGGTGGGCCCTTC
AGAGGGAGGGGTGGACCTGTTTCTCTTTCACTTTCATTTGCTGGTGTGAGCCATGGGGTGTGTATTTGTATGTGG
GGAGTAGGTGTTTGAGGTTCCCGTTCTTTCCCTTCCCAAGTCTCTGGGGGTGGAAAGGAGGAAGAGATACTAGTT
AAAGATTTTAAAAATGTAAATAAAATATACTTCCCAG

FIGURE 995

MDSGRRLGPEKWIRRLRRMESESESGAAADTPPLETLSFHGDEEIIEVVELDPGPPDPDDLAQEMEDVDFEEEEE
EEGNEEGWVLEPQEGVVGSMEGPDDSEVTFALHSASVFCVSLDPKTNTLAVTGGEDDKAFVWRLSDGELLFECAG
HKDSVTCAGFSHDSTLVATGDMSGLLKVWQVDTKEEVWSFEAGDLEWMEWHPRAPVLLAGTADGNTWMWKVPNGD
CKTFQGPNCPATCGRVLPDGKRAVVGYEDGTIRIWDLKQGSPIHVLKGTEGHQGPLTCVAANQDGSLILTGSVDC
QAKLVSATTGKVVGVFRPETVASQPSLGEGEESESNSVESLGFCSVMPLAAVGYLDGTLAIYDLATQTLRHQCQH
QSGIVQLLWEAGTAVVYTCSLDGIVRLWDARTGRLLTDYRGHTAEILDFALSKDASLVVTTSGDHKAKVFCVQRP
DR

FIGURE 996

GGCACGAGCTCTCCCTCCGTCCTTGCCTCCCTTACCCACCCTCACCGGCCCTTGTTTCTCCTTCCCCTGGGGGCA
GCCGCCGCC**ATG**ATCCTGCTGGAGGTGAACAACCGCATCATCGAGGAGACGCTCGCGCTCAAGTTCGAGAACGCG
GCCGCCGGAAACAAACCGGAAGCAGTAGAAGTAACATTTGCAGATTTCGATGGGGTCCTCTATCATATTTCAAAT
CCTAATGGAGACAAAACAAAAGTGATGGTCAGTATTTCTTTGAAATTCTACAAGGAACTTCAGGCACATGGTGCT
GATGAGTTATTAAAGAGGGTGTACGGGAGTTTCTTGGTAAATCCAGAATCAGGATACAATGTCTCTTTGCTATAT
GACCTTGAAAATCTTCCGGCATCCAAGGATTCCATTGTGCATCAAGCTGGCATGTTGAAGCGAAATTGTTTTGCC
TCTGTCTTTGAAAAATACTTCCAATTCCAAGAAGAGGGCAAGGAAGGAGAGAACAGGGCAGTTATCCATTATAGG
GATGATGAGACCATGTATGTTGAGTCTAAAAAGGACAGAGTCACAGTAGTCTTCAGCACAGTGTTTAAGGATGAC
GACGATGTGGTCATTGGAAAGGTGTTCATGCAGGAGTTCAAAGAAGGACGCAGAGCCAGCCACACAGCCCCACAG
GTCCTCTTTAGCCACAGGGAACCTCCTCTGGAGCTGAAAGACACAGACGCCGCTGTGGGTGACAACATTGGCTAC
ATTACCTTTGTGCTGTTCCCTCGTCACACCAATGCCAGTGCTCGAGACAACACCATCAACCTGATCCACACGTTC
CGGGACTACCTGCACTACCACATCAAGTGCTCTAAGGCCTATATTCACACACGTATGCGGGCGAAAACGTCTGAC
TTCCTCAAGGTGCTGAACCGCGCACGCCCAGATGCCGAGAAAAAAGAAATGAAAACAATCACGGGGAAGACGTTT
TCATCCCGC**TAA**TCTTGGGAATAAGAGGAGGAAGCGGCTGGCAACTGAAGGCTGGAACACTTGCTACTGGATAAT
CGTAGCTTTTAATGTTGCGCCTCTTCAGGTTCTTAAGGGATTCTCCGTTTTGGTTCCATTTTGTACACGTTTGGA
AAATAATCTGCAGAAACGAGCTGTGCTTGCAAAGACTTCATAGTTCCCAAGAATTAAAAAAAAAAAAAAAAAA

FIGURE 997

MILLEVNNRIIEETLALKFENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTKVMVSISLKFYKELQAHGADEL
LKRVYGSFLVNPESGYNVSLLYDLENLPASKDSIVHQAGMLKRNCFASVFEKYFQFQEEGKEGENRAVIHYRDDE
TMYVESKKDRVTVVFSTVFKDDDDVVIGKVFMQEFKEGRRASHTAPQVLFSHREPPLELKDTDAAVGDNIGYITF
VLFPRHTNASARDNTINLIHTFRDYLHYHIKCSKAYIHTRMRAKTSDFLKVLNRARPDAEKKEMKTIITGKTFSSR

FIGURE 998

GCGGCGGCGAGAGGATGAACAACAAGTTCGACGCTTTGAAAGATGATGACAGTGGGGACCATGATCAGAATGAAG
AAAACAGCACACAGAAAGATGGTGAGAAGGAAAAAACGGAACGAGACAAGAATCAGAGCAGTAGCAAGAGAAAGG
CTGTTGTCCCTGGACCGGCAGAGCATCCCCTGCAGTACAACTACACTTTTTGGTACTCCAGGAGAACCCCCGGCC
GTCCCACGAGCTCACAGAGCTATGAACAGAATATCAAACAGATTGGCACCTTTGCCTCTGTGGAGCAGTTCTGGA
GGTTTTATAGCCACATGGTACGTCCTGGGGACCTGACAGGCCACAGTGACTTCCATCTCTTCAAAGAAGGAATTA
AACCCATGTGGGAGGATGATGCAAATAAAAATGGTGGCAAGTGGATTATTCGGCTGCGGAAGGGCTTGGCCTCCC
GTTGCTGGGAGAATCTCATTTTGGCCATGCTGGGGGAACAGTTCATGGTTGGGGAGGAGATCTGTGGGGCTGTGG
TGTCTGTCCGCTTTCAGGAAGACATTATTTCAATATGGAATAAGACTGCCAGTGACCAAGCAACCACAGCCCGAA
TCCGGGACACACTTCGGCGAGTGCTTAACCTACCTCCCAACACCATTATGGAATACAAAACTCACACCGACAGCA
TCAAAATGCCAGGCAGGCTGGGCCCCCAAAGGCTCCTTTTTCAAAACCTCTGGAAGCCGCGGTTGAATGTGCCAT
GACCCTCTCCCTCTCTGGATGGCACCATCATTGAAGCTGGCGTCATCGGAGTCTGTTGTTCTGTTGGCGTGCTAC
CTGGAAGATCCTTCTGTGGTGGACAAGAGGAATTGGAAGAGCATTTTATGTTTTAAGAACAGGCTGACACGCAGC
AGCTACAACAACAGCTGAGATCACTTAATAAATGGTGCTAAACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 999

MNNKFDALKDDDSGDHDQNEENSTQKDGEKEKTERDKNQSSSKRKAVVPGPAEHPLQYNYTFWYSRRTPGRPTSS
QSYEQNIKQIGTFASVEQFWRFYSHMVRPGDLTGHSDFHLFKEGIKPMWEDDANKNGGKWIIRLRKGLASRCWEN
LILAMLGEQFMVGEEICGAVVSVRFQEDIISIWNKTASDQATTARIRDTLRRVLNLPPNTIMEYKTHTDSIKMPG
RLGPQRLLFQNLWKPRLNVP

FIGURE 1000

GGCACGAGGAGAGCCTCGAGCCTGCGAGGAGCGCGCCGCCCGCCAGCTCCCTGCGTCCCGTCCCGCGTCCCCGCG
TTCCCGCGTCCTGCGATCCGCCGCC**ATG**GCCAGTGAGGAGCTGGCGTGCAAGCTGGAGCGCCGGCTGCGGCGCGA
GGAGGCCGAGGAGAGTGGCCCCCAGCTGGCTCCCCTCGGCGCCCCAGCCCCGGAGCCCAAGCCCGAGCCCGAGCC
TCCCGCCCGTGCGCCCACGGCCAGCGCCGACGCGGAGCTGAGCGCCCAGCTGAGCCGGCGGCTGGACATCAACGA
GGGCGCTGCGCGGCCCCGGCGCTGCAGGGTCTTCAACCCCTACACGGAGTTCCCGGAGTTCAGCCGCCGCCTCAT
CAAGGACCTGGAGAGCATGTTCAAACTGTATGACGCTGGGCGGGATGGCTTCATCGACCTGATGGAGCTGAAGCT
GATGATGGAGAAGCTGGGGGCCCCCCAGACCCACCTGGGCCTGAAGAGCATGATCAAGGAGGTGGATGAGGACTT
CGATGGCAAGCTCAGCTTCCGGGAGTTCCTGCTCATTTTCCACAAGGCCGCGGCAGGGGAGCTGCAGGAGGACAG
TGGGCTGATGGCGCTGGCAAAGCTTTCTGAGATCGATGTGGCCCTGGAGGGTGTCAAAGGTGCCAAGAACTTCTT
TGAAGCCAAGGTCCAAGCCTTGTCATCGGCCAGTAAGTTTGAAGCAGAGTTGAAAGCTGAGCAAGATGAGCGGAA
GCGGGAGGAGGAGGAGAGGCGGCTCCGCCAGGCAGCCTTCCAGAAACTCAAGGCCAACTTCAATACA**TAG**TCCTG
CTGACCTTGCCCTCTGCCCACAGCTGTGCCTCACAGATGCCCCGAGAAGAGATGACTAGGCATCTTCATCACTGC
TGTCGGTCCCCTCCCTGAGCCAGCATCTCCATCCACCACCCCGTGCCAGCTCCCGTGCCAGCCTTCATTCCTCCC
AGTGTCCAAGCCCCTCCAGGAGGGTCCTGGGGTGGGCCAGATGCCTGCCCACCTCTGTCTCCTGCCTCTGCTCCT
CTGCCCTTCTTATAGCCAGAACTTGTATCTTCTCAGCAACCTTCACTTTGTCCTTGTCCCTTTACCATTCCCCAT
CAAAGAGTAGTCTGCTATATCAATTTGTGTAGATATGTCTGTCTTTTTGGGTCCTCAGAGAAAATGCCCATTTTC
TCGGAGAATTCTCTGCACTCCTCTCTGCTTCACATTCAACTTCCCTGTTCTCATCTTTGGTAGGATTCTGCCAGT
TGCTTTTGCATCTTCTGTTCCTGGGTAATGGTGGGTCTTAATGGAGGCTGGGTGGACCACTGCCCGTCCACTCTT
CAACAGGAGGAACAGCATGCCACCACAGTAACACACATTAGAGAAAGGACAGAGGTCTGCTCCTTCCTGCCACCT
TTCTCCTGGCCCCTTAGCATTCCCCCAGTCCCTCCCTCTTCACCTTGCTCCGTCTATGTCTTCCCAGCTCAGCCT
TTTCCCCACTCTTAAATACTGTACTACTTCACTGTAAGAACGAAAGAATAGTTAGGATACCAATGAGTAAAAGGG
TTCCTGTTCACTCTGACTCTGTGCAAATTGTATTACAGTAGACCGCTGACGTTCCCAAGTGACAGATCCAGGGCC
TTTCAAACATCCCCAAAGTCATGGCCATACTCACCATTAGCCAGTTTCTAACATCTGTTTCAGGGTATCCAGCTG
TAGATGTTCTTATCCCCCATACTTGTGAGTTATTGGGGTTGCTCACAAATACTAGGGGTTTTTGTTGTATTTTTA
ACAAATATATCCTAATGTCATATTTATTCTCTTTTGTAACTGCTGTCTTTACAATAAAGAAATCATCTGCCTTTC
TAAAAAAAAAAAAAAAAAAAAA

FIGURE 1001

MASEELACKLERRLRREEAEESGPQLAPLGAPAPEPKPEPEPPARAPTASADAELSAQLSRRLDINEGAARPRRC
RVFNPYTEFPEFSRRLIKDLESMFKLYDAGRDGFIDLMELKLMMEKLGAPQTHLGLKSMIKEVDEDFDGKLSFRE
FLLIFHKAAAGELQEDSGLMALAKLSEIDVALEGVKGAKNFFEAKVQALSSASKFEAELKAEQDERKREEEERRL
RQAAFQKLKANFNT

FIGURE 1002

ATGGTCCCCTGCTGGAACCATGGCAACATCACCCGCTCCAAGGCGGAGGAGCTGCTTTCCAGGACAGGCAAGGAC
GGGAGCTTCCTCGTGCGTGCCAGCGAGTCCATCTCCCGGGCATACGCGCTCTGCGTGCTGTATCGGAATTGCGTT
TACACTTACAGAATTCTGCCCAATGAAGATGATAAATTCACTGTTCAGAAATCTGAACCTGACTTCAGCCGATAC
TGGCAGAGAAAGGGTGTAAACGATGAGGAAGGAAGTGCACGCGCAGGATGCAGTAGTAGACAGGGAGCTGGACTC
AAGGTGTGGGGAGACCACAGGCAAGTCCCTGGAGGCAAAAATCCTCCAGAAGTTGTCAAGAGGGAGAGCGTGGTG
AGCAGAACGCCCCTCAGGAAGACAGCTTATGAGGATGGAAGGAATTGCTTCGAGGAGCGATGTGAT**TGA**

FIGURE 1003

MVPCWNHGNITRSKAEELLSRTGKDGSFLVRASESISRAYALCVLYRNCVYTYRILPNEDDKFTVQKSEPDFSRY
WQRKGVNDEEGSARAGCSSRQGAGLKVWGDHRQVPGGKNPPEVVKRESVVSRTPLRKTAYEDGRNCFEERCD

FIGURE 1004

CTTCGGGTGTACGTGCTCCGGGATCTTCAGCACCCGCGGCCGCCATCGCCGTCGCTTGGCTTCTTCTGGACTCAT
CTGCGCCACTTGTCCGCTTCACACTCCGCCGCCATC**ATG**GTGAAGCTCGCGAAGGCAGGTAAAAATCAAGGTGAC
CCCAAGAAAATGGCTCCTCCTCCAAAGGAGGTAGAAGAAGATAGTGAAGATGAGGAAATGTCAGAAGATGAAGAA
GATGATAGCAGTGGAGAAGAGGTCGTCATACCTCAGAAGAAAGGCAAGAAGGCTGCTGCAACCTCAGCAAAGAAG
GTGGTCGTTTCCCCAACAAAAAAGGTTGCAGTTGCCACACCAGCCAAGAAAGCAGCTGTCACTCCAGGCAAAAAG
GCAGCAGCAACACCTGCCAAGAAGACAGTTACACCAGCCAAAGCAGTTACCACACCTGGCAAGAAGGGAGCCACA
CCAGGCAAAGCATTGGTAGCAACTCCTGGTAAGAAGGGTGCTGCCATCCCAGCCAAGGGGGCAAAGAATGGCAAG
AATGCCAAGAAGGAAGACAGTGATGAAGAGGAGGATGATGACAGTGAGGAGGATGAGGAGGATGACGAGGACGAG
GATGAGGATGAAGATGAAATTGAACCAGCAGCGATGAAAGCAGCAGCTGCTGCCCCTGCCTCAGAGGATGAGGAC
GATGAGGATGACGAAGATGATGAGGATGACGATGACGATGAGGAAGATGACTCTGAAGAAGAAGCTATGGAGACT
ACACCAGCCAAAGGAAAGAAAGCTGCAAAAGTTGTTCCTGTGAAAGCCAAGAACGTGGCTGAGGATGAAGATGAA
GAAGAGGATGATGAGGACGAGGATGACGACGACGACGAAGATGATGAAGATGATGATGATGAAGATGATGAGGAG
GAGGAAGAAGAGGAGGAGGAAGAGCCTGTCAAAGAAGCACCTGGAAAACGAAAGAAGGAAATGGCCAAACAGAAA
GCAGCTCCTGAAGCCAAGAAACAGAAAGTGGAAGGCACAGAACCGACTACGGCTTTCAATCTCTTTGTTGGAAAC
CTAAACTTTAACAAATCTGCTCCTGAATTAAAAACTGGTATCAGCGATGTTTTTGCTAAAAATGATCTTGCTGTT
GTGGATGTCAGAATTGGTATGACTAGGAAATTTGGTTATGTGGATTTTGAATCTGCTGAAGACCTGGAGAAAGCG
TTGGAACTCACTGGTTTGAAAGTCTTTGGCAATGAAATTAAACTAGAGAAACCAAAAGGAAAAGACAGTAAGAAA
GAGCGAGATGCGAGAACACTTTTGGCTAAAAATCTCCCTTACAAAGTCACTCAGGATGAATTGAAAGAAGTGTTT
GAAGATGCTGCGGAGATCAGATTAGTCAGCAAGGATGGGAAAAGTAAAGGGATTGCTTATATTGAATTTAAGACA
GAAGCTGATGCAGAGAAAACCTTTGAAGAAAAGCAGGGAACAGAGATCGATGGGCGATCTATTTCCCTGTACTAT
ACTGGAGAGAAAGGTCAAAATCAAGACTATAGAGGTGGAAAGAATAGCACTTGGAGTGGTGAATCAAAAACTCTG
GTTTTAAGCAACCTCTCCTACAGTGCAACAGAAGAAACTCTTCAGGAAGTATTTGAGAAAGCAACTTTTATCAAA
GTACCCCAGAACCAAAATGGCAAATCTAAAGGGTATGCATTTATAGAGTTTGCTTCATTCGAAGACGCTAAAGAA
GCTTTAAATTCCTGTAATAAAAGGGAAATTGAGGGCAGAGCAATCAGGCTGGAGTTGCAAGGACCCAGGGGATCA
CCTAATGCCAGAAGCCAGCCATCCAAAACTCTGTTTGTCAAAGGCCTGTCTGAGGATACCACTGAAGAGACATTA
AAGGAGTCATTTGACGGCTCCGTTCGGGCAAGGATAGTTACTGACCGGGAAACTGGGTCCTCCAAAGGGTTTGGT
TTTGTAGACTTCAACAGTGAGGAGGATGCCAAAGCTGCCAAGGAGGCCATGGAAGACGGTGAAATTGATGGAAAT
AAAGTTACCTTGGACTGGGCCAAACCTAAGGGTGAAGGTGGCTTCGGGGGTCGTGGTGGAGGCAGAGGCGGCTTT
GGAGGACGAGGTGGTGGTAGAGGAGGCCGAGGAGGATTTGGTGGCAGAGGCCGGGGAGGCTTTGGAGGGCGAGGA
GGCTTCCGAGGAGGCAGAGGAGGAGGAGGAGGTGACCACAAGCCACAAGGAAAGAAGACGAAGTTTGAA**TAG**CTTCTG
TCCCTCTGCTTTCCCTTTTCCATTTGAAAGAAAGGACTCTGGGGTTTTTACTGTTACCTGATCAATGACAGAGCC
TTCTGAGGACATTCCAAGACAGTATACAGTCCTGTGGTCTCCTTGGAAATCCGTCTAGTTAACATTTCAAGGGCA
ATACCGTGTTGGTTTTGACTGGATATTCATATAAACTTTTTAAAGAGTTGAGTGATAGAGCTAACCCTTATCTGT
AAGTTTTGAATTTATATTGTTTCATCCCATGTACAAAACCATTTTTTCCTAC

FIGURE 1005

MVKLAKAGKNQGDPKKMAPPPKEVEEDSEDEEMSEDEEDDSSGEEVVIPQKKGKKAAATSAKKVVVSPTKKVAVA
TPAKKAAVTPGKKAAATPAKKTVTPAKAVTTPGKKGATPGKALVATPGKKGAAIPAKGAKNGKNAKKEDSDEEED
DDSEEDEEDDEDEDEDEDEIEPAAMKAAAAAPASEDEDDEDDEDDEDDDDDEEDDSEEEAMETTPAKGKKAAKVV
PVKAKNVAEDEDEEEDDEDEDDDDDEDDEDDDDEDDEEEEEEEEEEPVKEAPGKRKKEMAKQKAAPEAKKQKVEG
TEPTTAFNLFVGNLNFNKSAPELKTGISDVFAKNDLAVVDVRIGMTRKFGYVDFESAEDLEKALELTGLKVFGNE
IKLEKPKGKDSKKERDARTLLAKNLPYKVTQDELKEVFEDAAEIRLVSKDGKSKGIAYIEFKTEADAEKTFEEKQ
GTEIDGRSISLYYTGEKGQNQDYRGGKNSTWSGESKTLVLSNLSYSATEETLQEVFEKATFIKVPQNQNGKSKGY
AFIEFASFEDAKEALNSCNKREIEGRAIRLELQGPRGSPNARSQPSKTLFVKGLSEDTTEETLKESFDGSVRARI
VTDRETGSSKGFGFVDFNSEEDAKAAKEAMEDGEIDGNKVTLDWAKPKGEGGFGGRGGGRGGFGGRGGGRGGRGG
FGGRGRGGFGGRGGFRGGRGGGGDHKPQGKKTKFE

FIGURE 1006

TGAACTGAGCGGCCCCTGAGCTGACAGATACACTGCGCAGCTGGAACGGCGAGCGAGCCGACGGGCGAGTGAGGG
GCGCAGCCATGATCACCTCGGCCGCTGGAATTATTTCTCTTCTGGATGAAGATGAACCACAGCTTAAGGAATTTG
CACTACACAAATTGAATGCAGTTGTTAATGACTTCTGGGCAGAAATTTCCGAGTCCGTAGACAAAATAGAGGTTT
TATACGAAGATGAAGGTTTCCGGAGTCGGCAGTTTGCAGCCTTAGTGGCATCTAAAGTATTTTATCACCTGGGGG
CTTTTGAGGAGTCTCTGAATTATGCTCTTGGAGCAGGGGACCTCTTCAATGTCAATGATAACTCTGAATATGTGG
AAACTATTATAGCAAAATGCATTGATCACTACACCAAACAATGTGTGGAAAATGCAGATTTGCCTGAAGGAGAAA
AAAAACCAATTGACCAGAGATTGGAAGGCATCGTAAATAAAATGTTCCAGCGATGTCTAGATGATCACAAGTATA
AACAGGCTATTGGCATTGCTCTGGAGACACGAAGACTGGACGTCTTTGAAAAGACCATACTGGAGTCGAATGATG
TCCCAGGAATGTTAGCTTATAGCCTTAAGCTCTGCATGTCTTTAATGCAGAATAAACAGTTTCGGAATAAAGTAC
TAAGAGTTCTAGTTAAAATCTACATGAACTTGGAGAAACCTGATTTCATCAATGTTTGTCAGTGCTTAATTTTCT
TAGATGATCCTCAGGCTGTGAGTGATATCTTAGAGAAACTGGTAAAGGAAGACAACCTCCTGATGGCATATCAGA
TTTGTTTTGATTTGTATGAAAGTGCTAGCCAGCAGTTTTTGTCATCTGTAATCCAGAATCTTCGAACTGTTGGCA
CCCCTATTGCTTCTGTGCCTGGATCCACTAATACGGGTACTGTTCCGGGATCAGAGAAAGACAGTGACTCGATGG
AAACAGAAGAAAAGACAAGCAGTGCATTTGTAGGAAAGACACCAGAAGCCAGTCCAGAGCCTAAGGACCAGACTT
TGAAAATGATTAAAATTTTAAGTGGTGAAATGGCTATTGAGTTACATCTGCAGTTCTTAATACGAAACAATAATA
CAGACCTCATGATTCTAAAAAACACAAAGGATGCAGTACGGAATTCTGTATGTCATACTGCAACCGTTATAGCAA
ACTCTTTTATGCACTGTGGGACAACCAGTGACCAGTTTCTTAGAGATAATTTGGAATGGTTAGCCAGAGCCACTA
ACTGGGCAAAATTTACTGCTACAGCCAGTTTGGGTGTAATTCATAAGGGTCATGAAAAAGAAGCATTACAGTTAA
TGGCAACATACCTTCCCAAGGATACTTCTCCAGGATCAGCCTATCAGGAAGGTGGAGGTCTCTATGCACTAGGTC
TTATTCATGCCAATCATGGTGGTGATATAATTGACTATCTGCTTAATCAGCTTAAGAACGCCAGCAATGATATCG
TTAGACACGGTGGCAGTCTGGGCCTTGGTTTGGCAGCCATGGGAACTGCACGTCAAGATGTTTATGATTTGCTAA
AAACAAACCTTTATCAGGATGATGCAGTAACAGGGGAAGCAGCTGGCCTGGCCCTAGGTTTGGTTATGTTGGGCT
CTAAAAATGCTCAGGCTATTGAGGACATGGTTGGTTATGCACAAGAAACTCAACATGAGAAGATTCTGCGTGGTC
TTGCAGTTGGCATAGCTTTAGTAATGTATGGGAGGATGGAAGAGGCTGATGCTCTCATTGAATCTCTCTGTCGTG
ACAAGGACCCAATTCTTCGAAGGTCTGGAATGTATACTGTAGCCATGGCTTATTGTGGCTCTGGTAACAACAAAG
CAATTCGACGCCTGCTACATGTTGCTGTAAGTGATGTTAATGATGATGTCAGGAGGGCAGCAGTAGAATCACTTG
GGTTCATTCTATTCAGAACCCCTGAACAGTGCCCAAGTGTTGTCTCTTTGTTGTCAGAGAGTTACAACCCTCATG
TGCGCTACGGAGCTGCAATGGCCTTGGGGATATGCTGTGCTGGTACAGGAAACAAGGAAGCCATTAATTTGCTAG
AACCAATGACAAACGACCCCGTGAACTACGTGAGGCAAGGGGCACTCATAGCTTCAGCTCTCATCATGATCCAGC
AGACTGAAATCACTTGTCCAAAGGTGAATCAGTTCAGACAGCTGTATTCCAAAGTCATCAATGATAAGCATGATG
ATGTCATGGCCAAGTTTGGCGCTATTCTGGCCCAGGGCATACTGGATGCAGGTGGTCATAATGTCACAATCTCCT
TGCAGTCCAGGACTGGGCATACTCATATGCCTTCTGTGGTTGGCGTCCTTGTATTTACCCAGTTTTGGTTCTGGT
TTCCTCTTTCACACTTCCTGTCATTGGCTTATACCCCTACCTGTGTCATTGGCCTTAACAAGGACTTAAAGATGC
CGAAAGTTCAGTATAAATCGAACTGTAAACCATCCACATTTGCATATCCTGCCCCTCTGGAAGTACCAAAAGAAA
AAGAAAAGGAAAAGGTTTCTACTGCTGTATTATCTATAACTGCCAAGGCTAAAAAGAAGGAAAAAGAAAAGGAAA
AAAAGGAGGAGGAGAAAATGGAAGTGGATGAGGCAGAGAAAAAGGAGGAAAAAGAGAAGAAAAAAGAACCTGAGC
CAAACTTCCAGTTATTGGATAACCCAGCCCGAGTTATGCCTGCCCAGCTTAAGGTCCTAACCATGCCGGAGACCT
GTAGATACCAGCCTTTCAAACCACTCTCTATTGGAGGCATCATCATTCTGAAGGATACCAGTGAAGACATTGAGG
AGCTGGTGGAACCTGTGGCAGCACATGGCCCAAAAATCGAGGAGGAGGAACAAGAGCCAGAACCCCCAGAACCAT
TTGAGTATATTGATGATTAAGGGCCAGAGGATCTCACTTGCTTATCTGAAGAAGATTGTCCAGGCTCATATTGGG
AATGCTTATGAGGAAATTCATGCCGAGACCTGCTATTCAATGCATGTATCGTTGCCTCTGCACTGACCTGAAGAA
CCCTGTCTCCAAGTCTTTGGTTGAAGAGAAGATATATGACTGTTGAGTGTGCTCTTTCACAGAACTTGGTTTTCA
AATAAATATAAGATCTCCAGATGGACAAG

FIGURE 1007

CTGCAAGCCGCCGGAGCCGGGCAACCAGTGGAAGGAGCCTGGGAGAGGCCAGGCCTCCCCGGACTGCTAGCCTGC
TTTTCCTGGGGTCCCTGGAGCCGGAGGAAGAACCAGGATGTTGCTGCCTGCAGAAGCTCAGCTCAGGAAGACTTC
CAGGAACCTGAGGAGGAGCTGCCACTAACAGCCATATTTCCCA**ATG**GAGACTGTGATGACCTTGGAAGGGGGTCA
AAAGCCTGTGATGGAGTCGTACACACTCCTGCTGAGCCCACCGGAGACTCAAGATGAAGGCTGGACCCTTGCGCT
GTCCCTGGCTCTAACCTACAGACTGGGGCCTGGCTCCGTCTTACTGGCCCCCAGGTCTCCATGGAGACTGCAGAA
ACCCCCGCCTGCTGGAGGCCTGCCACACTCACAGTTACCAGCTAGACAGTGGGGCTTACTAAGACAAGCAGGACC
TAAAACAGTGTCTCCCCTGGGAACCTACTCCCCACCCAGCATTTGC**TAA**GTCTGATCACAGGGAGGTTATTTTGT
CTCTCTGTCTCGGTTTCTCTGAGCCACTGAGACAGATGGCTGTCCGCTTTGAGGCTCTGCAGAGCTGTGGCACCC
CATGGTGTGTCTGCAGTGTTCTGGGCACATGCATGGGCACCCATCGTTGAGAGTGCAGCTGGGAAGAACTCTGAA
CCAGAAGTCATCAGAGCTGAGGCATGGCCTTGAACATGTCACTCAGTCTCTGGGGCTTCTGTTTCACAAATGCAT
GAGGGGGCCACCAGCCCAGTGGCTTTAAACCAGGGGCAGGTTGTCCCTCCAGGCAGCATTGGAAATGTGTGTGTG
TTGAGGGGGTCACAGTGACTGTGGGGGCACCCCTGGCATCTAGTGGGCATCCCACAATGTGCAGAACAGTCTCTG
ACAGCAAAGAATTGGTCCATTCAATGCCAATTGTAGTACCTTTGAGACATTCTGGCTGAGCCAATGCCTTCTCCC
TGTCAGAGTCCCCCAGAGCAGAGAGGGTCAGGCTTCCCTGGACCTTGGCTCCCAGAGCAAGCCAAAATAAAGACT
ACACTGTTGCCTTGGGGGCTTGTCGGGCCAGGGCCAAGACGGTCTGCGTGCTGCAGGGCCAGGACAGAAATAGCC
ACACATGCCGGTGAGAACAAAGAGCCTCTTTCTTTCTCATGTTGACATCGACTTTCTGTGCCAAGTCCTTTGGGT
ATAAGGATGCTAGGGAATTCCTATAGGCACCAAACAGAAGGAAAGCTAGGGGCTTGGACTACTGGGTATAGGACT
TGCTCTAGCTCTCAGGTCCTAGCCCAAGCTCAATGCAAACACAGCCCCTCCGGGCTCTCTGTTTCTGTGAGGTTC
TGGAATCCCTTCCTCTGTGTCCGTGAGTCTGACAGAATCGATGATGTTCCCTTAGAGCTGGGAAATCCATGTGTT
TATTCACGGAGGGAACTCACCATTACCTCCCTTGTCTTCTTTGCCTGCCTTGGAGAAATCCAGAGTCTTCGGAAT
GGCAAAGGCAGCTCCTGGATTTCCCTGGAGGGGAGGCACTAGCTGAGGGAAGTAGCTCCCTTCATTCATGATGCA
CAGTTTACGCAGCAGACACACAACTGCGCCTACTATTTGCTCGGTGCCCTGCAAGGTGCTGCCTAACTTTGATTT
GTTATTTCAGCTCTCTCCAGGATAGTGCCAAATGGTGCAATGGGAAACCTGTTTTGCTGGGGGGCTCTAGATCAC
TGGCTCCAGAACTCCCGGCTGCCAGGGTAGCCCCTACCCCCAGCCCCTTGCTCCTGGACAGCAGTGGGTCTCACC
TTTAGCCTCTGCCCCCAGTTCTGGTCTGACCCAACAGAGGGGCTCTATGATATTAAGAAGGGGCCCTTCCTGCTC
TGTGCCTCAACCTATTCTCCATAATAGGGAGTCTAATCCTATTCCTTCCCTGCCTGATGAGGATGGTGTGAGGAT
GAGGAGGACGGCATCTCATTTGGGGCTTTTTGGCAGTGGGCCTCATTTTAATCCTGCAGGGCTGCCTGCCAGTGG
ATCTATCCAGCTGCTTCCTTGTAGCCAAGAATGAGTTCAATGAATTGTGATTCACTGATTTTATTGATTTTGTTT
TAAAACAGGGAGACTGGTATTTTTGAAGCTGCTATCATTTTCTATTTCTTTATTAATTTCTTTGTAATCATCTTA
TTAAAGTTTTCTTATTTAGTGGG

FIGURE 1008

METVMTLEGGQKPVMESYTLLLSPPETQDEGWTLALSLALTYRLGPGSVLLAPRSPWRLQKPPPAGGLPHSQLPA
RQWGLLRQAGPKTVSPLGTYSPPSIC

FIGURE 1009

GGGACGCGAGCGGGATCCAAACTTCCGGTGCCTGCAGAGCTCGGAGCGGCGGAGGCAGAGACCGAGGCTGCACCG
GCAGAGGCTGCGGGGCGGACGCGCGGGCCGGCGCAGCC**ATG**GTGAAGATTAGCTTCCAGCCCGCCGTGGCTGGCA
TCAAGGGCGACAAGGCTGACAAGGCGTCGGCGTCGGCCCCTGCGCCGGCCTCGGCCACCGAGATCCTGCTGACGC
CGGCTAGGGAGGAGCAGCCCCCACAACATCGATCCAAGAGGGGGGGCTCAGTGGGCGGCGTGTGCTACCTGTCGA
TGGGCATGGTCGTGCTGCTCATGGGCCTCGTGTTCGCCTCTGTCTACATCTACAGATACTTCTTCCTTGCGCAGC
TGGCCCGAGATAACTTCTTCCGCTGTGGTGTGCTGTATGAGGACTCCCTGTCCTCCCAGGTCCGGACTCAGATGG
AGCTGGAAGAGGATGTGAAAATCTACCTCGACGAGAACTACGAGCGCATCAACGTGCCTGTGCCCCAGTTTGGCG
GCGGTGACCCTGCAGACATCATCCATGACTTCCAGCGGGGTCTGACTGCGTACCATGATATCTCCCTGGACAAGT
GCTATGTCATCGAACTCAACACCACCATTGTGCTGCCCCCTCGCAACTTCTGGGAGCTCCTCATGAACGTGAAGA
GGGGGACCTACCTGCCGCAGACGTACATCATCCAGGAGGAGATGGTGGTCACGGAGCATGTCAGTGACAAGGAGG
CCCTGGGGTCCTTCATCTACCACCTGTGCAACGGGAAAGACACCTACCGGCTCCGGCGCCGGGCAACGCGGAGGC
GGATCAACAAGCGTGGGGCCAAGAACTGCAATGCCATCCGCCACTTCGAGAACACCTTCGTGGTGGAGACGCTCA
TCTGCGGGGTGGTG**TGA**GGCCCTCCTCCCCCAGAACCCCCTGCCGTGTTCCTCTTTTCTTCTTTCCGGCTGCTCT
CTGGCCCTCCTCCTTCCCCCTGCTTAGCTTGTACTTTGGACGCGTTTCTATAGAGGTGACATGTCTCTCCATTCC
TCTCCAACCCTGCCCACCTCCCTGTACCAGAGCTGTGATCTCTCGGTGGGGGGCCCATCTCTGCTGACCTGGGTG
TGGCGGAGGGAGAGGCGATGCTGCAAAGTGTTTTCTGTGTCCCACTGTCTTGAAGCTGGGCCTGCCAAAGCCTGG
GCCCACAGCTGCACCGGCAGCCCAAGGGGAAGGACCGGTTGGGGGAGCCGGGCATGTGAGGCCCTGGGCAAGGGG
ATGGGGCTGTGGGGGCGGGGCGGCATGGGCTTCAGAAGTATCTGCACAATTAGAAAAGTCCTCAGAAGCTTTTTC
TTGGAGGGTACACTTTCTTCACTGTCCCTATTCCTAGACCTGGGGCTTGAGCTGAGGATGGGACGATGTGCCCAG
GGAGGGACCCACCAGAGCACAAGAGAAGGTGGCTACCTGGGGGTGTCCCAGGGACTCTGTCAGTGCCTTCAGCCC
ACCAGCAGGAGCTTGGAGTTTGGGGAGTGGGGATGAGTCCGTCAAGCACAACTGTTCTCTGAGTGGAACCAAAGA
AGCAAGGAGCTAGGACCCCCAGTCCTGCCCCCCAGGAGCACAAGCAGGGTCCCCTCAGTCAAGGCAGTGGGATGG
GCGGCTGAGGAACGGGGCAGGCAAGGTCACTGCTCAGTCACGTCCACGGGGGACGAGCCGTGGGTTCTGCTGAGT
AGGTGGAGCTCATTGCTTTCTCCAAGCTTGGAACTGTTTTGAAAGATAACACAGAGGGAAAGGGAGAGCCACCTG
GTACTTGTCCACCCTGCCTCCTCTGTTCTGAAATTCCATCCCCCTCAGCTTAGGGGAATGCACCTTTTTCCCTTT
CCTTCTCACTTTTGCATGTTTTTACTGATCATTCGATATGCTAACCGTTCTCAGCCCTGAGCCTTGGAGAGGAGG
GCTGTAACGCCTTCAGTCAGTCTCTGGGGATGAAACTCTTAAATGCTTTGTATATTTTCTCAATTAGATCTCTTT
TCAGAAGTGTCTATAGAACAATAAAAATCTTTTACTTCTG

FIGURE 1010

MVKISFQPAVAGIKGDKADKASASASAPAPASATEILLTPAREEQPPQHRSKRGGSVGGVCYLSMGMVVLLMGLVFA
SVYIIYRYFFLAQLARDNFFRCGVLYEDSLSSQVRTQMELEEDVKIYLDENYERINVPVPQFGGGDPADIIHDFQR
GLTAYHDISLDKCYVIELNTTIVLPPRNFWELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGK
DTYRLRRRATRRRINKRGAKNCNAIRHFENTFVVETLICGVV

FIGURE 1011

GATCACCACCATCGAGGCAGTGAAGTGCAAGATCCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGC
TGAGCACCTCCAGCGAGAAGTTGAGGGAGAAAGGCAGGCCCGGGAAGAGAGGTATGAAGGTTGTTGAAAATCGGG
CCTTAAAAGATGAAGAAAAGATGGAACTCCAGGAAATCTAACTCCAAGAAGCTAAGCACATTGCAGAAGAGGCAG
ATAGGAAGTATGAAGAGGTGGCTCATAAGTTGGTGATCATTGAAGGAGACTTGGAAGGCACGGAGGAACGAGCTG
AGCTGGGAGAGTCCCGTTGCCAAGAGATGGATGAGCAGATTAGACTGATGGACCAGAACCTGAAGTGTCTGAGTG
CTGCTGAAGAAATGTACTCTCAAAAAGAAGACAAATATGAGGAAGAGATCAAGATTCTTACTGATAAACTCAAGG
AGGCAGAGACCAGTGCTGAGTTTGCTGAGAGATCGGTAGCCAAGCTGGAAAAGACAATTGATGACTTGGAAGATA
AACTGAAACGCACCAAAGAGGAGCACCTCTGTACACAAAGGATGCTGGACCAGACTCTGATTGACCTGAATGAGA
TGTAGAACGCCCCAGTCCCACCCTGCTGCTGCTCCTCCCTCTTCTCAGAGAATCCAGCTGGGCTAGAGGCTGAGC
ACCTTTGGAAACAACATTTAAGGGAATGTGAGCACAATGCATAATGTCTTTAAAAAGCATGTTGTGATG

FIGURE 1012

GTTTTGCCTGCTAGCATCTCCCTGTAACTCTCCCAATCTTGAGGAGTGATCCCTGTCCCAGCCCCTGGAAAGGGG
CAGGAACGACAAACTCAAAGTCCAGG**ATG**TTCACCATGACAAGAGCCATGGAAGAGGCTCTTTTTCAGCACTTCA
TGCACCAGAAGCTGGGGATCGCCTATGCCATACACAAGCCATTTCCCTTCTTTGAAGGCCTCCTAGACAACTCCA
TCATCACTAAGAGAATGTACATGGAATCTCTGGAAGCCTGTAGAAATTTGATCCCTGTATCCAGAGTGGTGCACA
ACATTCTCACCCAACTGGAGAGGACTTTTAACCTGTCTCTTCTGGTGACATTGTTCAGTCAAATTAACCTGCGTG
AATATCCCAATCTGGTGACGATTTACAGAAGCTTCAAACGTGTTGGTGCTTCCTATGAACGGCAGAGCAGAGACA
CACCAATCCTACTTGAAGCCCCAACTGGCCTAGCAGAAGGAAGCTCCCTCCATACCCCACTGGCGCTGCCCCCAC
CACAACCCCCTCAACCAAGCTGTTCACCCTGTGCGCCAAGAGTCAGTGAGCCTGGAACATCCTCCCAGCAAAGCG
ATGAGATCCTGAGTGAGTCGCCCAGCCCATCTGACCCTGTCCTGCCTCTCCCTGCACTCATCCAGGAAGGAAGAA
GCACTTCAGTGACCAATGACAAGTTAACATCCAAAATGAATGCGGAAGAAGACTCAGAAGAGATGCCCAGCCTCC
TCACTAGCACTGTGCAAGTGGCCAGTGACAACCTGATCCCCCAAATAAGAGATAAAGAAGACCCTCAAGAGATGC
CCCACTCTCCCTTGGGCTCTATGCCAGAGATAAGAGATAATTCTCCAGAACCAAATGACCCAGAAGAGCCCCAGG
AGGTGTCCAGCACACCTTCAGACAAGAAAGGAAAGAAAAGAAAAAGATGTATCTGGTCAACTCCAAAAAGGAGAC
ATAAGAAAAAAAGCCTCCCAAGAGGGACAGCCTCATCTAGACACGGAATCCAAAAGAAGCTCAAAAGGGTGGATC
AGGTTCCTCAAAAGAAAGATGACTCAACTTGTAACTCCACGGTAGAGACAAGGGCCCAAAAGGCGAGAACTGAAT
GTGCCCGAAAGTCGAGATCAGAGGAGATCATTGATGGCACTTCAGAAATGAATGAAGGAAAGAGGTCCCAGAAGA
CGCCTAGTACACCACGAAGGGTCACACAAGGGGCAGCCTCACCTGGGCATGGCATCCAAGAGAAGCTCCAAGTGG
TGGATAAGGTGACTCAAAGGAAAGACGACTCAACCTGGAACTCAGAGGTCATGATGAGGGTCCAAAAGGCAAGAA
CTAAATGTGCCCGAAAGTCCAGATCGAAAGAAAAGAAAAAGGAGAAAGATATCTGTTCAAGCTCAAAAAGGAGAT
TTCAGAAAAATATTCACCGAAGAGGAAAACCCAAAAGTGACACTGTGGATTTTCACTGTTCTAAGCTCCCCGTGA
CCTGTGGTGAGGCGAAAGGGATTTTATATAAGAAGAAAATGAAACACGGATCCTCAGTGAAGTGCATTCGGAATG
AGGATGGAACTTGGTTAACACCAAATGAATTTGAAGTCGAAGGAAAAGGAAGGAACGCAAAGAACTGGAAACGGA
ATATACGTTGTGAAGGAATGACCCTAGGAGAGCTGCTGAAGCGGAAAAACTCGGATGAATGCGAGGTGTGCTGTC
AAGGGGGACAACTTCTCTGCTGCGGTACTTGTCCACGAGTCTTCCATGAGGACTGTCACATCCCCCCTGTGGAAG
CCAAGAGGATGCTGTGGAGTTGCACCTTCTGCAGGATGAAGAGGTCTTCAGGAAGCCAACAGTGCCATCATGTAT
CTAAGACCCTGGAGAGGCAGATGCAGCCTCAGGACCAGCTGATTCGAGATTACGGTGAGCCCTTTCAGGAAGCAA
TGTGGTTGGACCTGGTTAAGGAAAGGCTGATTACGGAAATGTACACGGTGGCATGGTTTGTGCGAGACATGCGCC
TGATGTTTCGCAACCATAAAACATTTTACAAGGCTTCTGACTTTGGCCAGGTAGGACTTGACTTAGAGGCAGAAT
TTGAAAAAGATCTCAAAGACGTGCTCGGTTTTCATGAAGCCAATGACGGCGGTTTCTGGACTCTTCCT**TGA**CCCT
GTTCTGTAAAGACTGAAGCATCCCCACCTCAGGATTCAGCTGATGGGACCCTGGCTTGGACTGTTGATTGCCAGT
GAGTCTGGGATGTAATTGGCTGCCCTCAGGACCCAAACCCAGACACTTCATAGGATTATCACACCCTCCATCTTT
ATTCTTTCTTTTTACCTTTAAAAGTCTATATCTA

FIGURE 1013

MFTMTRAMEEALFQHFMHQKLGIAYAIHKPFPFFEGLLDNSIITKRMYMESLEACRNLIPVSRVVHNILTQLERT
FNLSLLVTLFSQINLREYPNLVTIYRSFKRVGASYERQSRDTPILLEAPTGLAEGSSLHTPLALPPPQPPQPSCS
PCAPRVSEPGTSSQQSDEILSESPSPSDPVLPLPALIQEGRSTSVTNDKLTSKMNAEEDSEEMPSLLTSTVQVAS
DNLIPQIRDKEDPQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSTPSDKKGKKRKRCIWSTPKRRHKKKSLPRG
TASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSEMNEGKRSQKTPSTPRRVT
QGAASPGHGIQEKLQVVDKVTQRKDDSTWNSEVMMRVQKARTKCARKSRSKEKKKEKDICSSSKRRFQKNIHRRG
KPKSDTVDFHCSKLPVTCGEAKGILYKKKMKHGSSVKCIRNEDGTWLTPNEFEVEGKGRNAKNWKRNIRCEGMTL
GELLKRKNSDECEVCCQGGQLLCCGTCPRVFHEDCHIPPVEAKRMLWSCTFCRMKRSSGSQQCHHVSKTLERQMQ
PQDQLIRDYGEPFQEAMWLDLVKERLITEMYTVAWFVRDMRLMFRNHKTFYKASDFGQVGLDLEAEFEKDLKDVL
GFHEANDGGFWTLP

FIGURE 1014

GTTTTGCCTGCTAGCATCTCCCTGTAACTCTCCCAATCTTGAGGAGTGATCCCTGTCCCAGCCCCTGGAAAGGGG
CAGGAACGACAAACTCAAAGTCCAGG**ATG**TTCACCATGACAAGAGCCATGGAAGAGGCTCTTTTCAGCACTTCA
TGCACCAGAAGCTGGGGATCGCCTATGCCATACACAAGCCATTTCCCTTCTTTGAAGGCCTCCTAGACAACTCCA
TCATCACTAAGAGAATGTACATGGAATCTCTGGAAGCCTGTAGAAATTTGATCCCTGTATCCAGAGTGGTGCACA
ACATTCTCACCCAACTGGAGAGGACTTTTAACCTGTCTCTTCTGGTGACATTGTTCAGTCAAATTAACCTGCGTG
AATATCCCAATCTGGTGACGATTTACAGAAGCTTCAAACGTGTTGGTGCTTCCTATGAACGGCAGAGCAGAGACA
CACCAATCCTACTTGAAGCCCCAACTGGCCTAGCAGAAGGAAGCTCCCTCCATACCCCACTGGCGCTGCCCCCAC
CACAACCCCCTCAACCAAGCTGTTCACCCTGTGCGCCAAGAGTCAGTGAGCCTGGAACATCCTCCCAGCAAAGCG
ATGAGATCCTGAGTGAGTCGCCCAGCCCATCTGACCCTGTCCTGCCTCTCCCTGCACTCATCCAGGAAGGAAGAA
GCACTTCAGTGACCAATGACAAGTTAACATCCAAAATGAATGCGGAAGAAGACTCAGAAGAGATGCCCAGCCTCC
TCACTAGCACTGTGCAAGTGGCCAGTGACAACCTGATCCCCCAAATAAGAGATAAAGAAGACCCTCAAGAGATGC
CCCACTCTCCCTTGGGCTCTATGCCAGAGATAAGAGATAATTCTCCAGAACCAAATGACCCAGAAGAGCCCCAGG
AGGTGTCCAGCACACCTTCAGACAAGAAAGGAAAGAAAAGAAAAAGATGTATCTGGTCAACTCCAAAAAGGAGAC
ATAAGAAAAAAAGCCTCCCAAGAGGGACAGCCTCATCTAGACACGGAATCCAAAAGAAGCTCAAAAGGGTGGATC
AGGTTCCTCAAAAGAAAGATGACTCAACTTGTAACTCCACGGTAGAGACAAGGGCCCAAAAGGCGAGAACTGAAT
GTGCCCGAAAGTCGAGATCAGAGGAGATCATTGATGGCACTTCAGAAATGAATGAAGGAAAGAGGTCCCAGAAGA
CGCCTAGTACACCACGAAGGGTCACACAAGGGGCAGCCTCACCTGGGCATGGCATCCAAGAGAAGCTCCAAGTGG
TGGATAAGGTGACTCAAAGGAAAGACGACTCAACCTGGAACTCAGAGGTCATGATGAGGGTCCAAAAGGCAAGAA
CTAAATGTGCCCGAAAGTCCAGATCGAAAGAAAAGAAAAAGGAGAAAGATATCTGTTCAAGCTCAAAAAGGAGAT
TTCAGAAAAATATTCACCGAAGAGGAAAACCCAAAAGTGACACTGTGGATTTTCACTGTTCTAAGCTCCCCGTGA
CCTGTGGTGAGGCGAAAGGGATTTTATATAAGAAGAAAATGAAACACGGATCCTCAGTGAAGTGCATTCGGAATG
AGGATGGAACTTGGTTAACACCAAATGAATTTGAAGTCGAAGGAAAAGGAAGGAACGCAAAGAACTGGAAACGGA
ATATACGTTGTGAAGGAATGACCCTAGGAGAGCTGCTGAAGAGTGGACTTTTGCTCTGTCCTCCAAGAATAAATC
TCAAGAGAGAGTTAAATAGCAAG**TGA**ATTTCTACTACCCTCTCAGTCACCATGTTGCAGACTTTCCCTGTCTGGA
GGCTCACCTTAGAGCTTCTGAGTTTCCAAGCTCTGAGTCACCTCCACATTTGGGCATGGCATCTTCAAAACAATT
AATTTGCATAGTTAATTTGGGATGGGGAAGCAAATGACTCTAAAATAAAAATTAAATGAAAAAGCTCAAAAAAAA
AAAAAAAAAAAA

FIGURE 1015

MFTMTRAMEEALFQHFMHQKLGIAYAIHKPFPFFEGLLDNSIITKRMYMESLEACRNLIPVSRVVHNILTQLERT
FNLSLLVTLFSQINLREYPNLVTIYRSFKRVGASYERQSRDTPILLEAPTGLAEGSSLHTPLALPPPQPPQPSCS
PCAPRVSEPGTSSQQSDEILSESPSPSDPVLPLPALIQEGRSTSVTNDKLTSKMNAEEDSEEMPSLLTSTVQVAS
DNLIPQIRDKEDPQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSTPSDKKGKKRKRCIWSTPKRRHKKKSLPRG
TASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSEMNEGKRSQKTPSTPRRVT
QGAASPGHGIQEKLQVVDKVTQRKDDSTWNSEVMMRVQKARTKCARKSRSKEKKKEKDICSSSKRRFQKNIHRRG
KPKSDTVDFHCSKLPVTCGEAKGILYKKKMKHGSSVKCIRNEDGTWLTPNEFEVEGKGRNAKNWKRNIRCEGMTL
GELLKSGLLLCPPRINLKRELNSK

FIGURE 1016

GTTTTGCCTGCTAGCATCTCCCTGTAACTCTCCCAATCTTGAGGAGTGATCCCTGTCCCAGCCCCTGGAAAGGGG
CAGGAACGACAAACTCAAAGTCCAGG**ATG**TTCACCATGACAAGAGCCATGGAAGAGGCTCTTTTTCAGCACTTCA
TGCACCAGAAGCTGGGGATCGCCTATGCCATACACAAGCCATTTCCCTTCTTTGAAGGCCTCCTAGACAACTCCA
TCATCACTAAGAGAATGTACATGGAATCTCTGGAAGCCTGTAGAAATTTGATCCCTGTATCCAGAGTGGTGCACA
ACATTCTCACCCAACTGGAGAGGACTTTTAACCTGTCTCTTCTGGTGACATTGTTCAGTCAAATTAACCTGCGTG
AATATCCCAATCTGGTGACGATTTACAGAAGCTTCAAACGTGTTGGTGCTTCCTATGAACGGCAGAGCAGAGACA
CACCAATCCTACTTGAAGCCCCAACTGGCCTAGCAGAAGGAAGCTCCCTCCATACCCCACTGGCGCTGCCCCCAC
CACAACCCCCTCAACCAAGCTGTTCACCCTGTGCGCCAAGAGTCAGTGAGCCTGGAACATCCTCCCAGCAAAGCG
ATGAGATCCTGAGTGAGTCGCCCAGCCCATCTGACCCTGTCCTGCCTCTCCCTGCACTCATCCAGGAAGGAAGAA
GCACTTCAGTGACCAATGACAAGTTAACATCCAAAATGAATGCGGAAGAAGACTCAGAAGAGATGCCCAGCCTCC
TCACTAGCACTGTGCAAGTGGCCAGTGACAACCTGATCCCCCAAATAAGAGATAAAGAAGACCCTCAAGAGATGC
CCCACTCTCCCTTGGGCTCTATGCCAGAGATAAGAGATAATTCTCCAGAACCAAATGACCCAGAAGAGCCCCAGG
AGGTGTCCAGCACACCTTCAGACAAGAAAGGAAAGAAAAGAAAAAGATGTATCTGGTCAACTCCAAAAAGGAGAC
ATAAGAAAAAAAGCCTCCCAAGAGGGACAGCCTCATCTAGACACGGAATCCAAAAGAAGCTCAAAAGGGTGGATC
AGGTTCCTCAAAAGAAAGATGACTCAACTTGTAACTCCACGGTAGAGACAAGGGCCCAAAAGGCGAGAACTGAAT
GTGCCCGAAAGTCGAGATCAGAGGAGATCATTGATGGCACTTCAGAAATGAATGAAGGAAAGAGGTCCCAGAAGA
CGCCTAGTACACCACGAAGGGTCACACAAGGGGCAGCCTCACCTGGGCATGGCATCCAAGAGAAGCTCCAAGTGG
TGGATAAGGTGACTCAAAGGAAAGACGACTCAACCTGGAACTCAGAGGTCATGATGAGGGTCCAAAAGGCAAGAA
CTAAATGTGCCCGAAAGTCCAGATCGAAAGAAAAGAAAAAGGAGAAAGATATCTGTTCAAGCTCAAAAAGGAGAT
TTCAGAAAAATATTCACCGAAGAGGAAAACCCAAAAGTGACACTGTGGATTTTCACTGTTCTAAGCTCCCCGTGA
CCTGTGGTGAGGCGAAAGGGATTTTATATAAGAAGAAAATGAAACACGGATCCTCAGTGAAGTGCATTCGGAATG
AGGATGGAACTTGGTTAACACCAAATGAATTTGAAGTCGAAGGAAAAGGAAGGAACGCAAAGAACTGGAAACGGA
ATATACGTTGTGAAGGAATGACCCTAGGAGAGCTGCTGAAGCGGAAAAACTCGGATGAATGCGAGGTGTGCTGTC
AAGGGGGACAACTTCTCTGCTGCGGTACTTGTCCACGAGTCTTCCATGAGGACTGTCACATCCCCCCTGTGGAAG
CCAAGAGGATGCTGTGGAGTTGCACCTTCTGCAGGATGAAGAGGTCTTCAGGAAGCCAACAGTGCCATCATGTAT
CTAAGACCCTGGAGAGGCAGATGCAGCCTCAGGACCAGCTGAAATGTGAGTTCCTCCTCTTGAAGGCCTACTGTC
ATCCACAAAGCTCCTTTTTTACGGGCATCCCATTTAATATTCGAGATTACGGTGAGCCCTTTCAGGAAGCAATGT
GGTTGGACCTGGTTAAGGAAAGGCTGATTACGGAAATGTACACGGTGGCATGGTTTGTGCGAGACATGCGCCTGA
TGTTTCGCAACCATAAAACATTTTACAAGGCTTCTGACTTTGGCCAGGTAGGACTTGACTTAGAGGCAGAATTTG
AAAAAGATCTCAAAGACGTGCTCGGTTTTCATGAAGCCAATGACGGCGGTTTCTGGACTCTTCCT**TGA**CCCTGTT
CTGTAAAGACTGAAGCATCCCCACCTCAGGATTCAGCTGATGGGACCCTGGCTTGGACTGTTGATTGCCAGTGAG
TCTGGGATGTAATTGGCTGCCCTCAGGACCCAAACCCAGACACTTCATAGGATTATCACACCCTCCATCTTTATT
CTTTCTTTTTACCTTTAAAAGTCTATATCTA

FIGURE 1017

MFTMTRAMEEALFQHFMHQKLGIAYAIHKPFPFFEGLLDNSIITKRMYMESLEACRNLIPVSRVVHNILTQLERT
FNLSLLVTLFSQINLREYPNLVTIYRSFKRVGASYERQSRDTPILLEAPTGLAEGSSLHTPLALPPPQPPQPSCS
PCAPRVSEPGTSSQQSDEILSESPSPSDPVLPLPALIQEGRSTSVTNDKLTSKMNAEEDSEEMPSLLTSTVQVAS
DNLIPQIRDKEDPQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSTPSDKKGKKRKRCIWSTPKRRHKKKSLPRG
TASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSEMNEGKRSQKTPSTPRRVT
QGAASPGHGIQEKLQVVDKVTQRKDDSTWNSEVMMRVQKARTKCARKSRSKEKKKEKDICSSSKRRFQKNIHRRG
KPKSDTVDFHCSKLPVTCGEAKGILYKKKMKHGSSVKCIRNEDGTWLTPNEFEVEGKGRNAKNWKRNIRCEGMTL
GELLKRKNSDECEVCCQGGQLLCCGTCPRVFHEDCHIPPVEAKRMLWSCTFCRMKRSSGSQQCHHVSKTLERQMQ
PQDQLKCEFLLLKAYCHPQSSFFTGIPFNIRDYGEPFQEAMWLDLVKERLITEMYTVAWFVRDMRLMFRNHKTFY
KASDFGQVGLDLEAEFEKDLKDVLGFHEANDGGFWTLP

FIGURE 1018

ATGCTGGGTACGCTGCGCGCCATGGAGGGCGAGGACGTGGAAGACGACCAGCTGCTGCAGAAGCTCAGGGCCAGT
CGCCGCCGCTTCCAGAGGCGCATGCAGCGGCTGATAGAGAAGTACAACCAGCCCTTCGAGGACACCCCGGTGGTG
CAAATGGCCACGCTGACCTACGAGACGCCACAGGGATTGAGAATTTGGGGTGGAAGACTAATAAAGGAAAGAAAC
AAAGGAGAGATCCAGGACTCCTCCATGAAGCCCGCGGACAGGACAGATGGCTCCGTGCAAGCTGCAGCCTGGGGT
CCTGAGCTTCCCTCGCACCGCACAGTCCTGGGAGCCGATTCAAAAAGCGGTGAGGTCGATGCCACGTCAGACCAG
GAAGAGTCAGTTGCTTGGGCCTTAGCACCTGCAGTGCCTCAAAGCCCTTTGAAAAATGAATTAAGAAGGAAATAC
TTGACCCAAGTGGATATACTGCTACAAGGTGCAGAGTATTTTGAGTGTGCAGGTAACAGAGCTGGAAGGGATGTA
CGTGTGACTCCGCTGCCTTCACTGGCCTCACCTGCCGTGCCTGCCCCCGGATACTGCAGTCGTATCTCCGGAAAG
AGTCCTGGTGACCCAGCGAAACCAGCTTCATCTCCCAGAGAATGGGATCCTTTGCATCCTTCCTCCACAGACATG
GCCTTAGTACCTAGAAATGACAGCCTCTCCCTACAAGAGACCAGTAGCAGCAGCTTCTTAAGCAGCCAGCCCTTT
GAAGATGATGACATTTGCAATGTGACCATCAGTGACCTGTACGCAGGG<u>ATG</u>CTGCACTCCATGAGCCGGCTGTTG
AGCACAAAGCCATCAAGCATCATCTCCACCAAAACGTTCATCATGCAAAACTGGAACTGCAGGAGGAGGCACAGA
TATAAGAGCAGGATGAACAAAACATATTGCAAAGGAGCCAGACGTTCTCAGAGGAGCTCCAAGGAGAACTTCATA
CCCTGCTCTGAGCCTGTGAAAGGGACAGGGGCATTAAGAGATTGCAAGAACGTATTAGATGTTTCTTGCCGTAAG
ACAGGTTTAAAATTGGAAAAAGCTTTTCTTGAAGTCAACAGACCCCAAATCCATAAGTTAGATCCAAGTTGGAAG
GAGCGCAAAGTGACACCCTCGAAGTATTCTTCCTTGATTTACTTCGACTCCAGTGCAACATATAATCTTGATGAG
GAAAATAGATTTAGGACATTAAAATGGTTAATTTCTCCTGTAAAAATAGTTTCCAGACCAACAATACGACAGGGC
CATGGAGAGAACCGTCAGAGGGAGATTGAAATCCGATTTGATCAGCTTCATCGGGAATATTGCCTGAGTCCCAGG
AACCAGCCTCGCCGGATGTGCCTCCCGGACTCCTGGGCCATGAACATGTACAGAGGGGGTCCTGCGAGTCCTGGT
GGCCTTCAGGGCTTAGAAACCCGCAGGCTGAGTTTACCTTCCAGCAAAGCAAAAGCAAAAAGTTTAAGTGAGGCT
TTTGAAAACCTAGGCAAAAGATCTCTGGAAGCAGGTAGGTGCCTGCCCAAGAGCGATTCATCTTCATCACTTCCA
AAGACCAACCCCACACACAGCGCAACTCGCCCGCAGCAGACATCTGACCTTCACGTTCAGGGAAATAGTTCTGGA
ATATTTAGAAAGTCAGTGTCACCCAGCAAAACTCTTTCAGTCCCAGATAAAGAAGTGCCAGGCCACGGAAGGAAT
CGTTACGATGAAATTAAAGAAGAATTTGACAAGCTTCATCAAAAGTATTGCCTCAAATCTCCTGGGCAGATGACA
GTGCCTTTATGTATTGGAGTGTCTACAGATAAAGCAAGTATGGAAGTTCGATATCAAACAGAAGGCTTCTTAGGA
AAATTAAATCCAGACCCTCACTTCCAGGGTTTCCAGAAGTTGCCATCATCACCCCTGGGGTGCAGAAAAAGTCTA
CTGGGCTCAACTGCAATTGAGGCTCCTTCATCTACATGTGTTGCTCGTGCCATCACGAGGGATGGCACGAGGGAC
CATCAGTTCCCTGCAAAAAGACCCAGGCTATCAGAACCCCAGGGCTCCGGACGCCAGGGCAATTCCCTGGGTGCC
TCAGATGGGGTGGACAACACCGTCAGACCGGGAGACCAGGGCAGCTCTTCACAGCCCAACTCAGAAGAGAGAGGA
GAGAACACGTCTTACAGGATGGAAGAGAAAAGTGATTTCATGCTAGAAAAATTGGAAACTAAAAGTGTG<u>TAG</u>CTA
GGTTATTTCGGAGTGTTATTTATCTTCCCACTTGCTCTCTGTTTGTATTTTTGTTTTGTTTTTGATTCTTGAGAC
TGTGAGGACTTGGTTGACTTCTCTGCCCTTAAAGTAAATATTAGTGAAATTGGTTCCATCAGAGATAACCTCGAG
TTCTTGGTGTAGAAATTATGTGAATAAAGTTGCTCAATTAGAAAAAAAAAAAAAAAAAA

FIGURE 1019

MLHSMSRLLSTKPSSIISTKTFIMQNWNCRRRHRYKSRMNKTYCKGARRSQRSSKENFIPCSEPVKGTGALRDCK
NVLDVSCRKTGLKLEKAFLEVNRPQIHKLDPSWKERKVTPSKYSSLIYFDSSATYNLDEENRFRTLKWLISPVKI
VSRPTIRQGHGENRQREIEIRFDQLHREYCLSPRNQPRRMCLPDSWAMNMYRGGPASPGGLQGLETRRLSLPSSK
AKAKSLSEAFENLGKRSLEAGRCLPKSDSSSSLPKTNPTHSATRPQQTSDLHVQGNSSGIFRKSVSPSKTLSVPD
KEVPGHGRNRYDEIKEEFDKLHQKYCLKSPGQMTVPLCIGVSTDKASMEVRYQTEGFLGKLNPDPHFQGFQKLPS
SPLGCRKSLLGSTAIEAPSSTCVARAITRDGTRDHQFPAKRPRLSEPQGSGRQGNSLGASDGVDNTVRPGDQGSS
SQPNSEERGENTSYRMEEKSDFMLEKLETKSV

FIGURE 1020

AAGACCGTCCCGGATGGCCTCGGGGACTGCCAGTGTGTGGAGGTGAGCTCCGGGATTGCCGGCATTCCCGCTTCT
GCTGGTTGCTTCATGCTGCAGGCTGCGGCCGTCAGCCCTCGCTCGCATTGGTGGCGCTGAGGTGCCGGGGCAGCA
AGTGAC<u>ATG</u>TCGTCGGGCCTCCGCGCCGCTGACTTCCCCCGCTGGAAGCGCCACATCTCGGAGCAACTGAGGCGC
CGGGACCGGCTGCAGAGACAGGCGTTCGAGGAGATCATCCTGCAGTATAACAAATTGCTGGAAAAGTCAGATCTT
CATTCAGTGTTGGCCCAGAAACTACAGGCTGAAAAGCATGACGTACCAAACAGGCACGAGATAAGTCCCGGACAT
GATGGCACATGGAATGACAATCAGCTACAAGAAATGGCCCAACTGAGGATTAAGCACCAAGAGGAACTGACTGAA
TTACACAAGAAACGTGGGGAGTTAGCTCAACTGGTGATTGACCTGAATAACCAAATGCAGCGGAAGGACAGGGAG
ATGCAGAAAGAGCTTGCAGAAGCAGCAAAGGAACCTCTACCAGTCGAACAGGATGATGACATTGAGGTCATTGTG
GATGAAACTTCTGATCACACAGAAGAGACCTCTCCTGTGCGAGCCATCAGCAGAGCAGCCACTAAGCGACTCTCG
CAGCCTGCTGGAGGCCTTCTGGATTCTGTCACTAATATCTTTGGGAGACGCTCTGTCTCTTCCTTCCCAGTCCCC
CAGGACAATGTGGATACTCATCCTGGTTCTGGTAAAGAAGTGAGGGTACCAGCTACTGCCTTGTGTGTCTTCGAT
GCACATGATGGGGAAGTCAACGCTGTGCAGTTCAGTCCAGGTTCCCGGTTACTGGCCACTGGAGGCATGGACCGC
AGGGTTAAGCTTTGGGAAGTATTTGGAGAAAAATGTGAGTTCAAGGGTTCCCTATCTGGCAGTAATGCAGGAATT
ACAAGCATTGAATTTGATAGTGCTGGATCTTACCTCTTAGCAGCTTCAAATGATTTTGCAAGCCGAATCTGGACT
GTGGATGATTATCGATTACGGGTAAGACCCAGT<u>TAA</u>GAAAGTTAGTGCAATCTCCAAACTTCATGTGGTGTTATC
AAGGCACAAACTGGCAGGTGCTTAATTAGGGGACTTTGTTTTCCCAAAAATCATGCTTGATTCACCCTGCCCTTC
CTTTCCTCCTTGGGGAAATCTGTGTTTCCACTTTATACTCTTTGTCCAAAACTCAGTTTCAAAATATTTGCAATG
GGACCCTCACATTTGCATGAAAACCTTGGAATACTCTTCATAAGGACTAAATACTTTGGTAGATAGCAATTTTGG
CTTAATGGCACAGAACTTAGCAACAGCATGTGAATTGTGATTCCTGTGGGCTCTAAAACCTAATTACCTAAAGTG
GGATATAGAAGTACAAATGGATGTATCATAGGGATAAGACAATTCTGAAACAAAAACTCCAAGCTGAGAAAGAGG
GGACAGGTGTCAGAGCAGGGAGAAATGATTGGATGTTGAGGAAAGCTGCATTTGAACCAAAACTTGCCAAGAATT
CTCTTGGCATCTGACAGAGAGACCAAAACTTGGTTGTATCATTTTTGATTGGGGCAGGGGGCGGAGGGCGAAGCA
TGTAACTTAATTTGCAGACATTTTTTTTCCCCATAAGCCTGAAGGAATCATCACATAAGCTTATTAAATACAAGC
TATTGAAAGATATAATGGAGGATGAATTTGGCATTAGTAGGCATTTTACT

FIGURE 1021

MSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIILQYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDG
TWNDNQLQEMAQLRIKHQEELTELHKKRGELAQLVIDLNNQMQRKDREMQKELAEAAKEPLPVEQDDDIEVIVDE
TSDHTEETSPVRAISRAATKRLSQPAGGLLDSVTNIFGRRSVSSFPVPQDNVDTHPGSGKEVRVPATALCVFDAH
DGEVNAVQFSPGSRLLATGGMDRRVKLWEVFGEKCEFKGSLSGSNAGITSIEFDSAGSYLLAASNDFASRIWTVD
DYRLRVRPS

FIGURE 1022A

AAGAGAGAAGGCTTCTGCCAGCTCCTGCAGCAG**ATG**AAGAACAAGCACTCAGAGCAGCCGGAGCCCGACATGATC
ACCATCTTCATCGGCACCTGGAACATGGGTAACGCCCCCCTCCCAAGAAGATCACGTCCTGGTTTCTCTCCAAG
GGGCAGGGAAAGACGCGGGACGACTCTGCGGACTACATCCCCCATGACATTTACGTGATCGGCACCCAAGAGGAC
CCCCTGAGTGAGAAGGAGTGGCTGGAGATCCTCAAACACTCCCTGCAAGAAATCACCAGTGTGACTTTTAAAACA
GTCGCCATCCACACGCTCTGGAACATCCGCATCGTGGTGCTGGCCAAGCCTGAGCACGAGAACCGGATCAGCCAC
ATCTGTACTGACAACGTGAAGACAGGCATTGCAAACACACTGGGGAACAAGGGAGCCGTGGGGGTGTCGTTCATG
TTCAATGGAACCTCCTTAGGGTTCGTCAACAGCCACTTGACTTCAGGAAGTGAAAAGAAACTCAGGCGAAACCAA
AACTATATGAACATTCTCCGGTTCCTGGCCCTGGGCGACAAGAAGCTGAGTCCCTTTAACATCACTCACCGCTTC
ACGCACCTCTTCTGGTTTGGGGATCTTAACTACCGTGTGGATCTGCCTACCTGGGAGGCAGAAACCATCATCCAG
AAAATCAAGCAGCAGCAGTACGCAGACCTCCTGTCCCACGACCAGCTGCTCACAGAGAGGAGGGAGCAGAAGGTC
TTCCTACACTTCGAGGAGGAAGAAATCACGTTTGCCCCAACCTACCGTTTTGAGAGACTGACTCGGGACAAATAC
GCCTACACCAAGCAGAAAGCGACAGGGATGAAGTACAACTTGCCTTCCTGGTGTGACCGAGTCCTCTGGAAGTCT
TATCCCCTGGTGCACGTGGTGTGTCAGTCTTATGGCAGTACCAGCGACATCATGACGAGTGACCACAGCCCTGTC
TTTGCCACATTTGAGGCAGGAGTCACTTCCCAGTTTGTCTCCAAGAACGGTCCCGGGACTGTTGACAGCCAAGGA
CAGATTGAGTTTCTCAGGTGCTATGCCACATTGAAGACCAAGTCCCAGACCAAATTCTACCTGGAGTTCCACTCG
AGCTGCTTGGAGAGTTTTGTCAAGAGTCAGGAAGGAGAAAATGAAGAAGGAAGTGAGGGGGAGCTGGTGGTGAAG
TTTGGTGAGACTCTTCCAAAGCTGAAGCCCATTATCTCTGACCCTGAGTACCTGCTAGACCAGCACATCCTCATC
AGCATCAAGTCCTCTGACAGCGACGAATCCTATGGCGAGGGCTGCATTGCCCTTCGGTTAGAGGCCACAGAAACG
CAGCTGCCCATCTACACGCCTCTCACCCACCATGGGGAGTTGACAGGCCACTTCCAGGGGGAGATCAAGCTGCAG
ACCTCTCAGGGCAAGACGAGGGAGAAGCTCTATGACTTTGTGAAGACGGAGCGTGATGAATCCAGTGGGCCAAAG
ACCCTGAAGAGCCTCACCAGCCACGACCCCATGAAGCAGTGGGAAGTCACTAGCAGGGCCCCTCCGTGCAGTGGC
TCCAGCATCACTGAAATCATCAACCCCAACTACATGGGAGTGGGGCCCTTTGGGCCACCAATGCCCCTGCACGTG
AAGCAGACCTTGTCCCCTGACCAGCAGCCCACAGCCTGGAGCTACGACCAGCCGCCCAAGGACTCCCCGCTGGGG
CCCTGCAGGGGAGAAAGTCCTCCGACACCTCCCGGCCAGCCGCCCATATCACCCAAGAAGTTTTACCCTCAACA
GCAAACCGGGGTCTCCCTCCCAGGACACAGGAGTCAAGGCCCAGTGACCTGGGAAGAACGCAGGGGACACGCTG
CCTCAGGAGGACCTGCCGCTGACGAAGCCCGAGATGTTTGAGAACCCCCTGTATGGGTCCCTGAGTTCCTTCCCT
AAGCCTGCTCCCAGGAAGGACCAGGAATCCCCCAAAATGCCGCGGAAGGAACCCCCGCCCTGCCCGGAACCCGGC
ATCTTGTCGCCCAGCATCGTGCTCACCAAAGCCCAGGAGGCTGATCGCGGCGAGGGGCCCGGCAAGCAGGTGCCC
GCGCCCCGGCTGCGCTCCTTCACGTGCTCATCCTCTGCCGAGGGCAGGGCGGCCGGCGGGGACAAGAGCCAAGGG
AAGCCCAAGACCCCGGTCAGCTCCCAGGCCCCGGTGCCGGCCAAGAGGCCCATCAAGCCTTCCAGATCGGAAATC
AACCAGCAGACCCCGCCCACCCCGACGCCGCGGCCGCCGCTGCCAGTCAAGAGCCCGGCGGTGCTGCACCTCCAG
CACTCCAAGGGCCGCGACTACCGCGACAACACCGAGCTCCCGCATCACGGCAAGCACCGGCCGGAGGAGGGGCCA
CCAGGGCCTCTAGGCAGGACTGCCATGCAG**TGA**AGCCCTCAGTGAGCTGCCACTGAGTCGGGAGCCCAGAGGAAC
GGCGTGAAGCCACTGGACCCTCTCCCGGGACCTCCTGCTGGCTCCTCCTGCCCAGCTTCCTATGCAAGGCTTTGT
GTTTTCAGGAAAGGGCCTAGCTTCTGTGTGGCCCACAGAGTTCACTGCCTGTGAGACTTAGCACCAAGTGCTGAG
GCTGGAAGAAAAACGCACACCAGACGGGCAACAAACAGTCTGGGTCCCCAGCTCGCTCTTGGTACTTGGGACCCC
AGTGCCTCGTTGAGGGCGCCATTCTGAAGAAAGGAACTGCAGCGCCGATTTGAGGGTGGAGATATAGATAATAAT
AATATTAATAATAATAATGGCCACATGGATCGAACACTCATGATGTGCCAAGTGCTGTGCTAAGTGCTTTACGAA
CATTCGTCATATCAGGATGACCTCGAGAGCTGAGGCTCTAGCCACCTAAAACCACGTGCCCAAACCCACCAGTTT
AAAACGGTGTGTGTTCGGAGGGGTGAAAGCATTAAGAAGCCCAGTGCCCTCCTGGAGTGAGACAAGGGCTCGGCC
TTAAGGAGCTGAAGAGTCTGGGTAGCTTGTTTAGGGTACAAGAAGCCTGTTCTGTCCAGCTTCAGTGACACAAGC
TGCTTTAGCTAAAGTCCCGCGGGTTCCGGCATGGCTAGGCTGAGAGCAGGGATCTACCTGGCTTCTCAGTTCTTT
GGTTGGAAGGAGCAGGAAATCAGCTCCTATTCTCCAGTGGAGAGATCTGGCCTCAGCTTGGGCTAGAGATGCCAA
GGCCTGTGCCAGGTTCCCTGTGCCCTCCTCGAGGTGGGCAGCCATCACCAGCCACAGTTAAGCCAAGCCCCCCAA
CATGTATTCCATCGTGCTGGTAGAAGAGTCTTTGCTGTTGCTCCCGAAAGCCGTGCTCTCCAGCCTGGCTGCCAG
GGAGGGTGGGCCTCTTGGTTCCAGGCTCTTGAAATAGTGCAGCCTTTTCTTCCTATCTCTGTGGCTTTCAGCTCT
GCTTCCTTGGTTATTAGGAGAATAGATGGGTGATGTCTTTCCTTATGTTGCTTTTTCAACATAGCAGAATTAATG
TAGGGAGCTAAATCCAGTGGTGTGTGTGAATGCAGAAGGGAATGCACCCCACATTCCCATGATGGAAGTCTGCGT

FIGURE 1022B

AACCAATAAATTGTGCCTTTCTCACTCA

FIGURE 1023

MKNKHSEQPEPDMITIFIGTWNMGNAPPPKKITSWFLSKGQGKTRDDSADYIPHDIYVIGTQEDPLSEKEWLEIL
KHSLQEITSVTFKTVAIHTLWNIRIVVLAKPEHENRISHICTDNVKTGIANTLGNKGAVGVSFMFNGTSLGFVNS
HLTSGSEKKLRRNQNYMNILRFLALGDKKLSPFNITHRFTHLFWFGDLNYRVDLPTWEAETIIQKIKQQQYADLL
SHDQLLTERREQKVFLHFEEEEITFAPTYRFERLTRDKYAYTKQKATGMKYNLPSWCDRVLWKSYPLVHVVCQSY
GSTSDIMTSDHSPVFATFEAGVTSQFVSKNGPGTVDSQGQIEFLRCYATLKTKSQTKFYLEFHSSCLESFVKSQE
GENEEGSEGELVVKFGETLPKLKPIISDPEYLLDQHILISIKSSDSDESYGEGCIALRLEATETQLPIYTPLTHH
GELTGHFQGEIKLQTSQGKTREKLYDFVKTERDESSGPKTLKSLTSHDPMKQWEVTSRAPPCSGSSITEIINPNY
MGVGPFGPPMPLHVKQTLSPDQQPTAWSYDQPPKDSPLGPCRGESPPTPPGQPPISPKKFLPSTANRGLPPRTQE
SRPSDLGKNAGDTLPQEDLPLTKPEMFENPLYGSLSSFPKPAPRKDQESPKMPRKEPPPCPEPGILSPSIVLTKA
QEADRGEGPGKQVPAPRLRSFTCSSSAEGRAAGGDKSQGKPKTPVSSQAPVPAKRPIKPSRSEINQQTPPTPTPR
PPLPVKSPAVLHLQHSKGRDYRDNTELPHHGKHRPEEGPPGPLGRTAMQ

FIGURE 1024

CGAGCGGACTCGACTCGGCACCGCTGTGCACCATGGCCCGGGCCCTGTGCCGCCTCCCGCGGCGCGGCCTCTGGC
TGCTCCTGGCCCATCACCTCTTCATGACCACTGCCTGCCAGGAGGCTAACTACGGTGCCCTCCTCCGGGAGCTCT
GCCTCACCCAGTTCCAGGTAGACATGGAGGCCGTCGGGGAGACGCTGTGGTGTGACTGGGGCAGGACCATCAGGA
GCTACAGGGAGCTGGCCGACTGCACCTGGCACATGGCGGAGAAGCTGGGCTGCTTCTGGCCCAATGCAGAGGTGG
ACAGGTTCTTCCTGGCAGTGCATGGCCGCTACTTCAGGAGCTGCCCCATCTCAGGCAGGGCCGTGCGGGACCCGC
CCGGCAGCATCCTCTACCCCTTCATCGTGGTCCCCATCACGGTGACCCTGCTGGTGACGGCACTGGTGGTCTGGC
AGAGCAAGCGCACTGAGGGCATTGTGTAGGCGGGGCCCAGGCTGCCCGCGGGTGCACCCAGGCTGCAGGGTGAGG
CCAGGCAGGCCTGGGTAGGGGCAGCTTCTGGAGCCTTGGGACAGAGCAGGCCCACAATGCCCCCCTTCTTCCAGC
CAAGAAGAGCTCACAGGAGTCCAGAGTAGCCGAGGCTCTGGTATTAACCTGGAAGCCCCCCTGGCTGGAGGCCAC
CGCCACCCTAGGAAGGGGGCAGGGACGTGACCTTGACTTACCTCTGGAAAGGGTCCCAGCCTAGACTGCTTACCC
CATAGCCACATTTGTGGATGAGTGGTTTGTGATTAAAAGGATGTTCTTG

FIGURE 1025

MARALCRLPRRGLWLLLAHHLFMTTACQEANYGALLRELCLTQFQVDMEAVGETLWCDWGRTIRSYRELADCTWH
MAEKLGCFWPNAEVDRFFLAVHGRYFRSCPISGRAVRDPPGSILYPFIVVPITVTLLVTALVVWQSKRTEGIV

FIGURE 1026A

GGCACGAGGCCGCTCCCCGGCGGGCTGGCTCCTGGCCCCGGAAGCGCGAGCGTTCACTTAGCGGCGAGTGGCTCC
GTCTCCGCGGACAGAGCGCGCGCCCCCTGGCCCGGCCCGCGAGGGGCTCCCGGCGCGGTCCCCGAGCATTTCCCG
CCGGGTGGAGCGGGCCGAGCCCGGCAGGATGACCAGCCCCGCGGCCGCTCAAAGCCGGGAGATCGACTGTTTGAG
CCCGGAAGCGCAGAAGCTGGCGGAAGCCCGGCTCGCTGCAAAACGGGCGGCCCGCGCGGAGGCTCGCGAGATCCG
CATGAAGGAGCTGGAGCGGCAGCAGAAGGAGGAAGACAGTGAGCGCTACTCTCGTAGATCCAGAAGAAACACATC
GGCTTCTGATGAAGACGAGCGCATGTCAGTGGGTAGTCGTGGAAGCCTGAGGGTAGAAGAGAGACCAGAAAAAGA
TTTTACTGAGAAGGGGTCTCGTAACATGCCGGGCCTGTCTGCAGCCACGCTGGCCTCTCTGGGTGGGACTTCCTC
TCGGAGAGGCAGCGGAGACACCTCCTTCTCCATCGACACCGAGGCATCCATCAGGGAAATCAAGGACTCTCTAGC
AGAAGTTGAAGAGAAATATAAGAAGGCTATGGTTTCCAATGCTCAGCTAGACAATGAAAAGACAAACTTCATGTA
CCAGGTTGATACCCTAAAAGATATGTTGCTGGAGCTTGAAGAACAGCTGGCTGAATCTAGGCGGCAGTACGAAGA
GAAAAACAAAGAATTTGAAAGGGAAAAACACGCCCACAGTATACTGCAATTTCAGTTTGCTGAAGTCAAGGAGGC
CCTGAAGCAAAGAGAGGAAATGCTCGAGAAACATGGAATAATCCTAAATTCAGAAATAGCTACCAATGGAGAGAC
TTCCGACACCCTCAATAATGTTGGATACCAAGGTCCTACCAAGATGACAAAAGAAGAGTTAAATGCCCTCAAGTC
TACAGGGGATGGGACCCTAGGAAGAGCCAGTGAAGTGGAGGTGAAAAATGAAATCGTGGCGAATGTGGGGAAAAG
AGAAATCTTGCACAATACTGAGAAAGAACAACACACAGAGGACACAGTGAAGGACTGTGTGGACATAGAGGTATT
CCCTGCTGGTGAGAATACCGAGGACCAGAAATCCTCTGAAGACACTGCCCCATTCCTAGGAACCTTAGCAGGTGC
TACCTATGAAGAACAGGTTCAAAGCCAAATTCTTGAGAGCAGTTCTCTCCCTGAAAACACAGTACAGGTTGAGTC
AAATGAGGTCATGGGTGCACCAGATGACAGGACCAGAACTCCCCTTGAGCCATCCAACTGTTGGAGTGACTTAGA
TGGTGGGAACCACACAGAGAATGTGGGAGAGGCAGCAGTGACTCAGGTTGAAGAGCAGGCAGGCACAGTGGCCTC
GTGTCCTTTAGGGCATAGTGATGACACAGTTTATCATGATGACAAATGTATGGTAGAGGTCCCCCAAGAGTTAGA
GACAAGCACAGGGCATAGTTTAGAGAAAGAATTCACCAACCAGGAAGCAGCTGAGCCCAAGGAGGTTCCAGCGCA
CAGTACAGAAGTAGGTAGGGATCACAACGAAGAAGAGGGTGAAGAAACAGGATTAAGGGACGAGAAACCAATCAA
GACAGAAGTTCCTGGTTCTCCAGCAGGAACTGAGGGCAACTGTCAGGAAGCGACAGGTCCAAGTACAGTAGACAC
TCAAAATGAACCCTTAGATATGAAAGAGCCCGATGAAGAAAAGAGTGACCAACAGGGAGAGGCATTGGACTCATC
GCAGAAGAAGACAAAGAACAAGAAAAAGAAAAACAAGAAGAAAAAATCCCCAGTACCCGTAGAAACCCTTAAAGA
TGTTAAAAAAGAGTTAACGTATCAGAACACAGATTTAAGTGAAATTAAGGAAGAAGAGCAGGTAAAGTCTACTGA
CAGAAAGTCAGCAGTGGAAGCCCAAAACGAGGTGACTGAAAATCCAAAACAGAAAATTGCAGCAGAAAGCAGTGA
AAATGTTGATTGTCCGGAGAATCCTAAAATTAAGTTGGATGGAAAACTTGACCAAGAAGGTGATGATGTACAAAC
AGCAGCTGAGGAGGTACTAGCTGATGGAGACACATTAGATTTTGAGGATGACACCGTTCAATCATCAGGCCCGAG
GGCTGGTGGTGAAGAATTAGATGAAGGTGTTGCAAAAGATAATGCTAAAATAGATGGTGCCACTCAAAGCAGTCC
TGCAGAACCAAAGAGCGAAGACGCAGATCGCTGCACCCTGCCCGAACATGAAAGTCCCTCACAGGACATTAGTGA
TGCCTGTGAAGCAGAAAGTACAGAGAGGTGTGAGATGTCAGAACATCCAAGTCAGACCGTCAGGAAAGCTTTAGA
CAGCAATAGCCTAGAGAACGATGACTTGTCGGCACCAGGAAGAGAGCCAGGGCACTTCAATCCAGAAAGCAGAGA
AGATACCAGAGGAGGGAATGAGAAGGGCAAAAGCAAAGAAGACTGTACCATGTCCTAAGCTGAGGCAGGCGGCAG
GCGCGGTGCACAGGAAGTCTCAGTGTGAAGGGGTCTTTTCTCTCCACTGCCAATGTAAGTAGAATGTTCTAAATT
CATAGAGAGGCACTGTATGACAATTACCAGGTGCTCTACTGCTTTAAGTTATAGACTGTTACTTGTAGATTTCCA
TGTAATCATTGAGGTTATCACCCAGATTAGAAAGACATATTTGTTATCAGTGTACGTTCTAATTGAGAGCATTCC
AGTAGTATCAAACAATAATGTCTACTGTTTATAGTCCACTTAATAAAAATAGAGGCATTTACTATTTGCCTTAGG
CTGATAGGAATGTGGGTTTTCTTGACCAAATATATCAGCATCTAATTGAAATGACCAAATAGCATTCTTAGACTT
CTGTATTATGAATATAATTGATATTTAAATTAATGTCTTGTTCACATATGTGTACTTTCATATTTGATTTTAAAA
TGTACATTATAACCTGTATGGTATTTTATTTAAAGGAGATAAACAGCCAAATAGCAAATAGGTCACTGAATGATA
AGATTTGCACCTTAGAACAATAATCATTTTAAGGATAACAAGTAAATGTCTGAAAGCATGAGGGGCTTTATTTGC
CTTTACCTCATATGAGTCTTTGATCTTGAACCGATACTTTTGGATCTCATTGTTGATATACCTGAATTTACTTTG
TAAGAGATTTTAACTTCACTTCATGCTGATGATGTATCAAATTCATTTTATAGAAAGATTTAAAGTTTTTTTCTG
GAAGTGATATATGTCAAATTACATTTCCTACTGCAGTATTTGAGCAGGGACAGTCATTTTTTAAATGTTTTTGGC
CGGGCGTGGTGGCTCATGCCTGTAATCTCAGTACATTGGGAGGCCAAGGCAGGTGGATCACCTGAGGTCAAGAGT
TCGAGGCCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTGGCCGGGCGTGATGGTG
GGCGCCTGTAATCCCAGCCACTCCAGAGGCTGAGGCAGGAGAATCGCTTGAACCTGCGAGGCAGAGATTGCAGTG

FIGURE 1026B

AGCCAAGATCAAGCCATTGTACTCCAGCCTGGACAACAAGAGCGAAACTCTGTCTA

FIGURE 1027

MTSPAAAQSREIDCLSPEAQKLAEARLAAKRAARAEAREIRMKELERQQKEEDSERYSRRSRRNTSASDEDERMS
VGSRGSLRVEERPEKDFTEKGSRNMPGLSAATLASLGGTSSRRGSGDTSFSIDTEASIREIKDSLAEVEEKYKKA
MVSNAQLDNEKTNFMYQVDTLKDMLLELEEQLAESRRQYEEKNKEFEREKHAHSILQFQFAEVKEALKQREEMLE
KHGIILNSEIATNGETSDTLNNVGYQGPTKMTKEELNALKSTGDGTLGRASEVEVKNEIVANVGKREILHNTEKE
QHTEDTVKDCVDIEVFPAGENTEDQKSSEDTAPFLGTLAGATYEEQVQSQILESSSLPENTVQVESNEVMGAPDD
RTRTPLEPSNCWSDLDGGNHTENVGEAAVTQVEEQAGTVASCPLGHSDDTVYHDDKCMVEVPQELETSTGHSLEK
EFTNQEAAEPKEVPAHSTEVGRDHNEEEGEETGLRDEKPIKTEVPGSPAGTEGNCQEATGPSTVDTQNEPLDMKE
PDEEKSDQQGEALDSSQKKTKNKKKKNKKKKSPVPVETLKDVKKELTYQNTDLSEIKEEEQVKSTDRKSAVEAQN
EVTENPKQKIAAESSENVDCPENPKIKLDGKLDQEGDDVQTAAEEVLADGDTLDFEDDTVQSSGPRAGGEELDEG
VAKDNAKIDGATQSSPAEPKSEDADRCTLPEHESPSQDISDACEAESTERCEMSEHPSQTVRKALDSNSLENDDL
SAPGREPGHFNPESREDTRGGNEKGKSKEDCTMS

FIGURE 1028A

CAGTTTGGAGCTCAGTCTTCCACCAAAGGCCGTTCAGTTCTCCTGGGCTCCAGCCTCCTGCAAGGACTGCAAGAG
TTTTCCTCCGCAGCTCTGAGTCTCCACTTTTTTGGTGGAGAAAGGCTGCAAAAAGAAAAAGAGACGCAGTGAGTG
GGAAAAGTATGCATCCTATTCAAACCTAATTGAATCGAGGAGCCCAGGGACACACGCCTTCAGGTTTGCTCAGGG
GTTCATATTTGGTGCTTAGACAAATTCAAAATGAGGAAACATCGGCACTTGCCCTTAGTGGCCGTCTTTTGCCTC
TTTCTCTCAGGCTTTCCTACAACTCATGCCCAGCAGCAGCAAGCAGATGTCAAAAATGGTGCGGCTGCTGATATA
ATATTTCTAGTGGATTCCTCTTGGACCATTGGAGAGGAACATTTCCAACTTGTTCGAGAGTTTCTATATGATGTT
GTAAAATCCTTAGCTGTGGGAGAAAATGATTTCCATTTTGCTCTGGTCCAGTTCAACGGAAACCCACATACCGAG
TTCCTGTTAAATACGTATCGTACTAAACAAGAAGTCCTTTCTCATATTTCCAACATGTCTTATATTGGGGGAACC
AATCAGACTGGAAAAGGATTAGAATACATAATGCAAAGCCACCTCACCAAGGCTGCTGGAAGCCGGGCCGGTGAC
GGAGTCCCTCAGGTTATCGTAGTGTTAACTGATGGACACTCGAAGGATGGCCTTGCTCTGCCCTCAGCGGAACTT
AAGTCTGCTGATGTTAACGTGTTTGCAATTGGAGTTGAGGATGCAGATGAAGGAGCGTTAAAAGAAATAGCAAGT
GAACCGCTCAATATGCATATGTTCAACCTAGAGAATTTTACCTCACTTCATGACATAGTAGGAAACTTAGTGTCC
TGTGTGCATTCATCCGTGAGTCCAGAAAGGGCTGGGGACACGGAAACCCTTAAAGACATCACAGCACAAGACTCT
GCTGACATTATTTTCCTTATTGATGGATCAAACAACACCGGAAGTGTCAATTTCGCAGTCATTCTCGACTTCCTT
GTAAATCTCCTTGAGAAACTCCCAATTGGAACTCAGCAGATCCGAGTGGGGGTGGTCCAGTTTAGCGATGAGCCC
AGAACCATGTTCTCCTTGGACACCTACTCCACCAAGGCCCAGGTTCTGGGTGCAGTGAAAGCCCTCGGGTTTGCT
GGTGGGGAGTTGGCCAATATCGGCCTCGCCCTTGATTTCGTGGTGGAGAACCACTTCACCCGGGCAGGGGGCAGC
CGCGTGGAGGAAGGGGTTCCCCAGGTGCTGGTCCTCATAAGTGCCGGGCCTTCTAGTGACGAGATTCGCTACGGG
GTGGTAGCACTGAAGCAGGCTAGCGTGTTCTCATTCGGCCTTGGAGCCCAGGCCGCCTCCAGGGCAGAGCTTCAG
CACATAGCTACCGATGACAACTTGGTGTTTACTGTCCCGGAATTCCGTAGCTTTGGGGACCTCCAGGAGAAATTA
CTGCCGTACATTGTTGGCGTGGCCCAAAGGCACATTGTCTTGAAACCGCCAACCATTGTCACACAAGTCATTGAA
GTCAACAAGAGAGACATAGTCTTCCTGGTGGATGGCTCATCTGCACTGGGACTGGCCAACTTCAATGCCATCCGA
GACTTCATTGCTAAAGTCATCCAGAGGCTGGAAATCGGACAGGATCTTATCCAGGTGGCAGTGGCCCAGTATGCA
GACACTGTGAGGCCTGAATTTTATTTCAATACCCATCCAACAAAAAGGGAAGTCATAACCGCTGTGCGGAAAATG
AAGCCCCTGGACGGCTCGGCCCTGTACACGGGCTCTGCTCTAGACTTTGTTCGTAACAACCTATTCACGAGTTCA
GCCGGCTACCGGGCTGCCGAGGGGATTCCTAAGCTTTTGGTGCTGATCACAGGTGGTAAGTCCCTAGATGAAATC
AGCCAGCCTGCCCAGGAGCTGAAGAGAAGCAGCATAATGGCCTTTGCCATTGGGAACAAGGGTGCCGATCAGGCT
GAGCTGGAAGAGATCGCTTTCGACTCCTCCCTGGTGTTCATCCCAGCTGAGTTCCGAGCCGCCCCATTGCAAGGC
ATGCTGCCTGGCTTGCTGGCACCTCTCAGGACCCTCTCTGGAACCCCTGAAGTTCACTCAAACAAAAGGGATATC
ATCTTTCTTTTGGATGGATCAGCCAACGTTGGAAAAACCAATTTCCCTTATGTGCGCGACTTTGTAATGAACCTA
GTTAACAGCCTTGATATTGGAAATGACAATATTCGTGTTGGTTTAGTGCAATTTAGTGACACTCCTGTAACGGAG
TTCTCTTTAAACACATACCAGACCAAGTCAGATATCCTTGGTCATCTGAGGCAGCTGCAGCTCCAGGGAGGTTCG
GGCCTGAACACAGGCTCAGCCCTAAGCTATGTCTATGCCAACCACTTCACGGAAGCTGGCGGCAGCAGGATCCGT
GAACACGTGCCGCAGCTCCTGCTTCTGCTCACAGCTGGGCAGTCTGAGGACTCCTATTTGCAAGCTGCCAACGCC
TTGACACGCGCGGGCATCCTGACTTTTTGTGTGGGAGCTAGCCAGGCGAATAAGGCAGAGCTTGAGCAGATTGCT
TTTAACCCAAGCCTGGTGTATCTCATGGATGATTTCAGCTCCCTGCCAGCTTTGCCTCAGCAGCTGATTCAGCCC
CTAACCACATATGTTAGTGGAGGTGTGGAGGAAGTACCACTCGCTCAGCCAGAGAGCAAGCGAGACATTCTGTTC
CTCTTTGACGGCTCAGCCAATCTTGTGGGCCAGTTCCCTGTTGTCCGTGACTTTCTCTACAAGATTATCGATGAG
CTCAATGTGAAGCCAGAGGGGACCCGAATTGCGGTGGCTCAGTACAGCGATGATGTCAAGGTGGAGTCCCGTTTT
GATGAGCACCAGAGTAAGCCTGAGATCCTGAATCTTGTGAAGAGAATGAAGATCAAGACGGGCAAAGCCCTCAAC
CTGGGCTACGCGCTGGACTATGCACAGAGGTACATTTTTGTGAAGTCTGCTGGCAGCCGGATCGAGGATGGAGTG
CTTCAGTTCCTGGTGCTGCTGGTCGCAGGAAGGTCATCTGACCGTGTGGATGGGCCAGCAAGTAACCTGAAGCAG
AGTGGGGTTGTGCCTTTCATCTTCCAAGCCAAGAACGCAGACCCTGCTGAGTTAGAGCAGATCGTGCTGTCTCCA
GCGTTTATCCTGGCTGCAGAGTCGCTTCCCAAGATTGGAGATCTTCATCCACAGATAGTGAATCTCTTAAAATCA
GTGCACAACGGAGCACCAGCACCAGTTTCAGGTGAAAAGGACGTGGTGTTTCTGCTTGATGGCTCTGAGGGCGTC
AGGAGCGGTTTCCCTCTGTTGAAAGAGTTTGTCCAGAGAGTGGTGGAAAGCCTGGATGTGGGCCAGGACCGGGTC
CGCGTGGCCGTGGTGCAGTACAGCGACCGGACCAGGCCCGAGTTCTACCTGAATTCATACATGAACAAGCAGGAC
GTCGTCAACGCTGTCCGCCAGCTGACCCTGCTGGGAGGGCCGACCCCCAACACCGGGGCCGCCCTGGAGTTTGTC

FIGURE 1028B

CTGAGGAACATCCTGGTCAGCTCTGCGGGAAGCAGGATAACAGAAGGTGTGCCCCAGCTGCTGATCGTCCTCACG
GCCGACAGGTCTGGGGATGATGTGCGGAACCCCTCCGTGGTCGTGAAGAGGGGTGGGGCTGTGCCCATTGGCATT
GGCATCGGGAACGCTGACATCACAGAGATGCAGACCATCTCCTTCATCCCGGACTTTGCCGTGGCCATTCCCACC
TTTCGCCAGCTGGGGACCGTCCAACAGGTCATCTCTGAGAGGGTGACCCAGCTCACCCGCGAGGAGCTGAGCAGG
CTGCAGCCGGTGTTGCAGCCTCTACCGAGCCCAGGTGTTGGTGGCAAGAGGGACGTGGTCTTTCTCATCGATGGG
TCCCAAAGTGCCGGGCCTGAGTTCCAGTACGTTCGCACCCTCATAGAGAGGCTGGTTGACTACCTGGACGTGGGC
TTTGACACCACCCGGGTGGCTGTCATCCAGTTCAGCGATGACCCCAAGGTGGAGTTCCTGCTGAACGCCCATTCC
AGCAAGGATGAAGTGCAGAACGCGGTGCAGCGGCTGAGGCCCAAGGGAGGGCGGCAGATCAACGTGGGCAATGCC
CTGGAGTACGTGTCCAGGAACATCTTCAAGAGGCCCCTGGGGAGCCGCATTGAAGAGGGCGTCCCGCAGTTCCTG
GTCCTCATCTCGTCTGGAAAGTCTGACGATGAGGTGGACGACCCGGCGGTGGAGCTCAAGCAGTTTGGCGTGGCC
CCTTTCACGATCGCCAGGAACGCAGACCAGGAGGAGCTGGTGAAGATCTCGCTGAGCCCCGAATATGTGTTCTCG
GTGAGCACCTTCCGGGAGCTGCCCAGCCTGGAGCAGAAACTGCTGACGCCCATCACGACCCTGACCTCAGAGCAG
ATCCAGAAGCTCTTAGCCAGCACTCGCTATCCACCTCCAGCAGTTGAGAGTGATGCTGCAGACATCGTCTTTCTG
ATCGACAGCTCTGAGGGAGTTAGGCCAGATGGCTTTGCACATATTCGAGATTTTGTTAGCAGGATTGTTCGAAGA
CTCAACATCGGCCCCAGTAAAGTGAGAGTTGGGGTCGTGCAGTTCAGCAATGATGTCTTCCCAGAATTCTATCTG
AAAACCTACAGATCCCAGGCCCCGGTGCTGGACGCCATACGGCGCCTGAGGCTCAGAGGGGGTTCCCCACTGAAC
ACTGGCAAGGCTCTCGAATTTGTGGCAAGAAACCTCTTTGTTAAGTCTGCGGGGAGTCGCATAGAAGACGGGGTG
CCCCAACACCTGGTCCTGGTCCTGGGTGGAAAATCCCAGGACGATGTGTCCAGGTTCGCCCAGGTGATCCGTTCC
TCGGGCATTGTGAGTTTAGGGGTAGGAGACCGGAACATCGACAGAACAGAGCTGCAGACCATCACCAATGACCCC
AGACTGGTCTTCACAGTGCGAGAGTTCAGAGAGCTTCCCAACATAGAAGAAAGAATCATGAACTCGTTTGGACCC
TCCGCAGCCACTCCTGCACCTCCAGGGGTGGACACCCCTCCTCCTTCACGGCCAGAGAAGAAGAAAGCAGACATT
GTGTTCCTGTTGGATGGTTCCATCAACTTCAGGAGGGACAGTTTCCAGGAAGTGCTTCGTTTTGTGTCTGAAATA
GTGGACACAGTTTATGAAGATGGCGACTCCATCCAAGTGGGGCTTGTCCAGTACAACTCTGACCCCACTGACGAA
TTCTTCCTGAAGGACTTCTCTACCAAGAGGCAGATTATTGACGCCATCAACAAAGTGGTCTACAAAGGGGGAAGA
CACGCCAACACTAAGGTGGGCCTTGAGCACCTGCGGGTAAACCACTTTGTGCCTGAGGCAGGCAGCCGCCTGGAC
CAGCGGGTCCCTCAGATTGCCTTTGTGATCACGGGAGGAAAGTCGGTGGAAGATGCACAGGATGTGAGCCTGGCC
CTCACCCAGAGGGGGGTCAAAGTGTTTGCTGTTGGAGTGAGGAATATCGACTCGGAGGAGGTTGGAAAGATAGCG
TCCAACAGCGCCACAGCGTTCCGCGTGGGCAACGTCCAGGAGCTGTCCGAACTGAGCGAGCAAGTTTTGGAAACT
TTGCATGATGCGATGCATGAAACCCTTTGCCCTGGTGTAACTGATGCTGCCAAAGCTTGTAATCTGGATGTGATT
CTGGGGTTTGATGGTTCTAGAGACCAGAATGTTTTTGTGGCCCAGAAGGGCTTCGAGTCCAAGGTGGACGCCATC
TTGAACAGAATCAGCCAGATGCACAGGGTCAGCTGCAGCGGTGGCCGCTCGCCCACCGTGCGTGTGTCAGTGGTG
GCCAACACGCCCTCGGGCCCGGTGGAGGCCTTTGACTTTGACGAGTACCAGCCAGAGATGCTCGAGAAGTTCCGG
AACATGCGCAGCCAGCACCCCTACGTCCTCACGGAGGACACCCTGAAGGTCTACCTGAACAAGTTCAGACAGTCC
TCGCCGGACAGCGTGAAGGTGGTCATTCATTTTACTGATGGAGCAGACGGAGATCTGGCTGATTTACACAGAGCA
TCTGAGAACCTCCGCCAAGAAGGAGTCCGTGCCTTGATCCTGGTGGGCCTTGAACGAGTGGTCAACTTGGAGCGG
CTAATGCATCTGGAGTTTGGGCGAGGGTTTATGTATGACAGGCCCCTGAGGCTTAACTTGCTGGACTTGGATTAT
GAACTAGCGGAGCAGCTTGACAACATTGCCGAGAAAGCTTGCTGTGGGGTTCCCTGCAAGTGCTCTGGGCAGAGG
GGAGACCGCGGGCCCATCGGCAGCATCGGGCCAAAGGGTATTCCTGGAGAAGACGGCTACCGAGGCTATCCTGGT
GATGAGGGTGGACCCGGTGAGCGTGGTCCGCCTGGTGTGAACGGCACTCAAGGTTTCCAGGGCTGCCCGGGCCAG
AGAGGAGTAAAGGGCTCTCGGGGATTCCCAGGAGAGAAGGGCGAAGTAGGAGAAATTGGACTGGATGGTCTGGAT
GGTGAAGATGGAGACAAAGGATTACCTGGTTCTTCTGGAGAGAAAGGGAATCCTGGAAGAAGGGGTGATAAAGGA
CCTCGAGGAGAGAAAGGAGAAAGAGGAGATGTTGGGATTCGAGGGGACCCGGGTAACCCAGGACAAGACAGCCAG
GAGAGAGGACCCAAAGGAGAAACCGGTGACCTCGGCCCCATGGGTGTCCCAGGGAGAGATGGAGTACCTGGAGGA
CCTGGAGAAACTGGGAAGAATGGTGGCTTTGGCCGAAGGGGACCCCCCGGAGCTAAGGGCAACAAGGGCGGTCCT
GGCCAGCCGGGCTTTGAGGGAGAGCAGGGGACCAGAGGTGCACAGGGCCCAGCTGGTCCTGCTGGTCCTCCAGGG
CTGATAGGAGAACAAGGCATTTCTGGACCTCGGGGAAGCGGAGGTGCCGCTGGTGCTCCTGGAGAACGAGGCAGA
ACCGGTCCACTGGGAAGAAAGGGTGAGCCCGGAGAGCCAGGACCAAAAGGAGGAATCGGGAACCGGGGCCCTCGT
GGGGAGACGGGAGATGACGGGAGAGACGGAGTTGGCAGTGAAGGACGCAGAGGCAAAAAAGGAGAAAGAGGATTT

FIGURE 1028C

CCTGGATACCCAGGACCAAAGGGTAACCCAGGTGAACCTGGGCTAAATGGAACAACAGGACCCAAAGGCATCAGA
GGCCGAAGGGGAAATTCGGGACCTCCAGGGATAGTTGGACAGAAGGGAGACCCTGGCTACCCAGGACCAGCTXXX
XXXXXXGGCAACAGGGGCGACTCCATCGATCAATGTGCCCTCATCCAAAGCATCAAAGATAAATGCCCTTGCTGT
TACGGGCCCCTGGAGTGCCCCGTCTTCCCAACAGAACTAGCCTTTGCTTTAGACACCTCTGAGGGAGTCAACCAA
GACACTTTCGGCCGGATGCGAGATGTGGTCTTGAGTATTGTGAATGACCTGACCATTGCTGAGAGCAACTGCCCA
CGGGGGGCCCGGGTGGCTGTGGTCACCTACAACAACGAGGTGACCACGGAGATCCGGTTTGCTGACTCCAAGAGG
AAGTCGGTCCTCCTGGACAAGATTAAGAACCTTCAGGTGGCTCTGACATCCAAACAGCAGAGTCTGGAGACTGCC
ATGTCGTTTGTGGCCAGGAACACATTTAAGCGTGTGAGGAATGGATTCCTAATGAGGAAAGTGGCTGTTTTCTTC
AGCAACACACCCACAAGAGCATCCCCACAGCTCAGAGAGGCTGTGCTCAAGCTCTCAGATGCGGGGATCACCCCC
TTGTTCCTTACAAGGCAGGAAGACCGGCAGCTCATCAACGCTTTGCAGATCAATAACACAGCAGTGGGGCATGCG
CTTGTCCTGCCTGCAGGGAGAGACCTCACAGACTTCCTGGAGAATGTCCTCACGTGTCATGTTTGCTTGGACATC
TGCAACATCGACCCATCCTGTGGATTTGGCAGTTGGAGGCCTTCCTTCAGGGACAGGAGAGCGGCAGGGAGCGAT
GTGGACATCGACATGGCTTTCATCTTAGACAGCGCTGAGACCACCACCCTGTTCCAGTTCAATGAGATGAAGAAG
TACATAGCGTACCTGGTCAGACAACTGGACATGAGCCCAGATCCCAAGGCCTCCCAGCACTTCGCCAGAGTGGCA
GTTGTGCAGCACGCGCCCTCTGAGTCCGTGGACAATGCCAGCATGCCACCTGTGAAGGTGGAATTCTCCCTGACT
GACTATGGCTCCAAGGAGAAGCTGGTGGACTTCCTCAGCAGGGGAATGACACAGTTGCAGGGAACCAGGGCCTTA
GGCAGTGCCATTGAATACACCATAGAGAATGTCTTTGAAAGTGCCCCAAACCCACGGGACCTGAAAATTGTGGTC
CTGATGCTGACGGGCGAGGTGCCGGAGCAGCAGCTGGAGGAGGCCCAGAGAGTCATCCTGCAGGCCAAATGCAAG
GGCTACTTCTTCGTGGTCCTGGGCATTGGCAGGAAGGTGAACATCAAGGAGGTATACACCTTCGCCAGTGAGCCA
AACGACGTCTTCTTCAAATTAGTGGACAAGTCCACCGAGCTCAACGAGGAGCCTTTGATGCGCTTCGGGAGGCTG
TTGCCATCCTTCGTCAGCAGTGAAAATGCTTTTTACTTGTCCCCAGATATCAGGAAACAGTGTGATTGGTTCCAA
GGGGACCAACCCACAAAGAACCTTGTGAAGTTTGGTCACAAACAAGTAAATGTTCCGAATAACGTTACTTCAAGT
CCTACATCCAACCCAGTGACGACAACGAAGCCGGTGACTACGACGAAGCCGGTGACCACCACAACAAAGCCTGTA
ACCACCACAACAAAGCCTGTGACTATTATAAATCAGCCATCTGTGAAGCCAGCCGCTGCAAAGCCGGCCCCTGCG
AAACCTGTGGCTGCCAAGCCTGTGGCCACAAAGACGGCCACTGTTAGACCCCCAGTGGCGGTGAAGCCAGCAACG
GCAGCGAAGCCTGTAGCAGCAAAGCCAGCAGCTGTAAGACCCCCCGCTGCTGCTGCAAAACCAGTGGCGACCAAG
CCTGAGGTCCCTAGGCCACAGGCAGCCAAACCAGCTGCCACCAAGCCAGCCACCACTAAGCCCATGGTTAAGATG
TCCCGTGAAGTCCAGGTGTTTGAGATAACAGAGAACAGCGCCAAACTCCACTGGGAGAGGCCTGAGCCCCCCGGT
CCTTATTTTTATGACCTCACCGTCACCTCAGCCCATGATCAGTCCCTGGTTCTGAAGCAGAACCTCACGGTCACG
GACCGCGTCATTGGAGGCCTGCTCGCTGGGCAGACATACCATGTGGCTGTGGTCTGCTACCTGAGGTCTCAGGTC
AGAGCCACCTACCATGGAAGTTTCAGTACAAAGAAATCTCAGCCCCCACCTCCACAGCCAGCAAGGTCAGCTTCT
AGTTCAACCATCAATCTAATGGTGAGCACAGAACCATTGGCTCTCACTGAAACAGATATATGCAAGTTGCCGAAA
GACGAAGGAACTTGCAGGGATTTCATATTAAAATGGTACTATGATCCAAACACCAAAAGCTGTGCAAGATTCTGG
TATGGAGGTTGTGGTGGAAACGAAAACAAATTTGGATCACAGAAAGAATGTGAAAAGGTTTGCGCTCCTGTGCTC
GCCAAACCCGGAGTCATCAGTGTGATGGGAACCTAAGCGTGGGTGGCCAACATCATATACCTCTTGAAGAAGAAG
GAGTCAGCCATCGCCAACTTGTCTCTGTAGAAGCTCCGGGTGTAGATTCCCTTGCACTGTATCATTTCATGCTTT
GATTTACACTCGAACTCGGGAGGGAACATCCTGCTGCATGACCTATCAGTATGGTGCTAATGTGTCTGTGGACCC
TCGCTCTCTGTCTCCAGGCAGTTCTCTCGAATACTTTGAATGTTGTGTAACAGTTAGCCACTGCTGGTGTTTATG
TGAACATTCCTATCAATCCAAATTCCCTCTGGAGTTTCATGTTATGCCTGTTGCAGGCAAATGTAAAGTCTAGAA
AATAATGCAAATGTCACGGCTACTCTATATACTTTTGCTTGGTTCATTTTTTTTCCCTTTTAGTTAAGCATGACT
TTAGATGGGAAGCCTGTGTATCGTGGAGAAACAAGAGACCAACTTTTTCATTCCCTGCCCCCAATTTCCCAGACT
AGATTTCAAGCTAATTTTCTTTTTCTGAAGCCTCTAACAAATGATCTAGTTCAGAAGGAAGCAAAATCCCTTAAT
CTATGTGCACCGTTGGGACCAATGCCTTAATTAAAGAATTTAAAAAAGTTGTAATAGAGAATATTTTTGGCATTC
CTCTAATGTTGTGTGTTTTTTTTTTTTTGTGTGCTGGAGGGAGGGGATTTAATTTTAATTTTAAAATGTTTAGGAA
ATTTATACAAAGAAACTTTTTAATAAAGTATATTGAAAGTTT

FIGURE 1029

AGCCCAGCGAGGCCTGTGCTGTGAGGGGCTGTGCTGTGCCAGGGGAGGCCCCGCACCCGGGAAGCCCAGAGGAGA
GTGTGCACTCACGGAGCCCTCCTGGCAGGGCCGCGTCTCTGGAGCAGCAGACCCGTGTCCCTCTGGGAGGTCAAC
TGCGGCCTCACAGCTGGGCCTGTCCCAGCACAGCCCTTGTTGGAGGGCGCACCCCCGTGTCCTCAGCACCCCAGT
GTTGAGTGCCTTGACCTGCAGAGGGGAGCCTGTGCTGGTCCCGGGCGTCTGTGTGGCTCCTGGGTGCCCATCTGC
ACCCCTGGCCCTGCTCTGGGCTTCAGTGGAGCCGTGCCACCGTGGGAGTGTCCAGGGTCCTGACGTAGCCCTGAG
ACGTGGCCAGCTCCCTGGCCTGCTGCCCGCACAGTGGGCCCTTGTCTCTGCTCTGGGTCAGGCGAGGCAGCCACC
CATGATGAGCTCTGCAGCCTTCCCAAGGTGGCTGAGCATGGGGGTCCCTCGTACCCCTTCACGGACAGTGCTCTT
CGAGCGGGAGAGGACGGGCCTGACCTACCGCGTGCCCTCGTTGCTCCCCGTGCCCCCCGGGCCCACCCTGCTGGC
CTTTGTGGAGCAGCGGCTCAGCCCTGACGACTCCCACGCCCACCGCCTGGTGCTGAGGAGGGGCACGCTGGCCGG
GGGCTCCGTGCGGTGGGGTGCCCTGCACGTGCTGGGGACAGCAGCCCTGGCGGAGCACCGGTCCATGAACCCCTG
CCCTGTGCACGATGCTGGCACGGGCACCGTCTTCCTCTTCTTCATCGCGGTGCTGGGCCACACGCCTGAGGCCGT
GCAGATCGCCACGGGAAGGAACGCCGCGCGCCTCTGCTGTGTGGCCAGCCGTGACGCCGGCCTCTCGTGGGGCAG
CGCCCGGGACCTCACCGAGGAGGCCATCGGTGGTGCCGTGCAGGACTGGGCCACATTCGCTGTGGGTCCCGGCCA
CGGCGTGCAGCTGCCCTCAGGCCGCCTGCTGGTACCCGCCTACACCTACCGCGTGGACCGCCGAGAGTGTTTTGG
CAAGATCTGCCGGACCAGCCCTCACTCCTTCGCCTTCTACAGCGATGACCACGGCCGCACCTGGCGCTGTGGAGG
CCTCGTGCCCAACCTGCGCTCAGGCGAGTGCCAGCTGGCGGCGGTGGACGGTGGGCAGGCCGGCAGCTTCCTCTA
CTGCAATGCCCGGAGCCCACTGGGCAGCCGTGTGCAGGCGCTCAGCACTGACGAGGGCACCTCCTTCCTGCCCGC
AGAGCGCGTGGCTTCCCTGCCCGAGACTGCCTGGGGCTGCCAGGGCAGCATCGTGGGCTTCCCAGCCCCCGCCCC

FIGURE 1030

GAATTGGCAGCCAAC**ATG**GCGGCGGAACGCGGCGCGGGGCAGCAACAGTCGCAGGAGATGATGGAGGTTGACAGG
CGGGTCGAGTCTGAAGAATCCGGCGATGAAGAAGGGAAGAAACACAGCAGTGGCATCGTGGCCGACCTCAGTGAA
CAGAGCCTGAAGGATGGGGAGGAGCGGGGGGAGGAGGACCCAGAAGAAGAACATGAGCTGCCTGTGGACATGGAA
ACCATCAACCTGGACAGAGATGCAGAGGATGTTGATTTGAATCACTATCGCATAGGGAAGATTGAAGGATTTGAG
GTACTGAAGAAAGTGAAGACTCTCTGCCTCCGCCAAAATTTAATTAAATGCATTGAGAATCTGGAGGAGCTACAG
AGTCTTCGAGAGCTGGATCTTTACGACAACCAGATCAAGAAGATTGAGAATCTGGAGGCGCTAACAGAGCTGGAG
ATTCTAGATATTTCTTTTAATCTGCTGAGAAACATCGAAGGGGTTGACAAGTTGACACGACTGAAAAAACTCTTC
TTGGTCAACAATAAAATCAGTAAAATTGAGAACTTAAGCAACTTACATCAACTACAGATGCTAGAGCTGGGATCT
AACCGCATCCGGGCAATCGAAAATATCGACACCTTAACCAACCTGGAGAGTTTGTTTTTGGGGAAAAACAAAATT
ACTAAACTTCAGAACCTGGATGCGCTCACCAACCTGACAGTCCTCAGTATGCAGAGCAACCGGCTGACCAAGATC
GAGGGTCTGCAGAACCTGGTGAACCTGCGGGAGCTGTACCTTAGCCACAATGGCATCGAGGTCATCGAGGGCCTG
GAGAACAATAACAAACTCACGATGTTGGACATTGCATCAAATAGAATCAAAAAGATTGAAAATATCAGCCATCTA
ACAGAGCTGCAAGAGTTCTGGATGAACGACAATCTCCTTGAGAGCTGGAGCGACCTCGACGAGCTGAAGGGAGCC
AGGAGCCTGGAGACAGTGTACCTGGAGCGGAACCCCTTGCAGAAGGACCCCCAGTACCGGCGGAAGGTCATGCTC
GCCCTCCCCTCCGTGCGGCAGATCGATGCCACGTTCGTCAGGTTC**TGA**GTCCTTCTTGGCTCCTCATGTGGTCCC
TCTCCTCGGAAGAACTGCCCAGCCACGGGTTTTAACCCACCTGTTGCTCCTGAGGTCGTCACTATATCAACAGT
CACAAACCCAATGGCAATAAAGGCACTGACGATAGCTGGCGCGCGCGACGCCACACACCATTTTCAGATGCCGTT
GCAATTAAATCTTGCCACACTGTC

FIGURE 1031

MAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKHSSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLD
RDAEDVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLRELDLYDNQIKKIENLEALTELEILDIS
FNLLRNIEGVDKLTRLKKLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLESLFLGKNKITKLQN
LDALTNLTVLSMQSNRLTKIEGLQNLVNLRELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQE
FWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKVMLALPSVRQIDATFVRF

FIGURE 1032A

CAAAAGCTGGCAGGCTGACAGAGGCGGCCTCAGGACGGACCTTCTGGCTACTGACCGTTTTGCTGTGGTTTTCCC
GGATTGTGTGTAGGTGTGAGATCAACCATGAGTTCCGTTGCAGTTTTGACCCAAGAGAGTTTTGCTGAACACCGA
AGTGGGCTGGTTCCGCAACAAATCAAAGTTGCCACTCTAAATTCAGAAGAGGAGAGCGACCCTCCAACCTACAAG
GATGCCTTCCCTCCACTTCCTGAGAAAGCTGCTTGCCTGGAAAGTGCCCAGGAACCCTCTGGAGCCTGGGGGAAC
AAGATCCGACCCATCAAGGCTTCTGTCATCACTCAGGTGTTCCATGTACCCCTGGAGGAGAGAAAATACAAGGAT
ATGAACCAGTTTGGAGAAGGTGAACAAGCAAAAATCTGCCTTGAGATCATGCAGAGAACTGGTGCTCACTTGGAG
CTGTCTTTGGCCAAAGACCAAGGCCTCTCCATCATGGTGTCAGGAAAGCTGGATGCTGTCATGAAAGCTCGGAAG
GACATTGTTGCTAGACTGCAGACTCAGGCCTCAGCAACTGTTGCCATTCCCAAAGAACACCATCGCTTTGTTATT
GGCAAAAATGGAGAGAAACTGCAAGACTTGGAGCTAAAAACTGCAACCAAAATCCAGATCCCACGCCCAGATGAC
CCCAGCAATCAGATCAAGATCACTGGCACCAAAGAGGGCATCGAGAAAGCTCGCCATGAAGTCTTACTCATCTCT
GCCGAGCAGGACAAACGTGCTGTGGAGAGGCTAGAAGTAGAAAAGGCATTCCACCCCTTCATCGCTGGGCCGTAT
AATAGACTGGTTGGCGAGATCATGCAGGAGACAGGCACGCGCATCAACATCCCCCCACCCAGCGTGAACCGGACA
GAGATTGTCTTCACTGGAGAGAAGGAACAGTTGGCTCAGGCTGTGGCTCGCATCAAGAAGATTTATGAGGAGAAG
AAAAAGAAGACTACAACCATTGCAGTGGAAGTGAAGAAATCCCAACACAAGTATGTCATTGGGCCCAAGGGCAAT
TCATTGCAGGAGATCCTTGAGAGAACTGGAGTTTCCGTTGAGATCCCACCCTCAGACAGCATCTCTGAGACTGTA
ATACTTCGAGGCGAACCTGAAAAGTTAGGTCAGGCGTTGACTGAAGTCTATGCCAAGGCCAATAGCTTCACCGTC
TCCTCTGTCGCCGCCCCTTCCTGGCTTCACCGTTTCATCATTGGCAAGAAAGGGCAGAACCTGGCCAAAATCACT
CAGCAGATGCCAAAGGTTCACATCGAGTTCACAGAGGGCGAAGACAAGATCACCCTGGAGGGCCCTACAGAGGAT
GTCAATGTGGCCCAGGAACAGATAGAAGGCATGGTCAAAGATTTGATTAACCGGATGGACTATGTGGAGATCAAC
ATCGACCACAAGTTCCACAGGCACCTCATTGGGAAGAGCGGTGCCAACATAAACAGAATCAAAGACCAGTACAAG
GTGTCCGTGCGCATCCCTCCTGACAGTGAGAAGAGCAATTTGATCCGCATCGAGGGGGACCCACAGGGCGTGCAG
CAGGCCAAGCGAGAGCTGCTGGAGCTTGCATCTCGCATGGAAAATGAGCGTACCAAGGATCTAATCATTGAGCAA
AGATTTCATCGCACAATCATTGGGCAGAAGGGTGAACGGATCCGTGAAATTCGTGACAAATTCCCAGAGGTCATC
ATTAACTTTCCAGACCCAGCACAAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGC
ACAAAATACATGCAGAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAG
TTTCACAAGAATATCATTGGGAAAGGAGGCGCAAACATTAAAAAGATTCGTGAAGAAAGCAACACCAAAATCGAC
CTTCCAGCAGAGAATAGCAATTCAGAGACCATTATCATCACAGGCAAGCGAGCCAACTGCGAAGCTGCCCGGAGC
AGGATTCTGTCTATTCAGAAAGACCTGGCCAACATAGCCGAGGTAGAGGTCTCCATCCCTGCCAAGCTGCACAAC
TCCCTCATTGGCACCAAGGGCCGTCTGATCCGCTCCATCATGGAGGAGTGCGGCGGGGTCCACATTCACTTTCCC
GTGGAAGGTTCAGGAAGCGACACCGTTGTTATCAGGGGCCCTTCCTCGGATGTGGAGAAGGCCAAGAAGCAGCTC
CTGCATCTGGCGGAGGAGAAGCAAACCAAGAGTTTCACTGTTGACATCCGCGCCAAGCCAGAATACCACAAATTC
CTCATCGGCAAGGGGGGCGGCAAAATTCGCAAGGTGCGCGACAGCACTGGAGCACGTGTCATCTTCCCTGCGGCT
GAGGACAAGGACCAGGACCTGATCACCATCATTGGAAAGGAGGACGCCGTCCGAGAGGCACAGAAGGAGCTGGAG
GCCTTGATCCAAAACCTGGATAATGTGGTGGAAGACTCCATGCTGGTGGACCCCAAGCACCACCGCCACTTCGTC
ATCCGCAGAGGCCAGGTCTTGCGGGAGATTGCTGAAGAGTATGGCGGGGTGATGGTCAGCTTCCCACGCTCTGGC
ACACAGAGCGACAAAGTCACCCTCAAGGGCGCCAAGGACTGTGTGGAGGCAGCCAAGAAACGCATTCAGGAGATC
ATTGAGGACCTGGAAGCTCAGGTGACATTAGAATGTGCTATACCCCAGAAATTCCATCGATCTGTCATGGGCCCC
AAAGGTTCCAGAATCCAGCAGATTACTCGGGATTTCAGTGTTCAAATTAAATTCCCAGACAGAGAGGAGAACGCA
GTTCACAGTACAGAGCCAGTTGTCCAGGAGAATGGGGACGAAGCTGGGGAGGGGAGAGAGGCTAAAGATTGTGAC
CCCGGCTCTCCAAGGAGGTGTGACATCATCATCATCTCTGGCCGGAAAGAAAAGTGTGAGGCTGCCAAGGAAGCT
CTGGAGGCATTGGTTCCTGTCACCATTGAAGTAGAGGTGCCCTTTGACCTTCACCGTTACGTTATTGGGCAGAAA
GGAAGTGGGATCCGCAAGATGATGGATGAGTTTGAGGTGAACATACATGTCCCGGCACCTGAGCTGCAGTCTGAC
ATCATCGCCATCACGGGCCTCGCTGCAAATTTGGACCGGGCCAAGGCTGGACTGCTGGAGCGTGTGAAGGAGCTA
CAGGCCGAGCAGGAGGACCGGGCTTTAAGGAGTTTTAAGCTGAGTGTCACTGTAGACCCCAAATACCATCCCAAG
ATTATCGGGAGAAAGGGGGCAGTAATTACCCAAATCCGGTTGGAGCATGACGTGAACATCCAGTTTCCTGATAAG
GACGATGGGAACCAGCCCCAGGACCAAATTACCATCACAGGGTACGAAAAGAACACAGAAGCTGCCAGGGATGCT
ATACTGAGAATTGTGGGTGAACTTGAGCAGATGGTTTCTGAGGACGTCCCGCTGGACCACCGCGTTCACGCCCGC
ATCATTGGTGCCCGCGGCAAAGCCATTCGCAAAATCATGGACGAATTCAAGGTGGACATTCGCTTCCCACAGAGC

FIGURE 1032B

GGAGCCCCAGACCCCAACTGCGTCACTGTGACGGGGCTCCCAGAGAATGTGGAGGAAGCCATCGACCACATCCTC
AATCTGGAGGAGGAATACCTAGCTGACGTGGTGGACAGTGAGGCGCTGCAGGTATACATGAAACCCCCAGCACAC
GAAGAGGCCAAGGCACCTTCCAGAGGCTTTGTGGTGCGGGACGCACCCTGGACCGCCAGCAGCAGTGAGAAGGCT
CCTGACATGAGCAGCTCTGAGGAATTTCCCAGCTTTGGGGCTCAGGTGGCTCCCAAGACCCTCCCTTGGGGCCCC
AAACGA**TAA**TGATCAAAAAGAACAGAACCCTCTCCAGCCTGCTGACCCAAACCCAACCACACAATGGTTTGTCTC
AATCTGACCCAGCGGCTGGACCCTCCGTAAATTGTTGACGCTCTTCCCCCTTCCCGAGGTCCCGCAGGGAGCCTA
GCGCCTGGCTGTGTGTGCGGCCGCTCCTCCAGGCCTGGCCGTGCCCGCTCAGGACCTGCTCCACTGTTTAACACT
AAACCAAGGTCATGAGCATTCGTGCTAAGATAACAGACTCCAGCTCCTGGTCCACCCGGCATGTCAGTCAGCACT
CTGGCCTTCATCACGAGAGCTCCGCAGCCGTGGCTAGGATTCCACTTCCTGTGTCATGACCTCAGGAAATAAACG
TCCTTGACTTTATAAAAGCC